

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: October 5, 2005, 17:19:28 ; Search time 93.2556 Seconds
(without alignments)
1197.068 Million cell updates/sec
Title: US-10-063-510-6_COPY_17_234
Perfect score: 1125
Sequence: 1 TRLLVQSLRAELSIQVSC.....ETEPFVENKAAPKNEAGFG 218

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| SUMMARIES | | | | |
|------------|-------|-------------|--------|-------------|
| Result No. | Score | Query Match | Length | Description |
| 1 | 1125 | 100.0 | 322 | Q9UNF4 |
| 2 | 1111 | 98.8 | 322 | Q8TC18 |
| 3 | 1106 | 98.3 | 322 | Q9Y5Y7 |
| 4 | 719 | 63.9 | 322 | Q6UC88 |
| 5 | 669 | 59.5 | 318 | Q99NE4 |
| 6 | 669 | 59.5 | 318 | Q8BHC0 |
| 7 | 520.5 | 46.3 | 201 | Q7YS22 |
| 8 | 241 | 21.4 | 441 | Q6QM56 |
| 9 | 226 | 20.1 | 437 | Q6P8A2 |
| 10 | 213.5 | 19.0 | 503 | CD44_RAT |
| 11 | 213.5 | 19.0 | 780 | Q08779 |
| 12 | 211.5 | 18.8 | 364 | Q70509 |
| 13 | 211 | 18.8 | 265 | Q98SR5 |
| 14 | 209.5 | 18.6 | 398 | Q90ZL8 |
| 15 | 209.5 | 18.6 | 778 | CD44_MOUSE |
| 16 | 207 | 18.4 | 362 | CD44_CRIGR |
| 17 | 205 | 18.2 | 431 | CD44_MESAU |
| 18 | 203.5 | 18.1 | 362 | CD44_FAPHA |
| 19 | 203 | 18.0 | 742 | Q9UJ36 |
| 20 | 202 | 18.0 | 742 | CD44_HUMAN |
| 21 | 200.5 | 17.8 | 580 | Q80X37 |
| 22 | 198.5 | 17.6 | 168 | Q90ZL6 |
| 23 | 198.5 | 17.6 | 493 | Q86Z27 |
| 24 | 197 | 17.5 | 396 | Q9W6S4 |
| 25 | 197 | 17.5 | 719 | Q9H5A5 |
| 26 | 196 | 17.4 | 294 | Q92493 |
| 27 | 196 | 17.4 | 361 | Q8N694 |
| 28 | 196 | 17.4 | 361 | Q86T72 |
| 29 | 195 | 17.3 | 364 | Q97569 |
| 30 | 194 | 17.2 | 351 | CD44_CANFA |
| 31 | 194 | 17.2 | 366 | CD44_BOVIN |

| | | | | | |
|-----|-------|------|------|------------|---------------------|
| 32 | 191.5 | 17.0 | 676 | Q9H5A7 | Q9H5a7 homo sapien |
| 33 | 191 | 17.0 | 271 | Q9H5A3 | Q9H5a3 homo sapien |
| 34 | 191 | 17.0 | 338 | Q9H5A4 | Q9H5a4 homo sapien |
| 35 | 191 | 17.0 | 470 | Q9H5A6 | Q9H5a6 homo sapien |
| 36 | 183.5 | 16.3 | 359 | CD44_HORSE | Q05078 equus caball |
| 37 | 150 | 13.3 | 537 | PGCA_PIG | Q29011 sus scrofa |
| 38 | 145.5 | 12.9 | 494 | Q9BGH3 | Q9bgh3 sus scrofa |
| 39 | 145.5 | 12.9 | 3562 | PGCV_CHICK | Q90953 gallus gall |
| 40 | 145 | 12.9 | 277 | TSG6_MOUSE | P98066 homo sapien |
| 41 | 144 | 12.8 | 275 | TSG6_MOUSE | Q08859 mus musculus |
| 42 | 143 | 12.7 | 2109 | PGCA_CHICK | P07898 gallus gall |
| 43 | 140 | 12.4 | 2571 | SGN1_MOUSE | Q8r3y4 mus musculus |
| 44 | 139.5 | 12.4 | 2333 | PGCA_CANFA | Q28343 canis famil |
| 45 | 139 | 12.4 | 2109 | P79787 | P79787 gallus gall |
| 46 | 137 | 12.2 | 276 | TSG6_RABIT | P98065 oryctolagus |
| 47 | 133 | 11.8 | 514 | Q629I3 | Q629i3 rattus norv |
| 48 | 132.5 | 11.8 | 721 | Q6PID9 | Q6pid9 homo sapien |
| 49 | 131.5 | 11.7 | 2124 | PGCA_RAT | P07897 rattus norv |
| 50 | 131 | 11.6 | 2132 | PGCA_MOUSE | Q61282 mus musculus |
| 51 | 130.5 | 11.6 | 883 | PGCB_MOUSE | Q61361 mus musculus |
| 52 | 130.5 | 11.6 | 883 | Q80WT7 | Q80wt7 mus musculus |
| 53 | 130.5 | 11.6 | 2415 | PGCA_HUMAN | P16112 homo sapien |
| 54 | 129 | 11.5 | 1431 | SN2_RAT | Q8cFm6 rattus norv |
| 55 | 128 | 11.4 | 2149 | Q6XL68 | Q6xl68 bos taurus |
| 56 | 128 | 11.4 | 2364 | PGCA_BOVIN | P13608 bos taurus |
| 57 | 128 | 11.4 | 2365 | Q6XL67 | Q6xl67 bos taurus |
| 58 | 127.5 | 11.3 | 883 | PGCB_RAT | P55068 rattus norv |
| 59 | 127.5 | 11.3 | 911 | PGCB_HUMAN | Q96cw7 homo sapien |
| 60 | 123 | 10.9 | 2570 | SGN1_HUMAN | Q9ny15 homo sapien |
| 61 | 122 | 10.8 | 394 | PGCA_RABIT | Q28670 oryctolagus |
| 62 | 121.5 | 10.8 | 360 | HPL3_HUMAN | Q96886 homo sapien |
| 63 | 121 | 10.8 | 516 | Q8IWX2 | Q8iwx2 homo sapien |
| 64 | 121 | 10.8 | 1152 | Q90WM2 | Q90wm2 xenopus lae |
| 65 | 120.5 | 10.7 | 912 | PGCB_BOVIN | Q28062 bos taurus |
| 66 | 120.5 | 10.7 | 1570 | Q75Zi3 | Q75zi3 brachydanio |
| 67 | 120.5 | 10.7 | 2559 | SN2_MOUSE | Q8riu0 mus musculus |
| 68 | 119 | 10.6 | 359 | Q7ZX17 | Q7zx17 xenopus lae |
| 69 | 118.5 | 10.5 | 3396 | PGCV_HUMAN | P13611 homo sapien |
| 70 | 116 | 10.3 | 368 | Q8BS97 | Q8bs97 mus musculus |
| 71 | 116 | 10.3 | 2738 | PGCV_RAT | Q9erb4 rattus norv |
| 72 | 116 | 10.3 | 3358 | PGCV_MOUSE | Q62059 mus musculus |
| 73 | 115 | 10.2 | 370 | Q7M2W7 | Q7m2w7 sus scrofa |
| 74 | 115 | 10.2 | 394 | Q6DCI6 | Q6dc16 xenopus lae |
| 75 | 115 | 10.2 | 3381 | PGCV_BOVIN | P81282 bos taurus |
| 76 | 113.5 | 10.1 | 341 | HPL2_MOUSE | Q9esm3 mus musculus |
| 77 | 113.5 | 10.1 | 340 | HPL2_HUMAN | Q9g2v7 homo sapien |
| 78 | 112.5 | 10.0 | 417 | PGCB_FELCA | P41725 felis silve |
| 79 | 112 | 10.0 | 210 | Q8C9U7 | Q8c9u7 mus musculus |
| 80 | 112 | 10.0 | 2551 | SN2_HUMAN | Q8wqg8 h stabilin |
| 81 | 111 | 9.9 | 354 | Q86W61 | Q86w61 homo sapien |
| 82 | 110 | 9.8 | 363 | Q6NV41 | Q6nv41 brachydanio |
| 83 | 110 | 9.8 | 1290 | Q9W6E1 | Q9w6e1 gallus gall |
| 84 | 109.5 | 9.7 | 1257 | PGCN_RAT | P55067 rattus norv |
| 85 | 109 | 9.7 | 1321 | PGCN_HUMAN | O14594 homo sapien |
| 86 | 108.5 | 9.6 | 341 | HPL2_RAT | Q9esm2 rattus norv |
| 87 | 108 | 9.6 | 354 | HPL1_HUMAN | P10915 homo sapien |
| 88 | 108 | 9.6 | 359 | HPL3_MOUSE | Q80wm5 mus musculus |
| 89 | 107 | 9.5 | 354 | HPL1_RAT | P03994 rattus norv |
| 90 | 107 | 9.5 | 355 | HPL1_CHICK | P07354 gallus gall |
| 91 | 107 | 9.5 | 356 | HPL1_MOUSE | Q9qup5 mus musculus |
| 92 | 107 | 9.5 | 862 | Q9UF98 | Q9uf98 homo sapien |
| 93 | 107 | 9.5 | 1268 | PGCN_MOUSE | P55066 mus musculus |
| 94 | 107 | 9.5 | 1268 | Q6P1E3 | Q6pie3 mus musculus |
| 95 | 106.5 | 9.5 | 816 | O70474 | O70474 rattus norv |
| 96 | 105 | 9.3 | 354 | HPL1_BOVIN | P52552 bos taurus |
| 97 | 104.5 | 9.3 | 862 | PGCV_MACNE | P25858 macaca neme |
| 98 | 104 | 9.2 | 139 | Q95370 | Q95370 homo sapien |
| 99 | 104 | 9.2 | 354 | HPL1_HORSE | Q28381 equus caball |
| 100 | 104 | 9.2 | 354 | HPL1_PIG | P10859 sus scrofa |
| 101 | 103 | 9.2 | 80 | Q86UZ1 | Q86uz1 homo sapien |
| 102 | 102 | 9.1 | 739 | O02360 | O02360 caenorhabdi |
| 103 | 101.5 | 9.0 | 380 | O02343 | O02343 caenorhabdi |
| 104 | 101.5 | 9.0 | 411 | Q702X4 | Q702x4 human herpe |

| | | | | | | | | | | | | | |
|-----|-------|-----|------|---|------------|---------------------|-----|------|-----|------|---|------------|---------------------|
| 105 | 101.5 | 9.0 | 1853 | 2 | Q7KT96 | Q7kt96 drosophila | 178 | 88 | 7.8 | 1051 | 2 | Q6C1J9 | Q6c1j9 yarrowia li |
| 106 | 101.5 | 9.0 | 1893 | 2 | Q9NKC9 | Q9nkc9 drosophila | 179 | 88 | 7.8 | 1254 | 2 | Q94185 | Q94185 caenorhabdi |
| 107 | 101.5 | 9.0 | 1908 | 2 | Q18175 | Q18175 caenorhabdi | 180 | 87.5 | 7.8 | 555 | 2 | Q9U6R7 | Q9u6r7 dermatophag |
| 108 | 101 | 9.0 | 2535 | 2 | Q755B8 | Q755b8 ashbya goes | 181 | 87.5 | 7.8 | 653 | 2 | Q8NK55 | Q8nk55 candida alb |
| 109 | 100.5 | 8.9 | 402 | 1 | HPL4_HUMAN | Q86uw8 homo sapien | 182 | 87.5 | 7.8 | 987 | 1 | VGNM_APMV | P38485 andean pouta |
| 110 | 100.5 | 8.9 | 665 | 2 | Q7Q4E5 | Q7q4e5 anopheles g | 183 | 87.5 | 7.8 | 1085 | 1 | CASR_BOVIN | P35384 bos taurus |
| 111 | 99.5 | 8.8 | 397 | 2 | Q702X3 | Q702x3 human herpe | 184 | 87.5 | 7.8 | 9234 | 2 | Q7KTE5 | Q7kt95 drosophila |
| 112 | 98.5 | 8.8 | 573 | 2 | Q8GJD9 | Q8gjd9 rattus norv | 185 | 87 | 7.7 | 235 | 2 | Q63349 | Q63349 rattus norv |
| 113 | 98 | 8.7 | 2112 | 2 | Q9VEL9 | Q9vel9 drosophila | 186 | 87 | 7.7 | 264 | 2 | Q80X85 | Q80x85 mus musculu |
| 114 | 97.5 | 8.7 | 260 | 2 | Q7PR65 | Q7pr65 anopheles g | 187 | 87 | 7.7 | 391 | 2 | Q753G3 | Q753g3 ashbya goes |
| 115 | 97 | 8.6 | 390 | 1 | VGL1_HRV11 | P06487 human herpe | 188 | 87 | 7.7 | 661 | 2 | O13444 | O13444 cladosporiu |
| 116 | 97 | 8.6 | 390 | 2 | Q702X7 | Q702x7 human herpe | 189 | 87 | 7.7 | 673 | 2 | Q7QJB6 | Q7qjb6 anopheles g |
| 117 | 96 | 8.5 | 3178 | 1 | YS89_CAEEL | Q09624 caenorhabdi | 190 | 87 | 7.7 | 701 | 2 | Q8ZMG4 | Q8zmg4 pyrobaculum |
| 118 | 95.5 | 8.5 | 481 | 2 | Q9XUF4 | Q9xuf4 caenorhabdi | 191 | 87 | 7.7 | 721 | 2 | Q97UG7 | Q97ug7 sulfolobus |
| 119 | 95 | 8.4 | 424 | 2 | Q8FGW0 | Q8fgw0 arabisdopsis | 192 | 87 | 7.7 | 722 | 2 | O59644 | O59644 sulfolobus |
| 120 | 94.5 | 8.4 | 182 | 2 | Q810D8 | Q810d8 drosophila | 193 | 87 | 7.7 | 1506 | 2 | P79927 | P79927 xenopus lae |
| 121 | 94.5 | 8.4 | 183 | 2 | Q9VT37 | Q9vt37 drosophila | 194 | 86.5 | 7.7 | 260 | 2 | Q7PYX0 | Q7pyx0 anopheles g |
| 122 | 94.5 | 8.4 | 519 | 2 | Q7YTR7 | Q7ytr7 caenorhabdi | 195 | 86.5 | 7.7 | 400 | 1 | MUAI_XENLA | P10667 xenopus lae |
| 123 | 94.5 | 8.4 | 1079 | 2 | Q9N4S7 | Q9n4s7 caenorhabdi | 196 | 86.5 | 7.7 | 768 | 2 | O60279 | O60279 homo sapien |
| 124 | 94.5 | 8.4 | 1795 | 2 | Q76894 | Q76894 drosophila | 197 | 86.5 | 7.7 | 838 | 2 | Q7UNP4 | Q7unp4 rhodopirell |
| 125 | 93.5 | 8.3 | 397 | 2 | Q702X6 | Q702x6 human herpe | 198 | 86.5 | 7.7 | 941 | 2 | Q9LTH0 | Q9lth0 arabidopsis |
| 126 | 93 | 8.3 | 405 | 2 | Q66HZ2 | Q66hz2 brachydanio | 199 | 86.5 | 7.7 | 965 | 2 | Q22286 | Q22286 caenorhabdi |
| 127 | 93 | 8.3 | 478 | 2 | Q7YX15 | Q7yx15 caenorhabdi | 200 | 86.5 | 7.7 | 980 | 2 | Q84FU6 | Q84fu6 chlamydia t |
| 128 | 93 | 8.3 | 916 | 2 | Q7YZI0 | Q7yzi0 monosiga br | 201 | 86.5 | 7.7 | 980 | 2 | Q84FU8 | Q84fu8 chlamydia t |
| 129 | 92.5 | 8.2 | 247 | 2 | Q8MKY7 | Q8mky7 drosophila | 202 | 86.5 | 7.7 | 981 | 2 | Q84FU7 | Q84fu7 chlamydia t |
| 130 | 92.5 | 8.2 | 248 | 2 | Q9NED0 | Q9ned0 leishmania | 203 | 86 | 7.6 | 477 | 2 | Q86YCS | Q86ycs homo sapien |
| 131 | 92.5 | 8.2 | 400 | 1 | HPL4_MOUSE | Q80wm4 mus musculu | 204 | 85.5 | 7.6 | 178 | 2 | Q8RFQ3 | Q8rfq3 corynebacte |
| 132 | 92 | 8.2 | 347 | 2 | Q8SYW5 | Q8syw5 drosophila | 205 | 85.5 | 7.6 | 510 | 2 | Q6SCJ8 | Q6scj8 aspergillus |
| 133 | 92 | 8.2 | 500 | 2 | Q864U4 | Q864u4 bos taurus | 206 | 85.5 | 7.6 | 616 | 2 | Q8R0X0 | Q8r0x0 mus musculu |
| 134 | 92 | 8.2 | 846 | 2 | O01699 | O01699 caenorhabdi | 207 | 85.5 | 7.6 | 656 | 2 | Q8BUE7 | Q8bue7 mus musculu |
| 135 | 92 | 8.2 | 989 | 2 | Q83U76 | Q83u76 chlamydia t | 208 | 85.5 | 7.6 | 734 | 2 | Q7S939 | Q7s939 neurospora |
| 136 | 92 | 8.2 | 989 | 2 | Q84FU9 | Q84fu9 chlamydia t | 209 | 85.5 | 7.6 | 786 | 2 | Q21027 | Q21027 caenorhabdi |
| 137 | 92 | 8.2 | 1121 | 2 | Q72884 | Q72884 candida alb | 210 | 85.5 | 7.6 | 841 | 2 | Q6R8J4 | Q6r8j4 brachydanio |
| 138 | 91.5 | 8.1 | 288 | 2 | Q6QPC9 | Q6qpc9 simian aden | 211 | 85.5 | 7.6 | 895 | 2 | O80973 | O80973 arabidopsis |
| 139 | 91.5 | 8.1 | 860 | 2 | Q7RZN3 | Q7rzn3 neurospora | 212 | 85.5 | 7.6 | 935 | 2 | Q6R8J3 | Q6r8j3 brachydanio |
| 140 | 91.5 | 8.1 | 1126 | 2 | Q9VGK5 | Q9vgk5 drosophila | 213 | 85.5 | 7.6 | 951 | 2 | Q9FVX8 | Q9fvx8 oryza sativ |
| 141 | 91 | 8.1 | 174 | 2 | Q7VTP1 | Q7vtp1 caenorhabdi | 214 | 85 | 7.6 | 977 | 2 | Q6R8J2 | Q6r8j2 brachydanio |
| 142 | 91 | 8.1 | 488 | 2 | Q09586 | Q09586 caenorhabdi | 215 | 85.5 | 7.6 | 1367 | 1 | AMVH_YEAST | P08640 saccharomyc |
| 143 | 91 | 8.1 | 624 | 2 | Q19780 | Q19780 caenorhabdi | 216 | 85.5 | 7.6 | 1367 | 2 | Q6LCS8 | Q6lcs8 saccharomyc |
| 144 | 90.5 | 8.0 | 411 | 2 | Q6P6W1 | Q6p6w1 rattus norv | 217 | 85.5 | 7.6 | 2448 | 2 | Q8WMQ5 | Q8wmq5 homo sapien |
| 145 | 90.5 | 8.0 | 497 | 2 | Q8QVC4 | Q8qvc4 eyach virus | 218 | 85.5 | 7.6 | 6995 | 2 | Q96RK2 | Q96rk2 homo sapien |
| 146 | 90.5 | 8.0 | 699 | 2 | Q8QVE9 | Q8qve9 eyach virus | 219 | 85 | 7.6 | 172 | 2 | Q8VC95 | Q8vc95 mus musculu |
| 147 | 90.5 | 8.0 | 952 | 2 | Q86AH0 | Q86ah0 dictyosteli | 220 | 85 | 7.6 | 265 | 2 | Q9GZES | Q9gzes caenorhabdi |
| 148 | 90.5 | 8.0 | 1175 | 2 | Q9VRL7 | Q9vrl7 drosophila | 221 | 85 | 7.6 | 319 | 2 | Q7QJA0 | Q7qja0 anopheles g |
| 149 | 90.5 | 8.0 | 1376 | 2 | Q9V9I8 | Q9v9i8 drosophila | 222 | 85 | 7.6 | 345 | 2 | Q891Y8 | Q891y8 anolis sagr |
| 150 | 90 | 8.0 | 388 | 1 | VE2_HPV27 | P36789 human papil | 223 | 85 | 7.6 | 429 | 2 | Q76430 | Q76430 caenorhabdi |
| 151 | 90 | 8.0 | 402 | 1 | ODP2_MYCPN | P75392 mycoplasma | 224 | 85 | 7.6 | 449 | 2 | Q71UN8 | Q71un8 caenorhabdi |
| 152 | 90 | 8.0 | 948 | 2 | Q86AV9 | Q86av9 dictyosteli | 225 | 85 | 7.6 | 569 | 2 | Q9KGV9 | Q9kgv9 listeria mo |
| 153 | 90 | 8.0 | 1167 | 2 | Q7RWQ7 | Q7rwq7 neurospora | 226 | 85 | 7.6 | 626 | 2 | Q9NDD1 | Q9ndd1 leishmania |
| 154 | 89.5 | 8.0 | 411 | 1 | LMP2_RAT | P17046 rattus norv | 227 | 85 | 7.6 | 627 | 1 | PKNB_LACUA | Q9cef5 lactococcus |
| 155 | 89.5 | 8.0 | 440 | 2 | Q9P566 | Q9p566 neurospora | 228 | 85 | 7.6 | 852 | 2 | Q6CIA5 | Q6cia5 yarrowia li |
| 156 | 89.5 | 8.0 | 471 | 2 | Q9VMG7 | Q9vmg7 drosophila | 229 | 85 | 7.6 | 961 | 2 | Q92223 | Q92223 emericeella |
| 157 | 89.5 | 8.0 | 1349 | 2 | Q8WQ4 | Q8wmq4 homo sapien | 230 | 85 | 7.6 | 991 | 2 | Q83UW2 | Q83uw2 chlamydia t |
| 158 | 89 | 7.9 | 307 | 1 | SGS3_DROME | P02840 drosophila | 231 | 85 | 7.6 | 991 | 2 | Q84FV0 | Q84fv0 chlamydia t |
| 159 | 89 | 7.9 | 416 | 1 | LMP1_HUMAN | P11279 homo sapien | 232 | 85 | 7.6 | 991 | 2 | Q84FV1 | Q84fv1 chlamydia t |
| 160 | 89 | 7.9 | 417 | 2 | Q8WU33 | Q8wu33 homo sapien | 233 | 85 | 7.6 | 1016 | 1 | PMFH_CHLTR | Q84880 chlamydia t |
| 161 | 89 | 7.9 | 429 | 2 | P79046 | P79046 humicola gr | 234 | 85 | 7.6 | 1049 | 2 | Q960E6 | Q960e6 drosophila |
| 162 | 89 | 7.9 | 482 | 2 | Q6BSZ9 | Q6bsz9 debaryomyce | 235 | 85 | 7.6 | 1049 | 2 | Q9V6L1 | Q9v6l1 drosophila |
| 163 | 89 | 7.9 | 503 | 2 | Q19269 | Q19269 caenorhabdi | 236 | 85 | 7.6 | 1170 | 2 | Q95011 | Q95011 caenorhabdi |
| 164 | 89 | 7.9 | 603 | 2 | Q6CE49 | Q6ce49 yarrowia li | 237 | 85 | 7.6 | 1225 | 2 | Q9VR49 | Q9vr49 drosophila |
| 165 | 89 | 7.9 | 1708 | 2 | Q7XWZ9 | Q7xwz9 oryza sativ | 238 | 85 | 7.6 | 3150 | 2 | Q7PMD5 | Q7pmd5 anopheles g |
| 166 | 88.5 | 7.9 | 316 | 2 | Q09UJ0 | Q09uj0 toxocara ca | 239 | 84.5 | 7.5 | 220 | 2 | Q9EQG0 | Q9eqg0 mus musculu |
| 167 | 88.5 | 7.9 | 582 | 2 | Q8IR74 | Q8ir74 drosophila | 240 | 84.5 | 7.5 | 350 | 2 | Q7Q1R0 | Q7qlr0 anopheles g |
| 168 | 88.5 | 7.9 | 901 | 2 | Q9H195 | Q9h195 homo sapien | 241 | 84.5 | 7.5 | 752 | 2 | Q9YCE1 | Q9yc61 aeropyrum p |
| 169 | 88.5 | 7.9 | 1101 | 1 | GUNC_CELFI | P14090 cellulomona | 242 | 84.5 | 7.5 | 814 | 2 | Q6C247 | Q6c247 yarrowia li |
| 170 | 88.5 | 7.9 | 1148 | 2 | Q6CBJ2 | Q6cbj2 yarrowia li | 243 | 84.5 | 7.5 | 834 | 2 | Q877B7 | Q877b7 aspergillus |
| 171 | 88.5 | 7.9 | 2273 | 2 | Q63HU2 | Q63hu2 burkholderi | 244 | 84.5 | 7.5 | 1161 | 1 | DAN4_YEAST | P47179 saccharomyc |
| 172 | 88 | 7.8 | 103 | 2 | Q9CTB3 | Q9ctb3 sus scrofa | 245 | 84.5 | 7.5 | 2152 | 2 | Q8WXI7 | Q8wxi7 homo sapien |
| 173 | 88 | 7.8 | 382 | 2 | Q6C971 | Q6c971 yarrowia li | 246 | 84 | 7.5 | 259 | 2 | Q9N3B9 | Q9n3b9 caenorhabdi |
| 174 | 88 | 7.8 | 456 | 2 | Q9U2W2 | Q9u2w2 caenorhabdi | 247 | 84 | 7.5 | 262 | 2 | P74577 | P74577 synechocyst |
| 175 | 88 | 7.8 | 602 | 2 | Q8YV91 | Q8yv91 anabaena sp | 248 | 84 | 7.5 | 273 | 2 | Q61002 | Q61002 mus musculu |
| 176 | 88 | 7.8 | 716 | 2 | Q9NVE4 | Q9nye4 homo sapien | 249 | 84 | 7.5 | 335 | 2 | Q9C7W2 | Q9c7w2 arabidopsis |
| 177 | 88 | 7.8 | 730 | 2 | Q86AZ8 | Q86az8 dictyosteli | 250 | 84 | 7.5 | 421 | 2 | Q6KCA6 | Q6kca6 candida dub |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|--------------------|-----|------|-----|------|---|------------|---------------------|
| 251 | 84 | 7.5 | 475 | 2 | Q8FQJ1 | Q8fgj1 corynebacte | 324 | 82 | 7.3 | 483 | 2 | Q9W4M2 | Q9w4m2 drosophila |
| 252 | 84 | 7.5 | 543 | 2 | Q14879 | Q14879 homo sapien | 325 | 82 | 7.3 | 538 | 2 | Q76H84 | Q76h84 streptococc |
| 253 | 84 | 7.5 | 641 | 2 | Q6AJU8 | Q6ajuh desulfotale | 326 | 82 | 7.3 | 630 | 2 | Q96VH6 | Q96vh6 sulfolobus |
| 254 | 84 | 7.5 | 648 | 2 | Q95QX0 | Q95qx0 caenorhabdi | 327 | 82 | 7.3 | 644 | 2 | Q6CF33 | Q6cf33 yarrowia li |
| 255 | 84 | 7.5 | 662 | 1 | MUC1_XENLA | Q05049 xenopus lae | 328 | 82 | 7.3 | 693 | 2 | Q27394 | Q27394 caenorhabdi |
| 256 | 84 | 7.5 | 927 | 2 | Q21811 | Q21811 caenorhabdi | 329 | 82 | 7.3 | 966 | 2 | Q203P1 | Q203p1 caenorhabdi |
| 257 | 84 | 7.5 | 1331 | 1 | MANB_CALSA | F22533 caldocellum | 330 | 82 | 7.3 | 973 | 2 | Q7CZH1 | Q7czh1 agrobacteri |
| 258 | 84 | 7.5 | 1362 | 2 | Q9V294 | Q9v294 pyrococcus | 331 | 82 | 7.3 | 977 | 2 | Q8WQF8 | Q8wqf8 agrobacteri |
| 259 | 84 | 7.5 | 1370 | 2 | Q6C3B8 | Q6c3b8 yarrowia li | 332 | 82 | 7.3 | 1099 | 2 | Q7TUJ6 | Q7tuj6 prochloroco |
| 260 | 84 | 7.5 | 1779 | 2 | O52374 | O52374 caldicellul | 333 | 82 | 7.3 | 1266 | 2 | Q6CAR3 | Q6car3 yarrowia li |
| 261 | 84 | 7.5 | 1832 | 2 | Q96503 | Q96503 cryptospori | 334 | 81.5 | 7.2 | 147 | 2 | O61043 | O61043 trypanosoma |
| 262 | 83.5 | 7.4 | 216 | 2 | Q28501 | Q28501 macaca mula | 335 | 81.5 | 7.2 | 171 | 1 | NUOE_BUCBP | Q89au3 clostridia |
| 263 | 83.5 | 7.4 | 279 | 2 | Q14888 | Q14888 homo sapien | 336 | 81.5 | 7.2 | 386 | 2 | Q97G38 | Q97g38 clostridium |
| 264 | 83.5 | 7.4 | 615 | 2 | Q9M6E8 | Q9m6e8 phaseolus v | 337 | 81.5 | 7.2 | 388 | 2 | Q7Q1W8 | Q7q1w8 anopheles g |
| 265 | 83.5 | 7.4 | 743 | 2 | Q7PQ19 | Q7pq19 anopheles g | 338 | 81.5 | 7.2 | 390 | 2 | Q6PND6 | Q6pnd6 emeritella |
| 266 | 83.5 | 7.4 | 788 | 2 | O18510 | O18510 trichoplusi | 339 | 81.5 | 7.2 | 411 | 2 | Q702X9 | Q702x9 human herpe |
| 267 | 83.5 | 7.4 | 800 | 2 | Q8TFG4 | Q8tfq4 schizosacch | 340 | 81.5 | 7.2 | 460 | 2 | O18984 | Q18984 cercopitheci |
| 268 | 83.5 | 7.4 | 807 | 2 | O18511 | O18511 trichoplusi | 341 | 81.5 | 7.2 | 584 | 1 | CEUL_CABEL | Q17802 caenorhabdi |
| 269 | 83.5 | 7.4 | 892 | 1 | LDL2_XENLA | Q99088 xenopus lae | 342 | 81.5 | 7.2 | 612 | 2 | Q6CD44 | Q6cd44 yarrowia li |
| 270 | 83.5 | 7.4 | 1286 | 2 | Q9TXR6 | Q9txr6 caenorhabdi | 343 | 81.5 | 7.2 | 741 | 2 | Q6CH88 | Q6ch88 yarrowia li |
| 271 | 83.5 | 7.4 | 5179 | 1 | MUC2_HUMAN | Q02817 homo sapien | 344 | 81.5 | 7.2 | 808 | 2 | O81123 | Q81123 caenorhabdi |
| 272 | 83 | 7.4 | 269 | 2 | Q9U9J2 | Q9u9j2 toxocara ca | 345 | 81.5 | 7.2 | 846 | 2 | Q6ZKY0 | Q6zky0 oryza sativ |
| 273 | 83 | 7.4 | 309 | 2 | Q63549 | Q63549 rattus norv | 346 | 81.5 | 7.2 | 860 | 1 | MUTS_LISIN | Q92bv3 listeria in |
| 274 | 83 | 7.4 | 316 | 2 | Q8TDP14 | Q8td14 homo sapien | 347 | 81.5 | 7.2 | 860 | 1 | VG12_BPB03 | Q37893 bacterioph |
| 275 | 83 | 7.4 | 329 | 2 | Q7QB72 | Q7qb72 anopheles g | 348 | 81.5 | 7.2 | 913 | 2 | Q7NP28 | Q7np28 gloebacter |
| 276 | 83 | 7.4 | 337 | 2 | Q7Z5K8 | Q7z5k8 homo sapien | 349 | 81.5 | 7.2 | 957 | 2 | Q9UKN0 | Q9ukn0 homo sapien |
| 277 | 83 | 7.4 | 378 | 2 | Q8SXS5 | Q8sxs5 drosophila | 350 | 81.5 | 7.2 | 1216 | 1 | VPX5_CAEEL | Q09277 caenorhabdi |
| 278 | 83 | 7.4 | 404 | 2 | Q702X0 | Q702x0 human herpe | 351 | 81.5 | 7.2 | 1320 | 2 | Q96KF5 | Q96kf5 homo sapien |
| 279 | 83 | 7.4 | 404 | 2 | Q702Y3 | Q702y3 human herpe | 352 | 81.5 | 7.2 | 1354 | 2 | Q9VKA7 | Q9vka7 drosophila |
| 280 | 83 | 7.4 | 409 | 1 | R23B_HUMAN | P54727 homo sapien | 353 | 81.5 | 7.2 | 1500 | 2 | Q6AUV2 | Q6auv2 oryza sativ |
| 281 | 83 | 7.4 | 419 | 2 | Q8TD11 | Q8td11 homo sapien | 354 | 81.5 | 7.2 | 1844 | 2 | Q22579 | Q22579 caenorhabdi |
| 282 | 83 | 7.4 | 422 | 2 | Q8TD13 | Q8td13 homo sapien | 355 | 81.5 | 7.2 | 2338 | 2 | Q6Z9N6 | Q6z9n6 burkholderi |
| 283 | 83 | 7.4 | 477 | 2 | Q14887 | Q14887 homo sapien | 356 | 81.5 | 7.2 | 3175 | 1 | RPOA_EAV | P19811 equine arte |
| 284 | 83 | 7.4 | 485 | 2 | Q9V8B0 | Q9v8b0 drosophila | 357 | 81 | 7.2 | 184 | 2 | Q7PPK1 | Q7ppk1 anopheles g |
| 285 | 83 | 7.4 | 492 | 2 | Q6CGC6 | Q6cgc6 yarrowia li | 358 | 81 | 7.2 | 221 | 1 | RL1_SULAC | P35024 sulfolobus |
| 286 | 83 | 7.4 | 559 | 2 | Q9VNS36 | Q9vns36 drosophila | 359 | 81 | 7.2 | 301 | 2 | Q924G0 | Q924g0 cratogeomys |
| 287 | 83 | 7.4 | 605 | 1 | WSC4_YEAST | P38739 saccharomyc | 360 | 81 | 7.2 | 315 | 2 | Q9VX11 | Q9vx11 drosophila |
| 288 | 83 | 7.4 | 769 | 2 | Q17921 | Q17921 caenorhabdi | 361 | 81 | 7.2 | 345 | 2 | Q691X0 | Q691x0 anolis sagr |
| 289 | 83 | 7.4 | 993 | 2 | Q83TJ6 | Q83tj6 chlamydia t | 362 | 81 | 7.2 | 355 | 2 | Q9NP13 | Q9np13 homo sapien |
| 290 | 83 | 7.4 | 1002 | 2 | Q6CBD5 | Q6cbd5 yarrowia li | 363 | 81 | 7.2 | 403 | 2 | Q702W8 | Q702w8 human herpe |
| 291 | 83 | 7.4 | 1030 | 2 | Q7QV30 | Q7qv30 giardia lam | 364 | 81 | 7.2 | 404 | 2 | Q702M6 | Q702m6 human herpe |
| 292 | 83 | 7.4 | 1066 | 2 | Q76NW3 | Q76nw3 dictyosteli | 365 | 81 | 7.2 | 404 | 2 | Q702Y0 | Q702y0 human herpe |
| 293 | 82.5 | 7.3 | 197 | 2 | Q26878 | Q26878 trypanosoma | 366 | 81 | 7.2 | 404 | 2 | Q702Y6 | Q702y6 human herpe |
| 294 | 82.5 | 7.3 | 252 | 2 | Q6GZ06 | Q6gz06 avian pneum | 367 | 81 | 7.2 | 453 | 2 | Q9U301 | Q9u301 caenorhabdi |
| 295 | 82.5 | 7.3 | 383 | 1 | VE2_HPV57 | P22155 human papil | 368 | 81 | 7.2 | 668 | 2 | Q6FWR2 | Q6fwr2 candida gla |
| 296 | 82.5 | 7.3 | 389 | 2 | Q64BB8 | Q64bb8 uncultured | 369 | 81 | 7.2 | 746 | 2 | Q82GM0 | Q82gm0 streptomyc |
| 297 | 82.5 | 7.3 | 389 | 2 | Q6GXX0 | Q6gxx0 swine hepat | 370 | 81 | 7.2 | 782 | 2 | Q6CNV3 | Q6cnv3 kluyveromyc |
| 298 | 82.5 | 7.3 | 389 | 2 | Q6GXX2 | Q6gxx2 swine hepat | 371 | 81 | 7.2 | 967 | 2 | Q08294 | Q08294 saccharomyc |
| 299 | 82.5 | 7.3 | 389 | 2 | Q6GXX3 | Q6gxx3 swine hepat | 372 | 81 | 7.2 | 1001 | 2 | Q05164 | Q05164 saccharomyc |
| 300 | 82.5 | 7.3 | 540 | 1 | CH60_STRAP | Q8KJ20 streptococc | 373 | 81 | 7.2 | 1128 | 1 | BEM3_YEAST | Q32873 saccharomyc |
| 301 | 82.5 | 7.3 | 599 | 2 | Q6C2K2 | Q6c2k2 yarrowia li | 374 | 81 | 7.2 | 1163 | 2 | O85AR1 | Q85ar1 dictyosteli |
| 302 | 82.5 | 7.3 | 627 | 2 | Q7RWT2 | Q7rwt2 neurospora | 375 | 81 | 7.2 | 1537 | 1 | FLO1_YEAST | P32768 saccharomyc |
| 303 | 82.5 | 7.3 | 635 | 2 | Q6G065 | Q6g065 fibrobacter | 376 | 81 | 7.2 | 1569 | 2 | Q6W4X9 | Q6w4x9 homo sapien |
| 304 | 82.5 | 7.3 | 726 | 1 | NF11_YEAST | Q12216 saccharomyc | 377 | 81 | 7.2 | 1609 | 1 | FIG2_YEAST | P25653 saccharomyc |
| 305 | 82.5 | 7.3 | 825 | 2 | Q03088 | Q03088 saccharomyc | 378 | 81 | 7.2 | 1713 | 2 | Q8TGE1 | Q8tge1 saccharomyc |
| 306 | 82.5 | 7.3 | 843 | 2 | Q9VYH8 | Q9vyh8 drosophila | 379 | 81 | 7.2 | 2282 | 1 | ZAN_RABIT | P57999 cryptotagus |
| 307 | 82.5 | 7.3 | 876 | 2 | Q6XLI5 | Q6xli5 brachydanio | 380 | 81 | 7.2 | 2977 | 2 | Q9VAP9 | Q9vap9 drosophila |
| 308 | 82.5 | 7.3 | 1206 | 1 | FM14_MOUSE | Q05859 mus muscul | 381 | 80.5 | 7.2 | 148 | 1 | SY02_RAT | P14844 rattus norv |
| 309 | 82.5 | 7.3 | 1261 | 2 | Q7R2F4 | Q7r2f4 giardia lam | 382 | 80.5 | 7.2 | 165 | 2 | Q6E877 | Q26877 trypanosoma |
| 310 | 82.5 | 7.3 | 1371 | 2 | Q9VU22 | Q9vu22 drosophila | 383 | 80.5 | 7.2 | 242 | 2 | Q86RS8 | Q86rs8 caenorhabdi |
| 311 | 82.5 | 7.3 | 1468 | 1 | FMN1_MOUSE | Q05860 mus muscul | 384 | 80.5 | 7.2 | 334 | 2 | Q6VAV6 | Q6vav6 anopheles g |
| 312 | 82.5 | 7.3 | 1472 | 2 | Q6V9R4 | Q6v9r4 strongyloce | 385 | 80.5 | 7.2 | 391 | 1 | VE2_HPV2A | P25482 human papil |
| 313 | 82.5 | 7.3 | 1478 | 1 | LHN2_BOVIN | Q97817 bos taurus | 386 | 80.5 | 7.2 | 410 | 2 | LMP2_CRIGR | Q25482 human papil |
| 314 | 82.5 | 7.3 | 1851 | 2 | Q9ESF3 | Q9eep3 rattus norv | 387 | 80.5 | 7.2 | 441 | 2 | Q9U2W3 | Q9u2w3 caenorhabdi |
| 315 | 82 | 7.3 | 236 | 2 | Q9LMO0 | Q9lm00 pinus taeda | 388 | 80.5 | 7.2 | 540 | 1 | CH60_STRAS | Q8cx22 streptococc |
| 316 | 82 | 7.3 | 318 | 2 | Q86HN3 | Q86hn3 dictyosteli | 389 | 80.5 | 7.2 | 540 | 1 | CH60_STRAS | Q8cx00 streptococc |
| 317 | 82 | 7.3 | 339 | 2 | Q9VUX8 | Q9vux8 drosophila | 390 | 80.5 | 7.2 | 659 | 2 | Q86AI8 | Q86ai8 dictyosteli |
| 318 | 82 | 7.3 | 345 | 2 | Q690W2 | Q690w2 anolis sagr | 391 | 80.5 | 7.2 | 747 | 2 | Q7S8F0 | Q7s8f0 neurospora |
| 319 | 82 | 7.3 | 346 | 2 | Q7S973 | Q7s973 neurospora | 392 | 80.5 | 7.2 | 758 | 2 | Q8TZI4 | Q8tzi4 caenorhabdi |
| 320 | 82 | 7.3 | 374 | 2 | Q9Z209 | Q9z209 cricetus | 393 | 80.5 | 7.2 | 765 | 2 | Q75I27 | Q75i27 oryza sativ |
| 321 | 82 | 7.3 | 389 | 2 | Q76573 | Q76573 caenorhabdi | 394 | 80.5 | 7.2 | 860 | 2 | Q71Z87 | Q71z87 listeria mo |
| 322 | 82 | 7.3 | 463 | 2 | Q42665 | Q42665 schizosacch | 395 | 80.5 | 7.2 | 896 | 2 | Q20253 | Q20253 caenorhabdi |
| 323 | 82 | 7.3 | 477 | 1 | MYPH_HUMAN | Q13203 homo sapien | 396 | 80.5 | 7.2 | 971 | 2 | Q6W3C4 | Q6w3c4 caenorhabdi |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|-------------|---------------------|-----|------|-----|------|---|------------|--------------------|
| 397 | 80.5 | 7.2 | 989 | 2 | Q19930 | Q19930 caenorhabdi | 470 | 79 | 7.0 | 213 | 2 | Q6ZU27 | Q6ZU27 homo sapien |
| 398 | 80.5 | 7.2 | 1184 | 2 | Q6F3A8 | Q6f3a8 oryza sativ | 471 | 79 | 7.0 | 249 | 2 | Q6BVK5 | Q6bvx5 debaryomyce |
| 399 | 80.5 | 7.2 | 1300 | 2 | Q6BZP6 | Q6bzp6 yarrowia li | 472 | 79 | 7.0 | 249 | 2 | Q8BJQ4 | Q8bjq4 arabidopsis |
| 400 | 80.5 | 7.2 | 1372 | 2 | Q8SX99 | Q8sx99 drosophila | 473 | 79 | 7.0 | 261 | 2 | Q70CC2 | Q70cc2 elmeria ten |
| 401 | 80.5 | 7.2 | 1372 | 2 | Q9VNV46 | Q9vn46 drosophila | 474 | 79 | 7.0 | 308 | 2 | Q74KF4 | Q74kf4 lactobacill |
| 402 | 80.5 | 7.2 | 2225 | 2 | Q45881 | Q45881 caenorhabdi | 475 | 79 | 7.0 | 333 | 2 | Q6VAV8 | Q6vav8 anopheles g |
| 403 | 80.5 | 7.2 | 3295 | 2 | Q66GT3 | Q66gt3 rattus norv | 476 | 79 | 7.0 | 345 | 2 | Q691T8 | Q691t8 anolis sagr |
| 404 | 80 | 7.1 | 103 | 2 | Q46380 | Q46380 oryctolagus | 477 | 79 | 7.0 | 352 | 2 | Q49782 | Q49782 arabidopsis |
| 405 | 80 | 7.1 | 272 | 2 | Q6ZSN5 | Q6zsn5 homo sapien | 478 | 79 | 7.0 | 353 | 2 | Q8VPM3 | Q8vpm3 micrococcus |
| 406 | 80 | 7.1 | 291 | 2 | Q6QFG5 | Q6qpg5 simian aden | 479 | 79 | 7.0 | 359 | 2 | Q9XZT0 | Q9xzt0 drosophila |
| 407 | 80 | 7.1 | 334 | 2 | Q6VAM0 | Q6vaw0 anopheles g | 480 | 79 | 7.0 | 390 | 2 | Q702W4 | Q702w4 human herpe |
| 408 | 80 | 7.1 | 349 | 2 | Q7XEC9 | Q7xec9 oryza sativ | 481 | 79 | 7.0 | 390 | 2 | Q702W9 | Q702w9 human herpe |
| 409 | 80 | 7.1 | 390 | 2 | Q7XETS5 | Q7xtcs5 phlebia tad | 482 | 79 | 7.0 | 410 | 1 | LMP2_HUMAN | P13473 homo sapien |
| 410 | 80 | 7.1 | 390 | 2 | Q70LM3 | Q70lm3 phlebia rad | 483 | 79 | 7.0 | 411 | 2 | Q6Q3G8 | Q6q3g8 homo sapien |
| 411 | 80 | 7.1 | 410 | 2 | Q9UD93 | Q9ud93 homo sapien | 484 | 79 | 7.0 | 446 | 2 | Q8UI37 | Q8ui37 leishmania |
| 412 | 80 | 7.1 | 429 | 2 | Q95Y50 | Q95y50 caenorhabdi | 485 | 79 | 7.0 | 447 | 2 | Q8BIY6 | Q8biy6 mus musculu |
| 413 | 80 | 7.1 | 449 | 2 | Q9VKS4 | Q9vks4 drosophila | 486 | 79 | 7.0 | 486 | 2 | Q8FRY2 | Q8fry2 corynebacte |
| 414 | 80 | 7.1 | 569 | 2 | Q71X10 | Q71x10 listeria mo | 487 | 79 | 7.0 | 489 | 2 | Q95Q80 | Q95q80 caenorhabdi |
| 415 | 80 | 7.1 | 657 | 2 | Q6AM00 | Q6am00 desulfotale | 488 | 79 | 7.0 | 503 | 2 | Q95Q82 | Q95q82 caenorhabdi |
| 416 | 80 | 7.1 | 725 | 1 | AGA1_YEAST | P32323 saccharomyc | 489 | 79 | 7.0 | 503 | 2 | Q9VCF0 | Q9vcf0 mus musculu |
| 417 | 80 | 7.1 | 729 | 2 | Q8QWY2 | Q8owiy2 mus musculu | 490 | 79 | 7.0 | 534 | 2 | Q86AL2 | Q86al2 dictyosteli |
| 418 | 80 | 7.1 | 732 | 2 | Q8QWY1 | Q8owiy1 mus musculu | 491 | 79 | 7.0 | 555 | 2 | Q9VH46 | Q9vh46 drosophila |
| 419 | 80 | 7.1 | 747 | 2 | Q8CCZ1 | Q8ccz1 mus musculu | 492 | 79 | 7.0 | 575 | 2 | Q62223 | Q62223 caenorhabdi |
| 420 | 80 | 7.1 | 881 | 1 | PRY3_YEAST | P47033 saccharomyc | 493 | 79 | 7.0 | 594 | 2 | Q6PAN1 | Q6pan1 mus musculu |
| 421 | 80 | 7.1 | 1082 | 1 | YK02_SCHPO | Q9hdy9 schizosacch | 494 | 79 | 7.0 | 601 | 2 | Q6V6S1 | Q6v6s1 drosophila |
| 422 | 80 | 7.1 | 1168 | 2 | Q9VZE8 | Q9vze8 drosophila | 495 | 79 | 7.0 | 601 | 2 | Q8V6S2 | Q8v6s2 drosophila |
| 423 | 80 | 7.1 | 1324 | 2 | Q8MMQ2 | Q8mmq2 dictyosteli | 496 | 79 | 7.0 | 629 | 2 | Q8KU05 | Q8kuu5 synecococc |
| 424 | 80 | 7.1 | 1325 | 2 | Q9BKV7 | Q9bkv7 leishmania | 497 | 79 | 7.0 | 629 | 2 | Q24017 | Q24017 drosophila |
| 425 | 80 | 7.1 | 4262 | 2 | Q685J2 | Q685j2 homo sapien | 498 | 79 | 7.0 | 629 | 2 | Q9V3H7 | Q9v3h7 drosophila |
| 426 | 80 | 7.1 | 4493 | 2 | Q685J3 | Q685j3 homo sapien | 499 | 79 | 7.0 | 669 | 2 | Q7EZY9 | Q7ezy9 oryza sativ |
| 427 | 79.5 | 7.1 | 129 | 2 | Q6UNH4 | Q6unh4 ictalurus p | 500 | 79 | 7.0 | 729 | 2 | Q8BW38 | Q8bw38 mus musculu |
| 428 | 79.5 | 7.1 | 161 | 2 | Q6IGP4 | Q6igp4 drosophila | 501 | 79 | 7.0 | 785 | 2 | Q7Q0I5 | Q7q0i5 giardia lam |
| 429 | 79.5 | 7.1 | 272 | 2 | Q8A3G1 | Q8a3g1 bacteroides | 502 | 79 | 7.0 | 893 | 2 | Q9LHT1 | Q9lht1 arabidopsis |
| 430 | 79.5 | 7.1 | 273 | 2 | Q6QK85 | Q6jqk85 neodiprion | 503 | 79 | 7.0 | 919 | 2 | Q76EQ4 | Q76eq4 streptococc |
| 431 | 79.5 | 7.1 | 333 | 2 | Q6VAV7 | Q6vav7 anopheles g | 504 | 79 | 7.0 | 980 | 2 | Q9MA13 | Q9ma13 arabidopsis |
| 432 | 79.5 | 7.1 | 354 | 2 | Q25402 | Q25402 litomosoid | 505 | 79 | 7.0 | 1031 | 2 | Q925N8 | Q925n8 mus musculu |
| 433 | 79.5 | 7.1 | 363 | 2 | Q91YK8 | Q91yk8 mus musculu | 506 | 79 | 7.0 | 1031 | 2 | Q9D071 | Q9d071 m mus muscu |
| 434 | 79.5 | 7.1 | 373 | 2 | Q76810 | Q76810 anopheles g | 507 | 79 | 7.0 | 1048 | 2 | Q9LAU3 | Q9lau3 legionella |
| 435 | 79.5 | 7.1 | 403 | 2 | Q8MVA9 | Q8mva9 ixodes scap | 508 | 79 | 7.0 | 1142 | 2 | Q6CCL7 | Q6ccl7 yarrowia li |
| 436 | 79.5 | 7.1 | 433 | 2 | Q88VC0 | Q88vc0 lactobacill | 509 | 79 | 7.0 | 1689 | 2 | Q8QZF4 | Q8qzf4 crimean-con |
| 437 | 79.5 | 7.1 | 461 | 2 | Q6C2X8 | Q6c2x8 yarrowia li | 510 | 79 | 7.0 | 1689 | 2 | Q8QZP5 | Q8qzf5 crimean-con |
| 438 | 79.5 | 7.1 | 462 | 2 | Q8TUE0 | Q8tue0 methanosarc | 511 | 79 | 7.0 | 1689 | 2 | Q991H9 | Q991h9 crimean-con |
| 439 | 79.5 | 7.1 | 463 | 2 | Q7RNE3 | Q7rne3 plasmodium | 512 | 79 | 7.0 | 1752 | 2 | Q9AE52 | Q9ae52 ruminococcu |
| 440 | 79.5 | 7.1 | 495 | 2 | Q9CV82 | Q9cv82 mus musculu | 513 | 79 | 7.0 | 2616 | 1 | NOL_DROME | P98159 drosophila |
| 441 | 79.5 | 7.1 | 497 | 2 | Q8QVC5 | Q8qvc5 eyach virus | 514 | 79 | 7.0 | 3550 | 2 | Q86GT4 | Q86gt4 rattus norv |
| 442 | 79.5 | 7.1 | 511 | 2 | Q8UYA8 | Q8uya8 human herpe | 515 | 78.5 | 7.0 | 94 | 2 | Q61030 | Q61030 trypanosoma |
| 443 | 79.5 | 7.1 | 511 | 2 | Q8UZ60 | Q8uz60 human herpe | 516 | 78.5 | 7.0 | 142 | 2 | Q26943 | Q26943 trypanosoma |
| 444 | 79.5 | 7.1 | 511 | 2 | Q8UZ61 | Q8uz61 human herpe | 517 | 78.5 | 7.0 | 161 | 2 | Q6CPZ3 | Q6cpz3 kluyveromyc |
| 445 | 79.5 | 7.1 | 511 | 2 | Q8UZ64 | Q8uz64 human herpe | 518 | 78.5 | 7.0 | 164 | 2 | Q14851 | Q14851 homo sapien |
| 446 | 79.5 | 7.1 | 511 | 2 | Q8UZ66 | Q8uz66 human herpe | 519 | 78.5 | 7.0 | 224 | 2 | Q8KKT9 | Q8kkt9 rhizobium e |
| 447 | 79.5 | 7.1 | 511 | 2 | Q8UZ67 | Q8uz67 human herpe | 520 | 78.5 | 7.0 | 231 | 2 | Q8EZM6 | Q8ezmw leptospira |
| 448 | 79.5 | 7.1 | 689 | 2 | Q7QN60 | Q7qn60 anopheles g | 521 | 78.5 | 7.0 | 232 | 2 | Q27423 | Q27423 drosophila |
| 449 | 79.5 | 7.1 | 796 | 2 | Q8MRG9 | Q8mr99 drosophila | 522 | 78.5 | 7.0 | 252 | 2 | Q80G93 | Q80g93 avian pneum |
| 450 | 79.5 | 7.1 | 796 | 2 | Q9VTR4 | Q9vtr4 drosophila | 523 | 78.5 | 7.0 | 258 | 2 | Q6TV72 | Q6tv72 bovine papu |
| 451 | 79.5 | 7.1 | 860 | 1 | MUT5_LITSMO | Q8y789 listeria mo | 524 | 78.5 | 7.0 | 262 | 2 | Q9JMF0 | Q9jmf0 mus musculu |
| 452 | 79.5 | 7.1 | 873 | 2 | Q9W458 | Q9w468 drosophila | 525 | 78.5 | 7.0 | 271 | 2 | Q71DD6 | Q71dd6 drosophila |
| 453 | 79.5 | 7.1 | 873 | 2 | Q9Y076 | Q9y076 leishmania | 526 | 78.5 | 7.0 | 283 | 2 | Q6CIR8 | Q6cir8 kluyveromyc |
| 454 | 79.5 | 7.1 | 887 | 2 | Q6XD56 | Q6xd56 gallus gall | 527 | 78.5 | 7.0 | 285 | 2 | Q86H76 | Q86h76 dictyosteli |
| 455 | 79.5 | 7.1 | 985 | 2 | Q67643 | Q67643 gallid herp | 528 | 78.5 | 7.0 | 294 | 2 | Q99322 | Q99322 homo sapien |
| 456 | 79.5 | 7.1 | 1203 | 2 | Q6ZQ56 | Q6zq56 mus musculu | 529 | 78.5 | 7.0 | 322 | 2 | Q62605 | Q62605 rattus norv |
| 457 | 79.5 | 7.1 | 1237 | 2 | Q7WYN2 | Q7wyn2 acetivibrio | 530 | 78.5 | 7.0 | 334 | 2 | Q6VAV5 | Q6vav5 anopheles g |
| 458 | 79.5 | 7.1 | 1441 | 2 | Q8S628 | Q8s628 oryza sativ | 531 | 78.5 | 7.0 | 334 | 2 | Q6VAV9 | Q6vav9 anopheles g |
| 459 | 79.5 | 7.1 | 1441 | 2 | Q8GU94 | Q8gu94 oryza sativ | 532 | 78.5 | 7.0 | 338 | 2 | Q95Y19 | Q95y19 caenorhabdi |
| 460 | 79.5 | 7.1 | 1459 | 1 | LHN2_HUMAN | Q95490 homo sapien | 533 | 78.5 | 7.0 | 402 | 2 | Q9N503 | Q9n503 caenorhabdi |
| 461 | 79.5 | 7.1 | 1486 | 2 | Q95RE5 | Q95re5 drosophila | 534 | 78.5 | 7.0 | 410 | 1 | GC5B_MOUSE | Q92320 mus musculu |
| 462 | 79.5 | 7.1 | 1486 | 2 | Q967Y2 | Q967y2 drosophila | 535 | 78.5 | 7.0 | 430 | 2 | Q9N4F8 | Q9n4f8 caenorhabdi |
| 463 | 79.5 | 7.1 | 1486 | 2 | Q7KRP7 | Q7krp7 drosophila | 536 | 78.5 | 7.0 | 525 | 2 | Q6CAQ5 | Q6caq5 yarrowia li |
| 464 | 79.5 | 7.1 | 1582 | 2 | Q7KRP6 | Q7krp6 drosophila | 537 | 78.5 | 7.0 | 540 | 1 | CH60_STRAG | Q6caq5 streptococc |
| 465 | 79.5 | 7.1 | 1707 | 2 | Q6PWR4 | Q6pmr4 swine hepat | 538 | 78.5 | 7.0 | 562 | 1 | NUPL_HUMAN | P52594 homo sapien |
| 466 | 79.5 | 7.1 | 1806 | 2 | Q659R4 | Q659r4 dictyosteli | 539 | 78.5 | 7.0 | 581 | 2 | Q7R0Z5 | Q7roz5 giardia lam |
| 467 | 79.5 | 7.1 | 5703 | 1 | MUSEB_HUMAN | Q9hc84 homo sapien | 540 | 78.5 | 7.0 | 589 | 2 | Q43419 | Q43419 homo sapien |
| 468 | 79 | 7.0 | 195 | 2 | Q9W4V3 | Q9w4v3 drosophila | 541 | 78.5 | 7.0 | 627 | 2 | Q8MP19 | Q8mp19 dictyosteli |
| 469 | 79 | 7.0 | 202 | 2 | Q7XLD8 | Q7xld8 oryza sativ | 542 | 78.5 | 7.0 | 647 | 2 | Q7RY11 | Q7ryy1 neurospora |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|---------------------|-----|------|-----|-------|---|------------|---------------------|
| 543 | 78.5 | 7.0 | 657 | 2 | Q861D0 | Q861d0 dictyosteli | 616 | 77.5 | 6.9 | 1212 | 2 | O42347 | O42347 gallus gall |
| 544 | 78.5 | 7.0 | 763 | 2 | Q965Y7 | Q965y7 caenorhabdi | 617 | 77.5 | 6.9 | 1383 | 2 | Q874K9 | Q874k9 candida alb |
| 545 | 78.5 | 7.0 | 830 | 2 | Q6CAY0 | Q6cay0 yarrowia li | 618 | 77.5 | 6.9 | 1845 | 2 | Q86JH8 | Q86jh8 dictyosteli |
| 546 | 78.5 | 7.0 | 858 | 2 | Q9H8D9 | Q9h8d9 homo sapien | 619 | 77.5 | 6.9 | 1873 | 2 | Q6S003 | Q6s003 dictyosteli |
| 547 | 78.5 | 7.0 | 1236 | 2 | Q9C105 | Q9c105 schizosacch | 620 | 77.5 | 6.9 | 1878 | 2 | Q6CP24 | Q6cp24 kluyveromyc |
| 548 | 78.5 | 7.0 | 1241 | 2 | Q75JC0 | Q75jc0 dictyosteli | 621 | 77.5 | 6.9 | 19522 | 2 | Q19522 | Q19522 caenorhabdi |
| 549 | 78.5 | 7.0 | 1487 | 1 | LHR2_RAT | LHR2r2 rattus norv | 622 | 77.5 | 6.9 | 4630 | 2 | Q7UWM5 | Q7uwm5 rhodopocell |
| 550 | 78.5 | 7.0 | 1740 | 2 | Q8ML25 | Q8ml25 rattus norv | 623 | 77.5 | 6.9 | 187 | 2 | Q77AU9 | Q77au9 lymphocytic |
| 551 | 78.5 | 7.0 | 1983 | 2 | Q9V696 | Q9v696 drosophila | 624 | 77.5 | 6.9 | 187 | 2 | Q77AV0 | Q77av0 lymphocytic |
| 552 | 78.5 | 7.0 | 2378 | 2 | Q7N7Y6 | Q7n7y6 photorabdu | 625 | 77.5 | 6.9 | 187 | 2 | Q9YJ85 | Q9yj85 lymphocytic |
| 553 | 78.5 | 7.0 | 5374 | 2 | Q99ND0 | Q99nd0 mus musculu | 626 | 77.5 | 6.9 | 187 | 2 | Q9YPM0 | Q9ypm0 lymphocytic |
| 554 | 78.5 | 7.0 | 119 | 2 | Q61034 | Q61034 trypanosoma | 627 | 77.5 | 6.9 | 213 | 2 | Q6M9S9 | Q6m9s9 neurospora |
| 555 | 78.5 | 7.0 | 248 | 2 | Q6CFU5 | Q6cfu5 yarrowia li | 628 | 77.5 | 6.9 | 262 | 2 | Q7PRM2 | Q7prm2 anopheles g |
| 556 | 78.5 | 7.0 | 253 | 2 | P74526 | P74526 synchocycet | 629 | 77.5 | 6.9 | 340 | 2 | Q8ZKQ1 | Q8zkg1 salmonella |
| 557 | 78.5 | 7.0 | 293 | 2 | Q9CCE9 | Q9cce9 mycobacteri | 630 | 77.5 | 6.9 | 341 | 2 | Q8IMS9 | Q8ime9 drosophila |
| 558 | 78.5 | 7.0 | 334 | 2 | Q6VAV4 | Q6vav4 anopheles g | 631 | 77.5 | 6.9 | 345 | 2 | Q690T8 | Q690t8 anolis sagr |
| 559 | 78.5 | 7.0 | 338 | 2 | Q7WZ11 | Q7wz11 bacillus th | 632 | 77.5 | 6.9 | 345 | 2 | Q690U2 | Q690u2 anolis sagr |
| 560 | 78.5 | 7.0 | 345 | 2 | Q690V2 | Q690v2 anolis sagr | 633 | 77.5 | 6.9 | 345 | 2 | Q690U5 | Q690u5 anolis sagr |
| 561 | 78.5 | 7.0 | 345 | 2 | Q690V6 | Q690v6 anolis sagr | 634 | 77.5 | 6.9 | 345 | 2 | Q690U6 | Q690u6 anolis sagr |
| 562 | 78.5 | 7.0 | 345 | 2 | Q690V7 | Q690v7 anolis sagr | 635 | 77.5 | 6.9 | 345 | 2 | Q690U8 | Q690u8 anolis sagr |
| 563 | 78.5 | 7.0 | 345 | 2 | Q690X3 | Q690x3 anolis sagr | 636 | 77.5 | 6.9 | 345 | 2 | Q690V1 | Q690v1 anolis sagr |
| 564 | 78.5 | 7.0 | 345 | 2 | Q692A4 | Q692a4 anolis sagr | 637 | 77.5 | 6.9 | 345 | 2 | Q690W8 | Q690w8 anolis sagr |
| 565 | 78.5 | 7.0 | 345 | 2 | Q692C2 | Q692c2 anolis quad | 638 | 77.5 | 6.9 | 345 | 2 | Q690X6 | Q690x6 anolis sagr |
| 566 | 78.5 | 7.0 | 356 | 2 | Q7TFJ3 | Q7tfj3 rheus cyco | 639 | 77.5 | 6.9 | 345 | 2 | Q690X8 | Q690x8 anolis sagr |
| 567 | 78.5 | 7.0 | 379 | 2 | Q42763 | Q42763 gossypium h | 640 | 77.5 | 6.9 | 345 | 2 | Q691U6 | Q691u6 anolis sagr |
| 568 | 78.5 | 7.0 | 400 | 2 | Q9SQF7 | Q9sqf7 brassica ju | 641 | 77.5 | 6.9 | 345 | 2 | Q691Y0 | Q691y0 anolis sagr |
| 569 | 78.5 | 7.0 | 405 | 2 | Q95XV0 | Q95xv0 caenorhabdi | 642 | 77.5 | 6.9 | 345 | 2 | Q691Y1 | Q691y1 anolis sagr |
| 570 | 78.5 | 7.0 | 434 | 2 | Q9SKN2 | Q9skn2 arabidopsis | 643 | 77.5 | 6.9 | 345 | 2 | Q691Y6 | Q691y6 anolis sagr |
| 571 | 78.5 | 7.0 | 453 | 2 | Q870S8 | Q870s8 neurospora | 644 | 77.5 | 6.9 | 345 | 2 | Q691Z2 | Q691z2 anolis sagr |
| 572 | 78.5 | 7.0 | 495 | 2 | Q74847 | Q74847 human immun | 645 | 77.5 | 6.9 | 350 | 2 | Q9RT72 | Q9rt72 deinococcus |
| 573 | 78.5 | 7.0 | 513 | 2 | Q43418 | Q43418 homo sapien | 646 | 77.5 | 6.9 | 453 | 1 | Q7YUQ4 | Q7yuyq4 trypanosoma |
| 574 | 78.5 | 7.0 | 530 | 2 | Q07701 | Q07701 herpesvirus | 647 | 77.5 | 6.9 | 549 | 2 | Q7L8E3 | Q7l8e3 homo sapien |
| 575 | 78.5 | 7.0 | 573 | 2 | Q8TOR9 | Q8tor9 drosophila | 648 | 77.5 | 6.9 | 577 | 2 | Q6FSJ1 | Q6fsj1 candida gla |
| 576 | 78.5 | 7.0 | 637 | 1 | C2AP_MOUSE | C2apm0 mus musculu | 649 | 77.5 | 6.9 | 598 | 2 | Q20747 | Q20747 caenorhabdi |
| 577 | 78.5 | 7.0 | 637 | 2 | Q7WTS5 | Q7wts5 rattus norv | 650 | 77.5 | 6.9 | 708 | 2 | Q7R9K7 | Q7r9k7 plasmodium |
| 578 | 78.5 | 7.0 | 689 | 2 | Q724Q0 | Q724q0 listeria mo | 651 | 77.5 | 6.9 | 713 | 2 | Q9Y253 | Q9y253 homo sapien |
| 579 | 78.5 | 7.0 | 699 | 2 | Q6CSM7 | Q6csm7 kluyveromyc | 652 | 77.5 | 6.9 | 717 | 2 | Q8U1H5 | Q8u1h5 pyrococcus |
| 580 | 78.5 | 7.0 | 759 | 2 | Q05143 | Q05143 ruminococcu | 653 | 77.5 | 6.9 | 750 | 2 | Q9HFZ4 | Q9hfz4 candida alb |
| 581 | 78.5 | 7.0 | 823 | 2 | Q6C159 | Q6c159 yarrowia li | 654 | 77.5 | 6.9 | 771 | 1 | TM88_HUMAN | TM88h8 homo sapien |
| 582 | 78.5 | 7.0 | 925 | 2 | Q7XFP0 | Q7xfp0 oryza sativ | 655 | 77.5 | 6.9 | 772 | 2 | Q82YF8 | Q82yf8 streptomyce |
| 583 | 78.5 | 7.0 | 1000 | 2 | Q95QH6 | Q95qh6 caenorhabdi | 656 | 77.5 | 6.9 | 802 | 2 | Q7YVP9 | Q7yvp9 trypanosoma |
| 584 | 78.5 | 7.0 | 1091 | 1 | NCAL_CHICK | NCALch0 gallus gall | 657 | 77.5 | 6.9 | 902 | 2 | Q8Q7H5 | Q8q7h5 human immun |
| 585 | 78.5 | 7.0 | 1822 | 2 | Q7ROW4 | Q7row4 giardia lam | 658 | 77.5 | 6.9 | 941 | 2 | Q7Z5R7 | Q7z5r7 homo sapien |
| 586 | 78.5 | 7.0 | 1955 | 1 | AGRN_CHICK | AGRNch0 gallus gall | 659 | 77.5 | 6.9 | 979 | 2 | Q8NDA4 | Q8nda4 homo sapien |
| 587 | 78.5 | 7.0 | 2162 | 2 | Q70PP2 | Q70pp2 drosophila | 660 | 77.5 | 6.9 | 1092 | 1 | NCAC863 | NCAC863 yarrowia li |
| 588 | 78.5 | 7.0 | 3218 | 2 | Q9W3V6 | Q9w3v6 drosophila | 661 | 77.5 | 6.9 | 1168 | 2 | Q8S7C7 | Q8s7c7 oryza sativ |
| 589 | 78.5 | 7.0 | 3529 | 2 | Q9GP30 | Q9gp30 theileria p | 662 | 77.5 | 6.9 | 1205 | 2 | Q6IE70 | Q6ie70 rattus norv |
| 590 | 77.5 | 6.9 | 215 | 2 | Q6CBZ1 | Q6cbz1 yarrowia li | 663 | 77.5 | 6.9 | 1223 | 2 | Q6ZS17 | Q6zsl7 homo sapien |
| 591 | 77.5 | 6.9 | 238 | 1 | COR3_MOUSE | COR3m0 mus musculu | 664 | 77.5 | 6.9 | 1462 | 2 | Q86AR5 | Q86ar5 dictyosteli |
| 592 | 77.5 | 6.9 | 250 | 2 | Q8F5I6 | Q8f5i6 corynebacte | 665 | 77.5 | 6.9 | 1513 | 1 | MUC2_RAT | MUC2r2 rattus norv |
| 593 | 77.5 | 6.9 | 260 | 2 | Q6ND60 | Q6nd60 rhodopeudo | 666 | 77.5 | 6.9 | 1521 | 2 | Q8CHS9 | Q8chs9 mus musculu |
| 594 | 77.5 | 6.9 | 270 | 2 | Q821Y9 | Q821y9 streptomyce | 667 | 77.5 | 6.9 | 1706 | 2 | Q7TGF2 | Q7tgf2 hepatitis e |
| 595 | 77.5 | 6.9 | 370 | 2 | Q9XW5 | Q9xw5 caenorhabdi | 668 | 77.5 | 6.9 | 1711 | 1 | N214_DROME | N214d4 drosophila |
| 596 | 77.5 | 6.9 | 425 | 2 | Q702W3 | Q702w3 human herpe | 669 | 77.5 | 6.9 | 2112 | 2 | Q80U93 | Q80u93 mus musculu |
| 597 | 77.5 | 6.9 | 430 | 2 | Q6K4M7 | Q6k4m7 oryza sativ | 670 | 77.5 | 6.9 | 2187 | 2 | P70670 | P70670 mus musculu |
| 598 | 77.5 | 6.9 | 447 | 2 | Q8SBG8 | Q8sbg8 bacterioph | 671 | 77.5 | 6.9 | 2300 | 2 | Q7SFP6 | Q7sfp6 neurospora |
| 599 | 77.5 | 6.9 | 497 | 2 | Q7XHL3 | Q7xhl3 oryza sativ | 672 | 77.5 | 6.9 | 2316 | 1 | P7P2_RAT | P7p2r2 rattus norv |
| 600 | 77.5 | 6.9 | 511 | 2 | Q8UZ62 | Q8uz62 human herpe | 673 | 77.5 | 6.9 | 2566 | 2 | Q8TSE7 | Q8tse7 methanosarc |
| 601 | 77.5 | 6.9 | 514 | 1 | AVP2_XENLA | AVP2x2 xenopus lae | 674 | 77.5 | 6.9 | 4782 | 2 | Q8K1G6 | Q8klg6 mus musculu |
| 602 | 77.5 | 6.9 | 540 | 1 | CH60_STRSA | CH60s0 streptococc | 675 | 77.5 | 6.9 | 123 | 2 | Q15773 | Q15773 trypanosoma |
| 603 | 77.5 | 6.9 | 547 | 2 | Q8IV81 | Q8iv81 homo sapien | 676 | 77.5 | 6.9 | 185 | 2 | Q7PEQ9 | Q7peq9 anopheles g |
| 604 | 77.5 | 6.9 | 592 | 2 | Q23036 | Q23036 caenorhabdi | 677 | 77.5 | 6.9 | 185 | 2 | Q7PZX2 | Q7pzx2 anopheles g |
| 605 | 77.5 | 6.9 | 624 | 2 | Q7SD58 | Q7sd58 neurospora | 678 | 76.5 | 6.8 | 232 | 2 | Q69EW2 | Q69ew2 streptococ |
| 606 | 77.5 | 6.9 | 658 | 2 | Q8MQZ8 | Q8mqz8 drosophila | 679 | 76.5 | 6.8 | 250 | 2 | Q8HFS1 | Q8hfs1 candida alb |
| 607 | 77.5 | 6.9 | 706 | 2 | Q9VNZ5 | Q9vnz5 drosophila | 680 | 76.5 | 6.8 | 299 | 2 | Q825U2 | Q825u2 streptomyce |
| 608 | 77.5 | 6.9 | 753 | 2 | Q9VCQ7 | Q9vcq7 drosophila | 681 | 76.5 | 6.8 | 304 | 2 | Q6CCZ0 | Q6ccz0 yarrowia li |
| 609 | 77.5 | 6.9 | 760 | 2 | Q6EJF7 | Q6ejf7 homo sapien | 682 | 76.5 | 6.8 | 304 | 2 | Q8AW28 | Q8aw28 bacillus th |
| 610 | 77.5 | 6.9 | 806 | 2 | Q960Q0 | Q960q0 drosophila | 683 | 76.5 | 6.8 | 308 | 2 | Q9BRD2 | Q9brd2 homo sapien |
| 611 | 77.5 | 6.9 | 951 | 1 | SFR8_HUMAN | SFR8h8 homo sapien | 684 | 76.5 | 6.8 | 345 | 2 | Q6UJMS | Q6ujms diploactyl |
| 612 | 77.5 | 6.9 | 982 | 2 | Q6CGV5 | Q6cgv5 yarrowia li | 685 | 76.5 | 6.8 | 349 | 2 | Q9UF43 | Q9uf43 homo sapien |
| 613 | 77.5 | 6.9 | 1050 | 2 | O16436 | O16436 caenorhabdi | 686 | 76.5 | 6.8 | | | | |
| 614 | 77.5 | 6.9 | 1118 | 2 | Q6CX19 | Q6cx19 kluyveromyc | 687 | 76.5 | 6.8 | | | | |
| 615 | 77.5 | 6.9 | 1127 | 2 | Q9C608 | Q9c608 arabidopsis | 688 | 76.5 | 6.8 | | | | |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|--------------------|-----|------|-----|------|---|------------|--------------------|
| 689 | 76.5 | 6.8 | 357 | 2 | Q8NJZ0 | Q8njz0 bionectria | 762 | 76 | 6.8 | 468 | 2 | O55279 | O55279 avian adeno |
| 690 | 76.5 | 6.8 | 358 | 2 | Q6CCM7 | Q6ccm7 yarrowia li | 763 | 76 | 6.8 | 508 | 2 | Q8GYU2 | Q8gyu2 arabidopsis |
| 691 | 76.5 | 6.8 | 385 | 2 | Q9NHU9 | Q9nhu9 drosophila | 764 | 76 | 6.8 | 509 | 2 | Q6UXI9 | Q6uxi9 homo sapien |
| 692 | 76.5 | 6.8 | 433 | 2 | Q9K6G1 | Q9k6g1 bacillus ha | 765 | 76 | 6.8 | 532 | 2 | O0I972 | O0i972 caenorhabdi |
| 693 | 76.5 | 6.8 | 452 | 2 | Q6SYY7 | Q6syy7 candida alb | 766 | 76 | 6.8 | 549 | 2 | Q7PAE0 | Q7pae0 rickettsia |
| 694 | 76.5 | 6.8 | 457 | 2 | Q8GAK1 | Q8gak1 dictyosteli | 767 | 76 | 6.8 | 549 | 2 | Q9M1B1 | Q9m1b1 arabidopsis |
| 695 | 76.5 | 6.8 | 490 | 2 | Q753Y1 | Q753y1 ashbya goss | 768 | 76 | 6.8 | 569 | 2 | Q9SLI0 | Q9sl10 arabidopsis |
| 696 | 76.5 | 6.8 | 505 | 2 | Q14395 | Q14395 homo sapien | 769 | 76 | 6.8 | 576 | 2 | Q06604 | Q06604 saccharomyc |
| 697 | 76.5 | 6.8 | 520 | 2 | Q6CTM5 | Q6ctm5 kluyveromyc | 770 | 76 | 6.8 | 595 | 2 | Q7R2J1 | Q7r2j1 giardia lam |
| 698 | 76.5 | 6.8 | 542 | 2 | Q59145 | Q59145 aeromonas s | 771 | 76 | 6.8 | 612 | 2 | Q7NY06 | Q7ny06 chromobacte |
| 699 | 76.5 | 6.8 | 623 | 2 | O17562 | O17562 caenorhabdi | 772 | 76 | 6.8 | 622 | 2 | Q6V6D8 | Q6v6d8 drosophila |
| 700 | 76.5 | 6.8 | 634 | 1 | HWP1_CANAL | Hwp1_canal | 773 | 76 | 6.8 | 622 | 2 | Q6V6E2 | Q6v6e2 drosophila |
| 701 | 76.5 | 6.8 | 653 | 1 | LRR4_HUMAN | Lrr4_human | 774 | 76 | 6.8 | 622 | 2 | Q6V6E4 | Q6v6e4 drosophila |
| 702 | 76.5 | 6.8 | 658 | 1 | SHK1_SCHPO | Shk1_schpo | 775 | 76 | 6.8 | 623 | 2 | O57602 | O57602 ictalurus p |
| 703 | 76.5 | 6.8 | 676 | 2 | Q9VB94 | Q9vb94 drosophila | 776 | 76 | 6.8 | 623 | 2 | Q6V6E1 | Q6v6e1 drosophila |
| 704 | 76.5 | 6.8 | 695 | 2 | Q802U4 | Q802u4 brachydanio | 777 | 76 | 6.8 | 653 | 2 | Q73TB8 | Q73tb8 mycobacteri |
| 705 | 76.5 | 6.8 | 703 | 2 | Q75YM4 | Q75ym4 streptococc | 778 | 76 | 6.8 | 679 | 2 | Q69HN9 | Q69hn9 ciona intes |
| 706 | 76.5 | 6.8 | 718 | 2 | Q23447 | Q23447 caenorhabdi | 779 | 76 | 6.8 | 686 | 2 | Q50194 | Q50194 mycobacteri |
| 707 | 76.5 | 6.8 | 750 | 2 | Q39307 | Q39307 equid herpe | 780 | 76 | 6.8 | 725 | 2 | Q7PP40 | Q7pp40 anopheles g |
| 708 | 76.5 | 6.8 | 862 | 2 | Q8K0T1 | Q8k0t1 mus muscula | 781 | 76 | 6.8 | 725 | 2 | Q6JAD6 | Q6jad6 zea mays lm |
| 709 | 76.5 | 6.8 | 907 | 2 | Q6CTD8 | Q6ctd8 kluyveromyc | 782 | 76 | 6.8 | 768 | 2 | Q8J2T4 | Q8j2t4 grifola fro |
| 710 | 76.5 | 6.8 | 1011 | 2 | Q9NHZ9 | Q9nhz9 helicoverpa | 783 | 76 | 6.8 | 812 | 2 | Q86AW3 | Q86aw3 dictyosteli |
| 711 | 76.5 | 6.8 | 1023 | 2 | Q7M009 | Q7m009 simian cyto | 784 | 76 | 6.8 | 922 | 2 | Q95U05 | Q95u05 drosophila |
| 712 | 76.5 | 6.8 | 1201 | 2 | Q8EZH2 | Q8ezh2 leptospira | 785 | 76 | 6.8 | 954 | 2 | Q7PMB9 | Q7pmb9 anopheles g |
| 713 | 76.5 | 6.8 | 1223 | 2 | Q68FE6 | Q68fe6 mus muscula | 786 | 76 | 6.8 | 981 | 2 | Q6QOI9 | Q6qoi9 xenopus lae |
| 714 | 76.5 | 6.8 | 1259 | 2 | Q72MU1 | Q72mu1 leptospira | 787 | 76 | 6.8 | 1067 | 2 | Q6BUL7 | Q6bul7 debaromyce |
| 715 | 76.5 | 6.8 | 1362 | 2 | Q80T73 | Q80t73 mus muscula | 788 | 76 | 6.8 | 1194 | 2 | Q6C4Z0 | Q6c4z0 yarrowia li |
| 716 | 76.5 | 6.8 | 1326 | 2 | Q6FR84 | Q6fr84 candida gla | 789 | 76 | 6.8 | 1228 | 2 | Q44334 | Q44334 agrobacteri |
| 717 | 76.5 | 6.8 | 1600 | 2 | Q9XE34 | Q9xe34 oryza sativ | 790 | 76 | 6.8 | 1240 | 1 | YQJ3_CAEEL | Yqj3_caeel |
| 718 | 76.5 | 6.8 | 1672 | 1 | PMPB_CHLMU | Pmpb_chlm | 791 | 76 | 6.8 | 1263 | 2 | Q8T0M2 | Q8t0m2 drosophila |
| 719 | 76.5 | 6.8 | 1674 | 2 | Q80Z18 | Q80z18 chlamydia m | 792 | 76 | 6.8 | 1360 | 2 | Q9TYK4 | Q9tyk4 caenorhabdi |
| 720 | 76.5 | 6.8 | 1696 | 2 | Q69Q09 | Q69q09 oryza sativ | 793 | 76 | 6.8 | 1392 | 2 | Q9SDG9 | Q9sdg9 oryza sativ |
| 721 | 76.5 | 6.8 | 2335 | 2 | Q7YXR5 | Q7yxr5 cryptospori | 794 | 76 | 6.8 | 1423 | 2 | Q6CRU1 | Q6crul kluyveromyc |
| 722 | 76.5 | 6.8 | 3088 | 2 | Q68CH7 | Q68ch7 streptomyce | 795 | 76 | 6.8 | 1426 | 2 | Q9X3P6 | Q9x3p6 caidicellul |
| 723 | 76.5 | 6.8 | 3176 | 2 | Q6V7J1 | Q6v7j1 equine arte | 796 | 76 | 6.8 | 1462 | 2 | Q9V5Q8 | Q9v5q8 drosophila |
| 724 | 76.5 | 6.8 | 3176 | 2 | Q6V7J1 | Q6v7j1 equine arte | 797 | 76 | 6.8 | 1489 | 2 | O23302 | O23302 arabidopsis |
| 725 | 76.5 | 6.8 | 4736 | 2 | Q7VT99 | Q7vt99 mytilus gal | 798 | 76 | 6.8 | 1689 | 2 | Q911R1 | Q911r1 crimean-con |
| 726 | 76 | 6.8 | 167 | 2 | Q14883 | Q14883 homo sapien | 799 | 76 | 6.8 | 1789 | 2 | Q8T145 | Q8t145 dictyosteli |
| 727 | 76 | 6.8 | 243 | 2 | Q25335 | Q25335 leishmania | 800 | 76 | 6.8 | 5376 | 1 | ZAN_MOUSE | Zan_mouse |
| 728 | 76 | 6.8 | 269 | 2 | Q9VLN8 | Q9vln8 drosophila | 801 | 75.5 | 6.7 | 127 | 2 | O61035 | O61035 trypanosoma |
| 729 | 76 | 6.8 | 301 | 2 | Q924F9 | Q924f9 geomys burs | 802 | 75.5 | 6.7 | 169 | 2 | Q870Y2 | Q870y2 neurospora |
| 730 | 76 | 6.8 | 309 | 2 | Q750P9 | Q750p9 neurospora | 803 | 75.5 | 6.7 | 193 | 2 | Q8XTI3 | Q8xti3 ralstonia s |
| 731 | 76 | 6.8 | 313 | 2 | Q8BEJ1 | Q8bej1 skunkpox vi | 804 | 75.5 | 6.7 | 194 | 2 | Q9Y9W0 | Q9y9w0 aeropyrum p |
| 732 | 76 | 6.8 | 340 | 2 | Q822X8 | Q822x8 salmonella | 805 | 75.5 | 6.7 | 228 | 2 | Q8HZB6 | Q8hzb6 gorilla gor |
| 733 | 76 | 6.8 | 345 | 2 | Q8WDI1 | Q8wdi1 anolis sagr | 806 | 75.5 | 6.7 | 232 | 2 | Q69EV5 | Q69ev5 streptococc |
| 734 | 76 | 6.8 | 345 | 2 | Q690T5 | Q690t5 anolis sagr | 807 | 75.5 | 6.7 | 232 | 2 | Q69EV7 | Q69ev7 streptococc |
| 735 | 76 | 6.8 | 345 | 2 | Q690T7 | Q690t7 anolis sagr | 808 | 75.5 | 6.7 | 232 | 2 | Q69EV8 | Q69ev8 streptococc |
| 736 | 76 | 6.8 | 345 | 2 | Q690U0 | Q690u0 anolis sagr | 809 | 75.5 | 6.7 | 232 | 2 | Q69EX1 | Q69ex1 streptococc |
| 737 | 76 | 6.8 | 345 | 2 | Q690U1 | Q690u1 anolis sagr | 810 | 75.5 | 6.7 | 260 | 2 | O27007 | O27007 methanobact |
| 738 | 76 | 6.8 | 345 | 2 | Q690U3 | Q690u3 anolis sagr | 811 | 75.5 | 6.7 | 273 | 2 | P87519 | P87519 bovine herp |
| 739 | 76 | 6.8 | 345 | 2 | Q690W5 | Q690w5 anolis sagr | 812 | 75.5 | 6.7 | 273 | 2 | Q99CZ0 | Q99cz0 bovine herp |
| 740 | 76 | 6.8 | 345 | 2 | Q690W9 | Q690w9 anolis sagr | 813 | 75.5 | 6.7 | 275 | 2 | Q8DLX5 | Q8dlx5 synchococc |
| 741 | 76 | 6.8 | 345 | 2 | Q691G5 | Q691g5 anolis sagr | 814 | 75.5 | 6.7 | 282 | 2 | Q8L8N4 | Q8l8n4 arabidopsis |
| 742 | 76 | 6.8 | 345 | 2 | Q691G8 | Q691g8 anolis sagr | 815 | 75.5 | 6.7 | 299 | 2 | Q8Z2P6 | Q8z2p6 pyrobaculum |
| 743 | 76 | 6.8 | 345 | 2 | Q691Q6 | Q691q6 anolis sagr | 816 | 75.5 | 6.7 | 300 | 2 | Q95XH5 | Q95xh5 caenorhabdi |
| 744 | 76 | 6.8 | 345 | 2 | Q691T7 | Q691t7 anolis sagr | 817 | 75.5 | 6.7 | 306 | 2 | Q8AV34 | Q8av34 lactobacill |
| 745 | 76 | 6.8 | 345 | 2 | Q691U4 | Q691u4 anolis sagr | 818 | 75.5 | 6.7 | 321 | 2 | Q9XUL7 | Q9xul7 caenorhabdi |
| 746 | 76 | 6.8 | 345 | 2 | Q692A0 | Q692a0 anolis sagr | 819 | 75.5 | 6.7 | 329 | 2 | Q6FIA0 | Q6fia0 homo sapien |
| 747 | 76 | 6.8 | 345 | 2 | Q692A2 | Q692a2 anolis sagr | 820 | 75.5 | 6.7 | 329 | 2 | Q9NWV8 | Q9nwv8 homo sapien |
| 748 | 76 | 6.8 | 345 | 2 | Q692A3 | Q692a3 anolis sagr | 821 | 75.5 | 6.7 | 330 | 2 | Q8GAR7 | Q8gar7 dictyosteli |
| 749 | 76 | 6.8 | 359 | 2 | Q43656 | Q43656 homo sapien | 822 | 75.5 | 6.7 | 346 | 2 | Q9TFU7 | Q9tfu7 teratoscinc |
| 750 | 76 | 6.8 | 368 | 1 | VE2_HPV45 | P36794 human papil | 823 | 75.5 | 6.7 | 385 | 2 | Q8T8L4 | Q8t8l4 drosophila |
| 751 | 76 | 6.8 | 370 | 2 | Q9FN39 | Q9fn39 arabidopsis | 824 | 75.5 | 6.7 | 385 | 2 | Q9N666 | Q9n666 drosophila |
| 752 | 76 | 6.8 | 372 | 2 | Q8CQM2 | Q8cqm2 staphylococ | 825 | 75.5 | 6.7 | 385 | 2 | Q9NHU6 | Q9nhu6 drosophila |
| 753 | 76 | 6.8 | 374 | 2 | Q8EC31 | Q8ec31 shewanella | 826 | 75.5 | 6.7 | 385 | 2 | Q9NHU7 | Q9nhu7 drosophila |
| 754 | 76 | 6.8 | 389 | 1 | ADHA_CLOAB | Q04944 clostridium | 827 | 75.5 | 6.7 | 397 | 2 | Q702W7 | Q702w7 human herpe |
| 755 | 76 | 6.8 | 415 | 2 | Q641C6 | Q641c6 xenopus lae | 828 | 75.5 | 6.7 | 397 | 2 | Q702X1 | Q702x1 human herpe |
| 756 | 76 | 6.8 | 428 | 2 | Q86DA4 | Q86da4 caenorhabdi | 829 | 75.5 | 6.7 | 420 | 2 | Q8N7W9 | Q8n7w9 homo sapien |
| 757 | 76 | 6.8 | 429 | 2 | Q7JMU4 | Q7jmu4 caenorhabdi | 830 | 75.5 | 6.7 | 430 | 1 | PO23_RAT | Po23_rat |
| 758 | 76 | 6.8 | 431 | 1 | YMR7_CAEEL | P34474 caenorhabdi | 831 | 75.5 | 6.7 | 464 | 2 | Q90WQ6 | Q90wq6 oncorhynch |
| 759 | 76 | 6.8 | 441 | 2 | Q72NAG | Q72na6 leptospira | 832 | 75.5 | 6.7 | 468 | 1 | VAS1_BOVIN | Va1_bovin |
| 760 | 76 | 6.8 | 441 | 2 | Q8FB95 | Q8fb95 leptospira | 833 | 75.5 | 6.7 | 476 | 2 | Q6C1S9 | Q6c1s9 humicola in |
| 761 | 76 | 6.8 | 452 | 2 | Q9ADQ9 | Q9adq9 staphylococ | 834 | 75.5 | 6.7 | 478 | 2 | O61122 | O61122 dictyosteli |

| | | | | | | | | | | | | | | | |
|------|------|-----|------|---|------------|---------|--------------|------|------|-----|------|---|------------|------------|--------------|
| 981 | 74.5 | 6.6 | 467 | 2 | Q6C5E7 | Q6C5E7 | Yarrowia li | 1054 | 74 | 6.6 | 435 | 2 | O45484 | O45484 | caenorhabdi |
| 982 | 74.5 | 6.6 | 469 | 2 | Q82340 | Q82840 | nitrosomona | 1055 | 74 | 6.6 | 437 | 2 | Q9EZF7 | Q9EZF7 | streptococ |
| 983 | 74.5 | 6.6 | 474 | 2 | Q7JPF8 | Q7JPF8 | caenorhabdi | 1056 | 74 | 6.6 | 441 | 1 | END2_HUMAN | END2_HUMAN | homo sapien |
| 984 | 74.5 | 6.6 | 475 | 2 | Q22794 | Q22794 | arabidopsis | 1057 | 74 | 6.6 | 451 | 2 | Q82DJ2 | Q82DJ2 | streptomyce |
| 985 | 74.5 | 6.6 | 482 | 2 | Q20858 | Q20858 | caenorhabdi | 1058 | 74 | 6.6 | 458 | 2 | O16285 | O16285 | caenorhabdi |
| 986 | 74.5 | 6.6 | 484 | 2 | Q872J7 | Q872J7 | neurospora | 1059 | 74 | 6.6 | 464 | 2 | Q8MN43 | Q8MN43 | dictyosteli |
| 987 | 74.5 | 6.6 | 507 | 2 | Q8R4H1 | Q8R4H1 | mus musculus | 1060 | 74 | 6.6 | 467 | 2 | Q8GM73 | Q8GM73 | streptococ |
| 988 | 74.5 | 6.6 | 507 | 2 | Q6P5D7 | Q6P5D7 | mus musculus | 1061 | 74 | 6.6 | 472 | 2 | O8PLF5 | O8PLF5 | xanthomonas |
| 989 | 74.5 | 6.6 | 511 | 2 | Q8U2P63 | Q8U2P63 | human herpe | 1062 | 74 | 6.6 | 472 | 2 | O8PLF5 | O8PLF5 | xanthomonas |
| 990 | 74.5 | 6.6 | 530 | 2 | Q8BLS0 | Q8BLS0 | m mus muscu | 1063 | 74 | 6.6 | 490 | 2 | Q6V6N2 | Q6V6N2 | drosophila |
| 991 | 74.5 | 6.6 | 530 | 2 | Q9X4R5 | Q9X4R5 | m mus muscu | 1063 | 74 | 6.6 | 490 | 2 | Q6V6N6 | Q6V6N6 | drosophila |
| 992 | 74.5 | 6.6 | 567 | 1 | CHI3_CANAL | Q9X4R5 | streptococ | 1064 | 74 | 6.6 | 505 | 2 | Q8TWN8 | Q8TWN8 | methanopyru |
| 993 | 74.5 | 6.6 | 567 | 1 | Q6FR51 | P40954 | candida alb | 1065 | 74 | 6.6 | 515 | 2 | Q8Y941 | Q8Y941 | listeria mo |
| 994 | 74.5 | 6.6 | 588 | 2 | Q9VGA8 | Q6FR51 | candida gla | 1066 | 74 | 6.6 | 518 | 2 | O16283 | O16283 | caenorhabdi |
| 995 | 74.5 | 6.6 | 606 | 2 | Q8E522 | Q9VGA8 | drosophila | 1067 | 74 | 6.6 | 538 | 2 | Q967D0 | Q967D0 | geodia cydo |
| 996 | 74.5 | 6.6 | 612 | 2 | Q9FS24 | Q8E522 | caenorhabdi | 1068 | 74 | 6.6 | 542 | 1 | SCWB_YEAST | SCWB_YEAST | saccharomyc |
| 997 | 74.5 | 6.6 | 626 | 2 | Q6UDE6 | Q9FS24 | vigna ungui | 1069 | 74 | 6.6 | 543 | 2 | Q7YZ30 | Q7YZ30 | cryptospori |
| 998 | 74.5 | 6.6 | 635 | 2 | Q9LJD5 | Q6UDE6 | schizophyll | 1070 | 74 | 6.6 | 551 | 2 | Q815U4 | Q815U4 | bagillus ce |
| 999 | 74.5 | 6.6 | 636 | 2 | Q66HZ5 | Q9LJD5 | lycopersico | 1071 | 74 | 6.6 | 578 | 2 | Q63ZX6 | Q63ZX6 | mus musculu |
| 1000 | 74.5 | 6.6 | 678 | 2 | Q92K48 | Q66HZ5 | brachydanio | 1072 | 74 | 6.6 | 581 | 2 | Q7SGW5 | Q7SGW5 | neurospora |
| 1001 | 74.5 | 6.6 | 709 | 2 | O16783 | Q92K48 | rhizobium m | 1073 | 74 | 6.6 | 586 | 2 | Q8A118 | Q8A118 | saccharomyc |
| 1002 | 74.5 | 6.6 | 751 | 2 | Q7RSB7 | O16783 | caenorhabdi | 1074 | 74 | 6.6 | 600 | 1 | PRCK_CHLCV | PRCK_CHLCV | chlamydophi |
| 1003 | 74.5 | 6.6 | 806 | 2 | Q7RXW7 | Q7RSB7 | neurospora | 1075 | 74 | 6.6 | 600 | 2 | Q9T0K6 | Q9T0K6 | arabidopsis |
| 1004 | 74.5 | 6.6 | 812 | 2 | O52504 | Q7RXW7 | thermotoga | 1076 | 74 | 6.6 | 601 | 2 | Q6V6S0 | Q6V6S0 | drosophila |
| 1005 | 74.5 | 6.6 | 813 | 2 | O87964 | O52504 | thermotoga | 1077 | 74 | 6.6 | 602 | 2 | Q8W4K6 | Q8W4K6 | arabidopsis |
| 1006 | 74.5 | 6.6 | 841 | 2 | O9A002 | Q87964 | candida alb | 1078 | 74 | 6.6 | 647 | 2 | Q7S5I2 | Q7S5I2 | neurospora |
| 1007 | 74.5 | 6.6 | 849 | 2 | P87107 | O9A002 | saccharomyc | 1079 | 74 | 6.6 | 666 | 2 | Q7QXK0 | Q7QXK0 | giardia lam |
| 1008 | 74.5 | 6.6 | 860 | 1 | CHI2_COCIM | P87107 | saccharomyc | 1080 | 74 | 6.6 | 691 | 2 | Q8BNQ7 | Q8BNQ7 | debaromyce |
| 1009 | 74.5 | 6.6 | 896 | 1 | MUTS_LACPL | P54197 | coccidioides | 1081 | 74 | 6.6 | 725 | 2 | Q9CV93 | Q9CV93 | mus musculu |
| 1010 | 74.5 | 6.6 | 909 | 1 | LDL1_XENLA | Q88U27 | lactobacill | 1082 | 74 | 6.6 | 783 | 2 | Q7SA55 | Q7SA55 | ashbya goss |
| 1011 | 74.5 | 6.6 | 910 | 2 | Q9D4H6 | Q99087 | xenopus lae | 1083 | 74 | 6.6 | 794 | 2 | Q6LP23 | Q6LP23 | photobacter |
| 1012 | 74.5 | 6.6 | 998 | 1 | EPB3_HUMAN | Q9D4H6 | m mus muscu | 1084 | 74 | 6.6 | 809 | 2 | Q7SDN1 | Q7SDN1 | neurospora |
| 1013 | 74.5 | 6.6 | 998 | 2 | Q7Z740 | P54753 | homo sapien | 1085 | 74 | 6.6 | 835 | 2 | Q7R2W3 | Q7R2W3 | giardia lam |
| 1014 | 74.5 | 6.6 | 1009 | 2 | Q6CTH0 | Q7Z740 | homo sapien | 1086 | 74 | 6.6 | 860 | 1 | ENV_HV2BE | ENV_HV2BE | human immun |
| 1015 | 74.5 | 6.6 | 1032 | 2 | Q6XLI7 | Q6CTH0 | kluyveromyc | 1087 | 74 | 6.6 | 873 | 2 | Q9NYU3 | Q9NYU3 | homo sapien |
| 1016 | 74.5 | 6.6 | 1074 | 2 | Q8COP8 | Q6XLI7 | rattus norv | 1088 | 74 | 6.6 | 906 | 2 | Q97YQ1 | Q97YQ1 | sulfolobus |
| 1017 | 74.5 | 6.6 | 1075 | 1 | FLOS_YEAST | Q8COP8 | mus musculu | 1089 | 74 | 6.6 | 1047 | 2 | Q24019 | Q24019 | drosophila |
| 1018 | 74.5 | 6.6 | 1089 | 2 | Q86KPF4 | P38894 | saccharomyc | 1090 | 74 | 6.6 | 1100 | 2 | Q9VUE7 | Q9VUE7 | drosophila |
| 1019 | 74.5 | 6.6 | 1091 | 2 | Q7SDT8 | Q86KPF4 | dictyosteli | 1091 | 74 | 6.6 | 1226 | 2 | Q9NZB6 | Q9NZB6 | homo sapien |
| 1020 | 74.5 | 6.6 | 1100 | 1 | TCGI_MOUSE | Q7SDT8 | neurospora | 1092 | 74 | 6.6 | 1248 | 2 | Q8AUP9 | Q8AUP9 | oryza sativ |
| 1021 | 74.5 | 6.6 | 1126 | 2 | Q9EQJ9 | Q8CGF7 | mus musculu | 1093 | 74 | 6.6 | 1342 | 2 | Q9GPP6 | Q9GPP6 | drosophila |
| 1022 | 74.5 | 6.6 | 1170 | 2 | Q69ZE1 | Q9EQJ9 | mus musculu | 1094 | 74 | 6.6 | 1342 | 2 | Q9VPZ7 | Q9VPZ7 | drosophila |
| 1023 | 74.5 | 6.6 | 1209 | 2 | Q7SZF4 | Q69ZE1 | mus musculu | 1095 | 74 | 6.6 | 1355 | 2 | Q86AM1 | Q86AM1 | dictyosteli |
| 1024 | 74.5 | 6.6 | 1233 | 1 | MUSA_HUMAN | Q7SZF4 | brachydanio | 1096 | 74 | 6.6 | 1371 | 2 | Q8BV57 | Q8BV57 | mus musculu |
| 1025 | 74.5 | 6.6 | 1388 | 1 | CAIE_HUMAN | P98088 | homo sapien | 1097 | 74 | 6.6 | 1378 | 2 | Q8SQI2 | Q8SQI2 | sarcophaga |
| 1026 | 74.5 | 6.6 | 1720 | 2 | Q81486 | P39059 | homo sapien | 1098 | 74 | 6.6 | 1455 | 2 | Q7RYI6 | Q7RYI6 | neurospora |
| 1027 | 74.5 | 6.6 | 1790 | 2 | Q81816 | Q81486 | plasmodium | 1099 | 74 | 6.6 | 1469 | 2 | Q7S3S3 | Q7S3S3 | neurospora |
| 1028 | 74.5 | 6.6 | 1838 | 1 | CAI5_HUMAN | Q81816 | aplysia cal | 1100 | 74 | 6.6 | 2071 | 2 | Q8GZY7 | Q8GZY7 | neurospora |
| 1029 | 74.5 | 6.6 | 1838 | 2 | Q15094 | P20908 | homo sapien | 1101 | 74 | 6.6 | 2414 | 1 | P300_HUMAN | P300_HUMAN | homo sapien |
| 1030 | 74.5 | 6.6 | 1969 | 2 | Q7SEZ5 | Q15094 | homo sapien | 1102 | 74 | 6.6 | 4060 | 2 | Q9THZ8 | Q9THZ8 | gill-associ |
| 1031 | 74.5 | 6.6 | 2888 | 1 | ZEPI_MOUSE | Q7SEZ5 | neurospora | 1103 | 74 | 6.6 | 4498 | 2 | Q9W2Z3 | Q9W2Z3 | drosophila |
| 1032 | 74 | 6.6 | 147 | 1 | IRI3_HCMVA | Q03172 | mus musculu | 1104 | 73.5 | 6.5 | 143 | 2 | O15776 | O15776 | trypanosoma |
| 1033 | 74 | 6.6 | 147 | 2 | Q7M575 | P16811 | human cytom | 1105 | 73.5 | 6.5 | 166 | 2 | Q94J61 | Q94J61 | oryza sativ |
| 1034 | 74 | 6.6 | 172 | 2 | Q8WTL2 | Q7M575 | human cytom | 1106 | 73.5 | 6.5 | 217 | 2 | Q6FM83 | Q6FM83 | candida gla |
| 1035 | 74 | 6.6 | 192 | 2 | O02817 | Q8WTL2 | caenorhabdi | 1107 | 73.5 | 6.5 | 225 | 2 | P89669 | P89669 | san miguel |
| 1036 | 74 | 6.6 | 218 | 2 | Q9XCK5 | Q02817 | oryctolagus | 1108 | 73.5 | 6.5 | 286 | 2 | O8CB51 | O8CB51 | mus musculu |
| 1037 | 74 | 6.6 | 223 | 2 | O02255 | Q9XCK5 | streptococ | 1109 | 73.5 | 6.5 | 290 | 1 | LECR_CLALU | LECR_CLALU | cladraetis |
| 1038 | 74 | 6.6 | 267 | 2 | Q6CLX9 | O02255 | caenorhabdi | 1110 | 73.5 | 6.5 | 304 | 2 | Q9QNN4 | Q9QNN4 | lymphocyctic |
| 1039 | 74 | 6.6 | 340 | 2 | Q88L40 | Q6CLX9 | kluyveromyc | 1111 | 73.5 | 6.5 | 304 | 2 | Q9QNN5 | Q9QNN5 | lymphocyctic |
| 1040 | 74 | 6.6 | 345 | 2 | Q690W7 | Q88L40 | pseudomonas | 1112 | 73.5 | 6.5 | 304 | 2 | Q9QNN6 | Q9QNN6 | lymphocyctic |
| 1041 | 74 | 6.6 | 345 | 2 | Q690X9 | Q690W7 | anolis sagr | 1113 | 73.5 | 6.5 | 304 | 2 | Q9QNN7 | Q9QNN7 | lymphocyctic |
| 1042 | 74 | 6.6 | 345 | 2 | Q691U5 | Q690X9 | anolis sagr | 1114 | 73.5 | 6.5 | 304 | 2 | Q9QNN8 | Q9QNN8 | lymphocyctic |
| 1043 | 74 | 6.6 | 358 | 2 | Q8FQU1 | Q691U5 | anolis sagr | 1115 | 73.5 | 6.5 | 304 | 2 | Q9QNN9 | Q9QNN9 | lymphocyctic |
| 1044 | 74 | 6.6 | 364 | 2 | Q96D42 | Q8FQU1 | corynebacte | 1116 | 73.5 | 6.5 | 304 | 2 | Q9QNP0 | Q9QNP0 | lymphocyctic |
| 1045 | 74 | 6.6 | 367 | 2 | Q7YUQ8 | Q96D42 | homo sapien | 1117 | 73.5 | 6.5 | 304 | 2 | Q9QNP1 | Q9QNP1 | lymphocyctic |
| 1046 | 74 | 6.6 | 369 | 2 | Q7YUQ3 | Q7YUQ8 | trypanosoma | 1118 | 73.5 | 6.5 | 304 | 2 | Q9QNP2 | Q9QNP2 | lymphocyctic |
| 1047 | 74 | 6.6 | 392 | 2 | Q89HN7 | Q7YUQ3 | trypanosoma | 1119 | 73.5 | 6.5 | 304 | 2 | Q9QNP3 | Q9QNP3 | lymphocyctic |
| 1048 | 74 | 6.6 | 397 | 2 | Q97GX2 | Q89HN7 | bradyrhizob | 1120 | 73.5 | 6.5 | 304 | 2 | Q9QNP4 | Q9QNP4 | lymphocyctic |
| 1049 | 74 | 6.6 | 408 | 2 | Q6UDF5 | Q97GX2 | clostridium | 1121 | 73.5 | 6.5 | 336 | 2 | Q9HF70 | Q9HF70 | candida dub |
| 1050 | 74 | 6.6 | 418 | 2 | Q21941 | Q6UDF5 | psittacid h | 1122 | 73.5 | 6.5 | 336 | 2 | Q6W762 | Q6W762 | homo sapien |
| 1051 | 74 | 6.6 | 431 | 2 | Q90410 | Q21941 | caenorhabdi | 1123 | 73.5 | 6.5 | 337 | 2 | Q872L8 | Q872L8 | neurospora |
| 1052 | 74 | 6.6 | 431 | 1 | MNS1_MACFA | Q90410 | brachydanio | 1124 | 73.5 | 6.5 | 338 | 2 | O43420 | O43420 | homo sapien |
| 1053 | 74 | 6.6 | 435 | 2 | Q783T5 | Q95KG7 | macaca fasc | 1125 | 73.5 | 6.5 | 358 | 2 | Q8YNI5 | Q8YNI5 | anabaena sp |
| | | | | | | Q783T5 | neurospora | 1126 | 73.5 | 6.5 | 365 | 1 | PMA2_MOUSE | PMA2_MOUSE | mus musculu |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|------------|---------------------|------|------|-----|------|---|------------|---------------------|
| 1127 | 73.5 | 6.5 | 367 | 2 | Q9P018 | Q9p018 homo sapien | 1200 | 73.5 | 6.5 | 1689 | 2 | Q8JS22 | Q8jazz2 crimean-con |
| 1128 | 73.5 | 6.5 | 369 | 2 | Q96V15 | Q96v15 pneumocysti | 1201 | 73.5 | 6.5 | 1752 | 2 | Q86XN2 | Q86xq7 dictyosteli |
| 1129 | 73.5 | 6.5 | 371 | 2 | Q25333 | Q25333 leishmania | 1202 | 73.5 | 6.5 | 1761 | 2 | Q86XN2 | Q86xq7 dictyosteli |
| 1130 | 73.5 | 6.5 | 385 | 2 | Q9NHV0 | Q9nhv0 drosophila | 1203 | 73.5 | 6.5 | 1937 | 2 | Q9VT17 | Q9vt17 drosophila |
| 1131 | 73.5 | 6.5 | 385 | 2 | Q9NHV2 | Q9nhv2 drosophila | 1204 | 73.5 | 6.5 | 2081 | 2 | Q8HJ37 | Q8hj37 thermoplas |
| 1132 | 73.5 | 6.5 | 385 | 2 | Q9NHV3 | Q9nhv3 drosophila | 1205 | 73.5 | 6.5 | 2232 | 2 | Q8HJ37 | Q8hj37 thermoplas |
| 1133 | 73.5 | 6.5 | 389 | 2 | Q6GXX1 | Q6gxx1 swine hepat | 1206 | 73.5 | 6.5 | 2338 | 2 | Q8HJ37 | Q8hj37 thermoplas |
| 1134 | 73.5 | 6.5 | 407 | 2 | Q865F6 | Q865f6 macaca neme | 1207 | 73.5 | 6.5 | 2527 | 2 | Q9V7F2 | Q9v7f2 drosophila |
| 1135 | 73.5 | 6.5 | 415 | 2 | Q7X148 | Q7x148 oryza sativ | 1208 | 73.5 | 6.5 | 3176 | 1 | CA36_HUMAN | P12111 homo sapien |
| 1136 | 73.5 | 6.5 | 447 | 2 | Q63348 | Q63348 rattus norv | 1209 | 73 | 6.5 | 143 | 2 | Q61028 | Q61028 trypanosoma |
| 1137 | 73.5 | 6.5 | 451 | 2 | Q95144 | Q95144 cercopithe | 1210 | 73 | 6.5 | 172 | 2 | Q7PRG9 | Q7prg9 anopheles g |
| 1138 | 73.5 | 6.5 | 460 | 2 | Q95144 | Q95144 cercopithe | 1211 | 73 | 6.5 | 256 | 2 | Q6L3V7 | Q6l3v7 solanum dem |
| 1139 | 73.5 | 6.5 | 464 | 2 | Q9C247 | Q9c247 neurospora | 1212 | 73 | 6.5 | 260 | 2 | Q90274 | Q90274 brachydanio |
| 1140 | 73.5 | 6.5 | 476 | 2 | Q6AYP5 | Q6ayp5 rattus norv | 1213 | 73 | 6.5 | 261 | 2 | Q844J7 | Q844j7 lactobacill |
| 1141 | 73.5 | 6.5 | 484 | 1 | GUX_CELFI | P07986 cellulomona | 1214 | 73 | 6.5 | 327 | 2 | Q25334 | Q25334 leishmania |
| 1142 | 73.5 | 6.5 | 485 | 2 | Q59277 | Q59277 cellulomona | 1215 | 73 | 6.5 | 335 | 2 | Q14652 | Q14652 homo sapien |
| 1143 | 73.5 | 6.5 | 510 | 2 | Q6M375 | Q6m375 bdellovibri | 1216 | 73 | 6.5 | 340 | 2 | Q8W763 | Q8w763 homo sapien |
| 1144 | 73.5 | 6.5 | 511 | 1 | VGJC_HHV1K | P28986 human herpe | 1217 | 73 | 6.5 | 343 | 2 | Q6GJP6 | Q6gjp6 staphylococ |
| 1145 | 73.5 | 6.5 | 534 | 2 | Q8KJ12 | Q8kj12 streptococc | 1218 | 73 | 6.5 | 345 | 2 | Q9VJ23 | Q9vj23 drosophila |
| 1146 | 73.5 | 6.5 | 534 | 2 | Q9Y156 | Q9y156 gallus gall | 1219 | 73 | 6.5 | 345 | 2 | Q690U4 | Q690u4 anolis sagr |
| 1147 | 73.5 | 6.5 | 537 | 2 | Q96UK5 | Q96uk5 coccidioide | 1220 | 73 | 6.5 | 345 | 2 | Q690W4 | Q690w4 anolis sagr |
| 1148 | 73.5 | 6.5 | 542 | 2 | Q18637 | Q18637 caenorhabdi | 1221 | 73 | 6.5 | 345 | 2 | Q891H0 | Q891h0 anolis sagr |
| 1149 | 73.5 | 6.5 | 558 | 2 | Q6M2G6 | Q6m2g6 homo sapien | 1222 | 73 | 6.5 | 345 | 2 | Q891H0 | Q891h0 anolis sagr |
| 1150 | 73.5 | 6.5 | 565 | 2 | Q6ND51 | Q6nd51 rhodospseudo | 1223 | 73 | 6.5 | 345 | 2 | Q691T6 | Q691t6 anolis sagr |
| 1151 | 73.5 | 6.5 | 566 | 2 | Q96M23 | Q96m23 homo sapien | 1224 | 73 | 6.5 | 345 | 2 | Q692B8 | Q692b8 anolis sagr |
| 1152 | 73.5 | 6.5 | 575 | 1 | CH61_CUCMA | Q05045 cucurbita m | 1225 | 73 | 6.5 | 365 | 2 | Q6G110 | Q6g110 bartonella |
| 1153 | 73.5 | 6.5 | 594 | 2 | Q75UN9 | Q75un9 haliotis di | 1226 | 73 | 6.5 | 385 | 2 | Q8T8I7 | Q8t8i7 drosophila |
| 1154 | 73.5 | 6.5 | 594 | 2 | Q86M37 | Q86m37 haliotis di | 1227 | 73 | 6.5 | 385 | 2 | Q8T8I9 | Q8t8i9 drosophila |
| 1155 | 73.5 | 6.5 | 595 | 1 | TNR8_HUMAN | P28908 homo sapien | 1228 | 73 | 6.5 | 395 | 2 | Q8CAU7 | Q8cau7 yarrowia li |
| 1156 | 73.5 | 6.5 | 601 | 2 | Q97YX7 | Q97yx7 sulfolobus | 1229 | 73 | 6.5 | 417 | 2 | Q9VLA9 | Q9vla9 drosophila |
| 1157 | 73.5 | 6.5 | 602 | 2 | Q9V1P0 | Q9v1p0 drosophila | 1230 | 73 | 6.5 | 418 | 2 | Q43421 | Q43421 homo sapien |
| 1158 | 73.5 | 6.5 | 608 | 2 | Q6NP13 | Q6np13 drosophila | 1231 | 73 | 6.5 | 441 | 2 | Q43421 | Q43421 homo sapien |
| 1159 | 73.5 | 6.5 | 626 | 2 | Q8Y5N1 | Q8y5n1 listeria mo | 1232 | 73 | 6.5 | 459 | 2 | Q9H915 | Q9h915 homo sapien |
| 1160 | 73.5 | 6.5 | 664 | 2 | Q96PV8 | Q96pv8 homo sapien | 1233 | 73 | 6.5 | 461 | 2 | Q9P3J7 | Q9p3j7 neurospora |
| 1161 | 73.5 | 6.5 | 670 | 1 | YFGG_SCHPO | O13854 schizosacch | 1234 | 73 | 6.5 | 472 | 1 | YACA_BACSU | P37563 bacillus su |
| 1162 | 73.5 | 6.5 | 677 | 2 | Q9FNB7 | Q9fnb7 arabidopsis | 1235 | 73 | 6.5 | 492 | 1 | GAA3_BOVIN | P10064 bos taurus |
| 1163 | 73.5 | 6.5 | 679 | 2 | Q8GY46 | Q8gy46 arabidopsis | 1236 | 73 | 6.5 | 495 | 2 | Q63P57 | Q63p57 burkholderi |
| 1164 | 73.5 | 6.5 | 708 | 2 | Q9CCY4 | Q9ccy4 mycobacteri | 1237 | 73 | 6.5 | 507 | 2 | Q9HA16 | Q9ha16 homo sapien |
| 1165 | 73.5 | 6.5 | 720 | 2 | Q8N6M6 | Q8n6m6 homo sapien | 1238 | 73 | 6.5 | 528 | 1 | FIT1_YEAST | Q04433 saccharomyc |
| 1166 | 73.5 | 6.5 | 720 | 2 | Q8NLF6 | Q8nlf6 corynebacte | 1239 | 73 | 6.5 | 530 | 2 | Q8FT30 | Q8ft30 candida gla |
| 1167 | 73.5 | 6.5 | 733 | 2 | Q618T9 | Q618t9 cucumis sat | 1240 | 73 | 6.5 | 533 | 2 | Q9BTQ8 | Q9btq8 homo sapien |
| 1168 | 73.5 | 6.5 | 734 | 2 | O35930 | Q35930 mus musculu | 1241 | 73 | 6.5 | 544 | 1 | GP10_DICDI | Q06885 dictyosteli |
| 1169 | 73.5 | 6.5 | 754 | 2 | Q6DFX1 | Q6dfx1 mus musculu | 1242 | 73 | 6.5 | 550 | 2 | Q9RY21 | Q9ry21 deinococcus |
| 1170 | 73.5 | 6.5 | 794 | 2 | O18742 | O18742 bos taurus | 1243 | 73 | 6.5 | 582 | 2 | Q24160 | Q24160 drosophila |
| 1171 | 73.5 | 6.5 | 806 | 2 | O28874 | O28874 archaeoglob | 1244 | 73 | 6.5 | 600 | 1 | PPCK_CHLPN | Q92755 chlamydia p |
| 1172 | 73.5 | 6.5 | 820 | 2 | O18743 | O18743 bos taurus | 1245 | 73 | 6.5 | 637 | 2 | Q80ZE7 | Q80ze7 rattus norv |
| 1173 | 73.5 | 6.5 | 825 | 2 | Q873Y0 | Q873y0 aspergillus | 1246 | 73 | 6.5 | 639 | 1 | CZAP_HUMAN | Q9Y5K6 homo sapien |
| 1174 | 73.5 | 6.5 | 829 | 2 | Q7RW40 | Q7rw40 neurospora | 1247 | 73 | 6.5 | 645 | 2 | Q7PWE4 | Q7pwe4 anopheles g |
| 1175 | 73.5 | 6.5 | 830 | 2 | O53129 | O53129 mycobacteri | 1248 | 73 | 6.5 | 652 | 2 | Q83364 | Q83364 murine leuk |
| 1176 | 73.5 | 6.5 | 835 | 2 | O57075 | O57075 bombyx mori | 1249 | 73 | 6.5 | 656 | 2 | Q76184 | Q76184 mus musculu |
| 1177 | 73.5 | 6.5 | 838 | 2 | Q9VOA9 | Q9vga9 drosophila | 1250 | 73 | 6.5 | 681 | 1 | VGP_MABVP | P35254 marburg vir |
| 1178 | 73.5 | 6.5 | 866 | 2 | O39781 | Q39781 equid herpe | 1251 | 73 | 6.5 | 681 | 2 | Q71VM1 | Q71vml lake victor |
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| 1182 | 73.5 | 6.5 | 939 | 2 | Q69ZZ9 | Q69zz9 mus musculu | 1255 | 73 | 6.5 | 719 | 2 | Q6DJ90 | Q6dj90 xenopus tro |
| 1183 | 73.5 | 6.5 | 943 | 1 | YL61_SCHPO | Q8tf99 schizosacch | 1256 | 73 | 6.5 | 728 | 2 | Q19182 | Q19182 caenorhabdi |
| 1184 | 73.5 | 6.5 | 968 | 2 | Q6BEV7 | Q6bev7 caenorhabdi | 1257 | 73 | 6.5 | 741 | 2 | Q7QVE9 | Q7qve9 giardia lam |
| 1185 | 73.5 | 6.5 | 976 | 2 | Q9A531 | Q9a531 caulobacter | 1258 | 73 | 6.5 | 748 | 2 | Q9Y6E1 | Q9y6e1 homo sapien |
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| 1189 | 73.5 | 6.5 | 1016 | 2 | Q17718 | Q17718 caenorhabdi | 1262 | 73 | 6.5 | 780 | 2 | Q6DFV2 | Q6dfv2 mus musculu |
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| 1191 | 73.5 | 6.5 | 1033 | 2 | Q6Q121 | Q6q121 aspergillus | 1264 | 73 | 6.5 | 782 | 1 | SP4_MOUSE | Q62445 mus musculu |
| 1192 | 73.5 | 6.5 | 1036 | 2 | Q9VUK6 | Q9vuk6 drosophila | 1265 | 73 | 6.5 | 784 | 2 | Q9H5A0 | Q9h5a0 homo sapien |
| 1193 | 73.5 | 6.5 | 1124 | 2 | Q810N9 | Q810n9 caenorhabdi | 1266 | 73 | 6.5 | 801 | 2 | Q6P2S1 | Q6p2e1 homo sapien |
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| 1280 | 73 | 6.5 | 1016 | 1 | ENGL1_SCHPO | Q9ut45 schizosacch | 1353 | 72.5 | 6.4 | 685 | 2 | O40935 | O40935 human herpe |
| 1281 | 73 | 6.5 | 1104 | 2 | Q9VQP6 | Q9vqp6 drosophila | 1354 | 72.5 | 6.4 | 691 | 2 | O92608 | O92608 human herpe |
| 1282 | 73 | 6.5 | 1163 | 2 | Q8F613 | Q8f613 leptospira | 1355 | 72.5 | 6.4 | 698 | 2 | Q8UKG8 | Q8ukg8 heliothis z |
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| 1298 | 73 | 6.5 | 8545 | 2 | Q6TME3 | Q6imp3 caenorhabdi | 1371 | 72.5 | 6.4 | 800 | 1 | ASNT_RAT | P41739 rattus norv |
| 1299 | 72.5 | 6.4 | 123 | 2 | Q61027 | Q61027 trypanosoma | 1372 | 72.5 | 6.4 | 800 | 2 | Q80T29 | Q80t29 rattus norv |
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| 1303 | 72.5 | 6.4 | 236 | 1 | SLR1_RALSO | P58590 ralstonia s | 1376 | 72.5 | 6.4 | 859 | 2 | Q8IWC2 | Q8iwc2 homo sapien |
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| 1307 | 72.5 | 6.4 | 311 | 2 | Q8VCV1 | Q8vcv1 mus musculu | 1380 | 72.5 | 6.4 | 907 | 2 | Q66537 | Q66537 human herpe |
| 1308 | 72.5 | 6.4 | 321 | 2 | Q8XUL6 | Q8xul6 caenorhabdi | 1381 | 72.5 | 6.4 | 907 | 2 | Q777F0 | Q777f0 human herpe |
| 1309 | 72.5 | 6.4 | 332 | 2 | Q8V0L9 | Q8v0l9 equid herpe | 1382 | 72.5 | 6.4 | 927 | 2 | Q6FXK6 | Q6fxk6 candida gla |
| 1310 | 72.5 | 6.4 | 333 | 2 | Q9JUJ2 | Q9juj2 mus musculu | 1383 | 72.5 | 6.4 | 930 | 2 | Q9YBL5 | Q9ybl5 aeropyrum p |
| 1311 | 72.5 | 6.4 | 333 | 2 | Q8C5Q8 | Q8c5q8 mus musculu | 1384 | 72.5 | 6.4 | 967 | 2 | Q8Y8G0 | Q8y8g0 candida alb |
| 1312 | 72.5 | 6.4 | 337 | 2 | P95738 | P95738 staphylococ | 1385 | 72.5 | 6.4 | 974 | 1 | EPB3_XENLA | EPB3 xenopus lae |
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| 1314 | 72.5 | 6.4 | 337 | 2 | Q8VOM1 | Q8v0m1 equid herpe | 1387 | 72.5 | 6.4 | 992 | 2 | Q7TT14 | Q7tt14 mus musculu |
| 1315 | 72.5 | 6.4 | 338 | 2 | Q9CLF8 | Q9clf8 pasteurella | 1388 | 72.5 | 6.4 | 1002 | 1 | RBMC_MOUSE | RBm4x3 mus musculu |
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| 1317 | 72.5 | 6.4 | 344 | 2 | Q6XAV5 | Q6axv5 rattus norv | 1390 | 72.5 | 6.4 | 1021 | 1 | BUB1_YEAST | B41695 saccharomyc |
| 1318 | 72.5 | 6.4 | 356 | 2 | Q8VOL7 | Q8v0l7 equid herpe | 1391 | 72.5 | 6.4 | 1060 | 2 | Q6E6AN6 | Q6e6an6 dictyosteli |
| 1319 | 72.5 | 6.4 | 357 | 2 | Q8VOM2 | Q8v0m2 equid herpe | 1392 | 72.5 | 6.4 | 1138 | 2 | Q6PHT6 | Q6pht6 mus musculu |
| 1320 | 72.5 | 6.4 | 362 | 2 | Q7NSJ3 | Q7nsj3 chromobacte | 1393 | 72.5 | 6.4 | 1149 | 2 | Q6PCL1 | Q6pcl1 xenopus lae |
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| 1322 | 72.5 | 6.4 | 374 | 2 | Q8XVL6 | Q8xvl6 equid herpe | 1395 | 72.5 | 6.4 | 1180 | 2 | Q9CHH4 | Q9chh4 lactococcus |
| 1323 | 72.5 | 6.4 | 382 | 2 | Q9XWQ0 | Q9xwq0 caenorhabdi | 1396 | 72.5 | 6.4 | 1243 | 2 | Q8JXK6 | Q8jxk6 heliothis z |
| 1324 | 72.5 | 6.4 | 383 | 2 | Q702X5 | Q702x5 human herpe | 1397 | 72.5 | 6.4 | 1284 | 2 | Q8RQU9 | Q8rqu9 bacillus gi |
| 1325 | 72.5 | 6.4 | 388 | 2 | Q966V2 | Q966v2 halocynthia | 1398 | 72.5 | 6.4 | 1490 | 2 | Q9U485 | Q9u485 drosophila |
| 1326 | 72.5 | 6.4 | 389 | 2 | Q8VOM0 | Q8v0m0 equid herpe | 1399 | 72.5 | 6.4 | 1666 | 2 | Q8MXG2 | Q8mxg2 caenorhabdi |
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| 1330 | 72.5 | 6.4 | 442 | 2 | Q758Q5 | Q758q5 ashbya goss | 1403 | 72.5 | 6.4 | 1811 | 2 | Q9QXM9 | Q9qxm9 mus musculu |
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| 1334 | 72.5 | 6.4 | 487 | 2 | Q75JY9 | Q75jy9 dictyosteli | 1407 | 72.5 | 6.4 | 1975 | 2 | Q6Y8G2 | Q6y8g2 candida alb |
| 1335 | 72.5 | 6.4 | 497 | 2 | Q8WY24 | Q8wy24 homo sapien | 1408 | 72.5 | 6.4 | 1986 | 2 | Q9QXN0 | Q9qxn0 mus musculu |
| 1336 | 72.5 | 6.4 | 498 | 1 | VGLY_LYCV | P09991 lymphocytic | 1409 | 72.5 | 6.4 | 2031 | 2 | Q6Y8G1 | Q6y8g1 candida alb |
| 1337 | 72.5 | 6.4 | 518 | 2 | Q72VW7 | Q72vw7 leptospira | 1410 | 72.5 | 6.4 | 2066 | 2 | Q9DDV8 | Q9ddv8 xenopus lae |
| 1338 | 72.5 | 6.4 | 518 | 2 | Q8F9H6 | Q8f9h6 leptospira | 1411 | 72.5 | 6.4 | 2297 | 2 | Q9HGK6 | Q9hgk6 candida alb |
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| 1341 | 72.5 | 6.4 | 540 | 1 | CH60_STRGN | Q8vc58 streptococ | 1414 | 72.5 | 6.4 | 155 | 2 | Q6GE28 | Q6ge28 staphylococ |
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| 1344 | 72.5 | 6.4 | 563 | 2 | Q72V40 | Q72v40 bacillus ce | 1417 | 72 | 6.4 | 171 | 1 | CASK_TRAJA | Q29137 tragulus ja |
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QY 121 NSCIPETITKDPINFNTQTATOTTEFIIVSDTSYVSPASTIPAPTTTPPAPASTSIPRR 180
Db 137 NSCIPETITKDPINFNTQTATOTTEFIIVSDTSYVSPASTIPAPTTTPPAPASTSIPRR 196
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RESULT 2
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DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Extracellular link domain containing 1.
GN Name=XLKD1;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RN [1]
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RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek A., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC026231; AAH26231.1; -.
DR HSSP; P98066; 107B.
DR Genew; HGNC:14687; XLKD1.
DR GO; GO:0005540; F-hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
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DR ProDom; PD000918; Link; 1.
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DR PROSITE; PS00963; LINK 2; 1.
SQ SEQUENCE 322 AA; 35183 MW; 0B1EDBD76CE4610A CRC64;

Query Match 98.8%; Score 1111; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 6.4e-89;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRLLVGSLRAELSLIVSCRMIGITLVSKKANQQLNFTEAKACRLGLSLAGKQDVET 60
Db 17 TRLLVGSLRAELSLIVSCRMIGITLVSKKANQQLNFTEAKACRLGLSLAGKQDVET 76
QY 61 ALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 197 KKLICVTEVFMTSTMTSTETETPFVFNKAAAFKNEAAGFG 234

RESULT 3
Q9Y5Y7
ID Q9Y5Y7 PRELIMINARY; PRT; 322 AA.
AC Q9Y5Y7;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
RA Jackson D.G.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
RL receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801 (1999).
DR EMBL; AF118108; AAD42764.1; -.
DR HSSP; P98066; 107B.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006928; P:cell motility; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
DR GO; GO:0009653; P:morphogenesis; TAS.
DR GO; GO:0009611; P:response to wounding; TAS.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS00963; LINK_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35238 MW; 0EBEA56729CEFF7 CRC64;

Query Match 98.3%; Score 1106; DB 2; Length 322;
Best Local Similarity 98.6%; Pred. No. 1.8e-88;
Matches 215; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TRLLVGSLRAELSLIVSCRMIGITLVSKKANQQLNFTEAKACRLGLSLAGKQDVET 60
Db 17 TRLLVGSLRAELSLIVSCRMIGITLVSKKANQQLNFTEAKACRLGLSLAGKQDVET 76
QY 61 ALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 77 ALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
QY 121 NSCIPETITKDPINFNTQTATOTTEFIIVSDTSYVSPASTIPAPTTTPPAPASTSIPRR 180
Db 137 NSRIPETITKDPINFNTQTATOTTEFIIVSDTSYVSPASTIPAPTTTPPAPASTSIPRR 196
QY 181 KKLICVTEVFMTSTMTSTETETPFVFNKAAAFKNEAAGFG 218
Db 197 KKLICVTEVFMTSTMTSTETETPFVFNKAAAFKNEAAGFG 234

RESULT 4
Q6UCB8

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ID Q9C88 PRELIMINARY; PRT; 322 AA.
AC Q9C88;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Cell surface retention sequence binding protein-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA Huang J.S.;
RT "Cloning, expression, characterization and role in autocrine cell
RT growth of cell surface retention sequence binding protein-1.";
RL J. Biol. Chem. 278:43855-43869(2003).
DR EMBL; AY32937; AAQ85130.1; -
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPRO00538; Link.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 322 AA; 35561 MW; 4901DA1BF92648AE CRC64;

Query Match 63.9%; Score 719; DB 2; Length 322;
Best Local Similarity 63.3%; Pred. No. 1.3e-54;
Matches 138; Conservative 31; Mismatches 49; Indels 0; Gaps 0;

QY 1 TRLVQGSRLARELSIQVSCRIMGTLVSKKANQQLNFTFAEACRLGLSLAGKDOVET 60
DB 17 TRLVQGSRLARELSIQVSCRIMGTLVSKKANQQLNFTFAEACRLGLSLAGKDOVET 76
QY 61 ALKASFTCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCVNSDWT 120
DB 77 ARKFGFTCSYGVWKNQFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCVNSDWT 136
QY 121 NSCIPETITTKDPIFNQTQTOTTEFTIVSDTSYVASPYSTIPAPTTTPAPASTSIPRR 180
DB 137 NSCLPEIITDDPFLNFTETATVTKLWSDSTHSELSDTGPDPVITTVAPPLASTSTPRK 196
QY 181 KKLICVTEVFMETSTMSTETETFPFVENKAAPKNEAAGFG 218
DB 197 RKLICITEAFMDTSAVATERESDIQNRPAFKNEAVGFG 234

RESULT 5
Q99NE4 PRELIMINARY; PRT; 318 AA.
ID Q99NE4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE Hyaluronan receptor precursor.
OS Mus musculus (Mouse).
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Digestive tract;
RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
RA Banerji S.;
RT "LYVE-1, a new homologue of the CD44 glycoprotein is a lymph-specific
RT receptor for hyaluronan.";
RL J. Cell Biol. 144:789-801(1999).
RN [2]
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RP SEQUENCE FROM N.A.
RX STRAIN=Balb/c; TISSUE=Digestive tract;
RX MEDLINE=21276443; PubMed=11278811; DOI=10.1074/jbc.M011004200;
RA Prevo R., Banerji S., Ferguson D.J.P., Clasper S., Jackson D.G.;
RT "Mouse LYVE-1 is an endocytic receptor for hyaluronan in lymphatic
RT endothelium.";
RL J. Biol. Chem. 276:19420-19430(2001).
DR EMBL; AJ311501; CAC33082.1; -
DR HSP; P98066; 107B.
DR MGD; MGI:2136348; Xlkdl.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005886; C:plasma membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006027; P:glycosaminoglycan catabolism; IEA.
DR InterPro; IPRO00538; Link.
DR Pfam; PF00193; Xlink; 1.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
KW Receptor; Signal.
FT SIGNAL 1 23
FT CHAIN 24 318
FT CHAIN 318
SQ SEQUENCE 318 AA; 34641 MW; 1248974A16113330 CRC64;

Query Match 59.5%; Score 669; DB 2; Length 318;
Best Local Similarity 61.0%; Pred. No. 3e-50;
Matches 133; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

QY 1 TRLVQGSRLARELSIQVSCRIMGTLVSKKANQQLNFTFAEACRLGLSLAGKDOVET 60
DB 17 TRHPVQGDVLVDLIS-TCRIMGVALVGNKNQPNFTFAEACRLGLTLASRDQVES 75
QY 61 ALKASFTCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCVNSDWT 120
DB 76 AQKSGFTCSYGVWGEQFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCVNSDWT 135
QY 121 NSCIPETITTKDPIFNQTQTOTTEFTIVSDTSYVASPYSTIPAPTTTPAPASTSIPRR 180
DB 136 NSCIPETITTKDPIFNQTQTOTTEFTIVSDTSYVASPYSTIPAPTTTPAPASTSIPRR 192
QY 181 KKLICVTEVFMETSTMSTETETFPFVENKAAPKNEAAGFG 218
DB 193 TKICITEVTEPITMATETEAFVSGAAPKNEAAGFG 230

RESULT 6
Q8BHC0 PRELIMINARY; PRT; 318 AA.
ID Q8BHC0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Extra cellular link domain-containing 1 (Mus musculus adult male lung
DE cDNA, RIKEN full-length enriched library, clone:1200012G08
DE product:extra cellular link domain-containing 1, full insert
DE sequence).
GN Name=Xlkdl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZECH II; TISSUE=Lung, and Mammary gland;
RX MEDLINE=2328257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061327; AAH61327.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR PRINTS; PR00658; CD44.
DR PRODom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS0963; LINK_2; 1.
KW Hypothetical protein.
SQ
SEQUENCE 437 AA; 49108 MW; 7088441D0E138C10 CRC64;

Query Match 20.1%; Score 226; DB 2; Length 437;
Best Local Similarity 34.1%; Pred. No. 2.5e-11;
Matches 61; Conservative 18; Mismatches 78; Indels 22; Gaps 4;

QY 18 VSCRWIGTGLVSKKANQOINFTAEACELLGLSLAGKQVETALKASFETCSYGVGDG 77
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 24 ISCRFGVPHVEKYDRYALNREDAIKLCHELNNTTIANLTLMIAQDIGFETCRYGWIEDR 83
QY 78 FVVISRISGNPKCGKNGVGLWKPVGROPAAYCVNSGSDTWTNSCIP-----E 126
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 84 -VPIRPNPFCANYYGIFLGNDSRLRYDAYCYNASETDKSCFVLLNEDTDLSHK 142
QY 127 IITTKDPIFNQTATQTTFEIVSDSTYSVASPYSTIPAP-----TTTPPA-PAST 175
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 143 TIDSVDPTLDTQNPTQNSKSGDVTDPGPMITPDGQWDWDIIQGTTPDHGDPFST 201

RESULT 10
CD44 RAT
ID CD44 RAT STANDARD; PRT; 503 AA.
AC P26051; Q99021;
DT 01-MAY-1992 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-1)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE 24).
GN Name=CD44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=BDIX; TISSUE=Pancreas;
RX MEDLINE=91191552; PubMed=1707342; DOI=10.1016/0092-8674(91)90403-L;
RA Guentert U., Hofmann M., Rudy W., Reber S., Zoeller M., Haussmann I.,
RA Matzku S., Wenzel A., Ponta H., Herrlich P.;
RT "A new variant of glycoprotein CD44 confers metastatic potential to
RT rat carcinoma cells.,"
RL Cell 65:13-24 (1991).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Stevens J.W., Midura R.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SULFATION OF TYR-288.
RX PubMed=9692903;
RA Slesman J.P., Rahmsdorf U., Steffen A., Ponta H., Herrlich P.;
RT "CD44 variant exon v5 encodes a tyrosine that is sulphated.,"
RL Eur. J. Biochem. 255:74-80 (1998).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

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CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=2; Synonyms=Long, Meta-1;
CC IsoId=P26051-1; Sequence=Displayed;
CC Name=1; Synonyms=Short;
CC IsoId=P26051-2; Sequence=VSP 005330;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; contains Chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).
CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-467 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-433 (By similarity).
CC -!- SIMILARITY: Contains 1 Link domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M61875; AAA53532.1; -.
CC EMBL; M61874; AAA53534.1; -.
CC EMBL; U52179; AAA97915.1; -.
CC EMBL; U46957; AAA92920.1; -.
CC FIR; B38745; B38745.
CC HSSP; P98066; 1TSG.
CC InterPro; IPR001231; CD44 antigen.
CC InterPro; IPR005538; Link.
CC Pfam; PF00193; XLink; 1.
CC PRINTS; PR00658; CD44.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 1.
CC PROSITE; PS01241; LINK_1; 1.
CC PROSITE; PS0963; LINK_2; 1.
CC KW Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
CC Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
CC Sulfation; Transmembrane.
CC SIGNAL 1 21
CC CHAIN 22 503 CD44 antigen.
CC DOMAIN 22 410 Extracellular (Potential).
CC TRANSMEM 411 431 Potential.
CC DOMAIN 432 503 Cytoplasmic (Potential).
CC DOMAIN 35 124 Link.
CC DOMAIN 154 162 Arg/Lys-rich (basic).
CC DOMAIN 228 410 Stem.
CC MOD_RES 22 22 Pyrrolidone carboxylic acid (Probable).
CC DISULFID 56 122 By similarity.
CC DISULFID 80 100 By similarity.
CC MOD_RES 288 288 Sulfotyrosine (in isoform 2).
CC MOD_RES 433 433 Phosphoserine (by PKC) (By similarity).
CC MOD_RES 467 467 Phosphoserine (By similarity).
CC CARBOHYD 28 28 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 60 60 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 103 103 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 114 114 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 124 124 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 266 266 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 274 274 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 306 306 N-linked (GlcNAc...) (Potential).
CC VARSPLIC 224 385 IATTPVSAHTKQERTQWNPPIHNSPEVLQTTTMTDID
CC RSTTSAHGNWTQPPFNHNYDEBETHATTTWADP
CC NSTTEAATQKEKFNENQKGNPTPEDSHVTEGTTASA
CC HNNHPSORMTTQSDVDVSTWTFDFDPIHPMGQCHQTESK
CC -> SDGSSMDPRGGFTVTGSELA (in isoform
CC 1).
CC /FTId=VSP 005330.
CC R -> S (in Ref. 2).
CC CONFLICT 74 74
CC SEQUENCE 503 AA; 55945 MW; FB489D009BD4EE22 CRC64;
Query Match 19.0%; Score 213.5; DB 1; Length 503;

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Best Local Similarity 32.1%; Pred. No. 3.6e-10;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 4 LVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTFEAKEACRLGLSLAGKQDVETALK 63
DQ 15 LLQLSLAQOQIDLNITCRVAGVHFVEKNGRYSISRTEADLCFAFNITLPTWAQMEALR 74
QY 64 ASPTCSYGVWGDGFVVISRISPNPKCGKNGVGLVWKVPVSRQFAAYCNSDDTWTNSC 123
DQ 75 KGFETCRYGFI-EGHVIVPRIHPNAICAAANTGVILLASNTSHYDTYCFNASAPLEEDC 133
QY 124 IPEIITTKDPIENTQTATQTTTEFIVSDST-YSVASPYST 161
DQ 134 -----TSVTDLPNSFDGVPVTITIVNRDGRTRYKKGGEYRT 167

RESULT 11
O08779 PRELIMINARY; PRT; 780 AA.
AC O08779;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CD44 protein.
GN Name-CD44;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BDX; TISSUE=Pancreas;
RA Hofmann M.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U96138; AAB54002.1; -.
DR HSP; P98056; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK; 1.
DR PROSITE; PS0963; LINK; 2; 1.
SQ SEQUENCE 780 AA; 85917 MW; CC435AB1EA7377C CRC64;

Query Match 19.0%; Score 213.5; DB 2; Length 780;
Best Local Similarity 32.1%; Pred. No. 6.2e-10;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 4 LVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTFEAKEACRLGLSLAGKQDVETALK 63
DQ 15 LLQLSLAQOQIDLNITCRVAGVHFVEKNGRYSISRTEADLCFAFNITLPTWAQMEALR 74
QY 64 ASPTCSYGVWGDGFVVISRISPNPKCGKNGVGLVWKVPVSRQFAAYCNSDDTWTNSC 123
DQ 75 KGFETCRYGFI-EGHVIVPRIHPNAICAAANTGVILLASNTSHYDTYCFNASAPLEEDC 133
QY 124 IPEIITTKDPIENTQTATQTTTEFIVSDST-YSVASPYST 161
DQ 134 -----TSVTDLPNSFDGVPVTITIVNRDGRTRYKKGGEYRT 167

RESULT 12
O07059 PRELIMINARY; PRT; 364 AA.
AC O07059;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glycoprotein CD44s (CD44 protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Lumbar spine;
RA Stevens J.W.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenck C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF065147; AAC17117.1; -.
DR EMBL; BC061531; AAB61531.1; -.
DR HSP; P98066; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44 antigen.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRODOM; PD000918; Link; 1.
DR PROSITE; PS01241; LINK; 1.
DR PROSITE; PS0963; LINK; 2; 1.
SQ SEQUENCE 364 AA; 39725 MW; BA249776C4419AA7 CRC64;

Query Match 18.8%; Score 211.5; DB 2; Length 364;
Best Local Similarity 32.1%; Pred. No. 3.7e-10;
Matches 51; Conservative 24; Mismatches 77; Indels 7; Gaps 3;

QY 4 LVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTFEAKEACRLGLSLAGKQDVETALK 63
DQ 15 LLQLSLAQOQIDLNITCRVAGVHFVEKNGRYSISRTEADLCFAFNITLPTWAQMEALR 74
QY 64 ASPTCSYGVWGDGFVVISRISPNPKCGKNGVGLVWKVPVSRQFAAYCNSDDTWTNSC 123
DQ 75 KGFETCRYGFI-EGHVIVPRIHPNAICAAANTGVILLASNTSHYDTYCFNASAPLEEDC 133
QY 124 IPEIITTKDPIENTQTATQTTTEFIVSDST-YSVASPYST 161
DQ 134 -----TSVTDLPNSFDGVPVTITIVNRDGRTRYKKGGEYRT 167
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RESULT 13
Q98SR5 PRELIMINARY; PRT; 265 AA.
AC Q98SR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE T cell antigen CD44 isoform b.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin;
RA Chan S.W.S., Warr G.W., Middleton D.L., Higgins D.A.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332869; AAK18277.1; -.
DR HSSP; P98066; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 265 AA; 29215 MW; 77C176E0A98D081 CRC64;

Query Match 18.8%; Score 211; DB 2; Length 265;
Best Local Similarity 28.4%; Pred. No. 2.8e-10;
Matches 62; Conservative 31; Mismatches 93; Indels 32; Gaps 5;

QY 13 ELSIOVSCRMGITLVSKKANQQLNFTKEACRLGLSLAGKQVETALKASFETCSYG 72
DB 21 ETQFNVSCRYRGVHFVEKNGRYSLTRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

QY 73 WYGDGFVVISRISPNPKCGKGVGLWIKVPVSRQFAAYCYNSSDTWTNSCIP----- 125
DB 81 FV-VGVIVIPRINPYHLCAANTGIYKLSANTGRDAYCYNATETRDKACFPIERDTS 139

QY 126 -----EIITTKDP-----IFNTQTATQTTEFIVSDTSYVASPYSTIPAPTT 174
DB 140 FLSNGEIVIDNEDGSRYNADGTRHSGDSSTSGVDENVVSGSGSHDTPVDTSIIRSSPS 199

QY 175 -----TSIPR-----RKKLICVTEVPMTSTWSTE 199
DB 200 YYGSVTFVPHLSDHSSGGGGEKFFVTNSDDEISPTSTD 237

RESULT 14
Q90ZL8 PRELIMINARY; PRT; 398 AA.
AC Q90ZL8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE T cell antigen CD44 isoform a.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin;
RA Chan S.W.S., Middleton D.L., Warr G.W., Higgins D.A.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029553; AAK40246.1; -.
DR HSSP; P98066; 107B.

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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 398 AA; 43673 MW; 25A944EE2F4AED6D CRC64;

Query Match 18.6%; Score 209.5; DB 2; Length 398;
Best Local Similarity 30.1%; Pred. No. 6.1e-10;
Matches 52; Conservative 27; Mismatches 75; Indels 19; Gaps 3;

QY 13 ELSIOVSCRMGITLVSKKANQQLNFTKEACRLGLSLAGKQVETALKASFETCSYG 72
DB 21 ETQFNVSCRYRGVHFVEKNGRYSLTRTEAADLCRALNSTLSTLEQLEKAHELGFETCRYG 80

QY 73 WYGDGFVVISRISPNPKCGKGVGLWIKVPVSRQFAAYCYNSSDTWTNSCIP----- 125
DB 81 FV-VGVIVIPRINPYHLCAANTGIYKLSANTGRDAYCYNATETRDKACFPIERDTS 139

QY 126 -----EIITTKDP-----IFNTQTATQTTEFIVSDTSYVASPYSTIPAPTT 167
DB 140 FLSNGEIVIDNEDGSRYNADGTRHSGDSSTSGVDENVVSGSGSHDTPVDTSI 192

RESULT 15
CD44_MOUSE STANDARD; PRT; 778 AA.
AC P15379; Q05732; Q61395; Q62060; Q62061; Q62062; Q62063; Q62408;
AC Q62409; Q64296; Q99J14; Q9QYX8;
DT 01-APR-1990 (Rel. 14, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor) (LY-
DE 24).
GN Name=Cd44;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 4; 6; 7 AND 12).
RC STRAIN=DBA/2; TISSUE=Lung;
RX MEDLINE=93107170; PubMed=1469058; DOI=10.1083/jcb.119.6.1711;
RA He Q., Lesley J., Hyman R., Ishihara K., Kincade P.W.;
RT "Molecular isoforms of murine CD44 and evidence that the membrane
RT proximal domain is not critical for hyaluronate recognition.";
RA J. Cell Biol. 119:1711-1719(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=90038499; PubMed=2681416;
RA Zhou D.F.H., Ding J.F., Picker L.J., Bargatze R.F., Butcher E.C.,
RA Goeddel D.V.;
RT "Molecular cloning and expression of Pgp-1. The mouse homolog of the
RT human H-CAM (Hermes) lymphocyte homing receptor.";
RL J. Immunol. 143:3390-3395(1989).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 13).
RX MEDLINE=90046829; PubMed=2682651;
RA Nottenburg C., Rees G., St John T.;
RT "Isolation of mouse CD44 cDNA: structural features are distinct from
RT the primate cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8521-8525(1989).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20318634; PubMed=10859330;
RA Wittig B.M., Johansson B., Zoeller M., Schwaerzler C., Guenther U.;

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RT "Abrogation of experimental colitis correlates with increased
RT apoptosis in mice deficient for CD44 variant exon 7 (CD44v7).";
RL J. Exp. Med. 191:2053-2064(2000).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 13)
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udell T.B., Toehlyuk S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan L., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 13)
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RL MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Oatso N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J.C., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Sempé C.A., Setou M., Shinada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wegner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Saito K., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [7]
RP SEQUENCE OF 8-778 FROM N.A. (ISOFORM 13).
RX MEDLINE=90094420; PubMed=2403559;
RA Wolffe E.J., Gause W.C., Pelfrey C.M., Holland S.M., Steinberg A.D.,
RA August J.T.,
RT "The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell
RT surface antigen and proteoglycan core/link proteins.";
RL J. Biol. Chem. 265:341-347(1990).
RN [8]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORMS 1; 2; 3; 4; 5; 6; 7 AND 8).
RX STRAIN=GR;
RL MEDLINE=93219085; PubMed=8464707;
RA Toelg C., Hofmann M., Herrlich P., Ponta H.,
RT "Splicing choice from ten variant exons establishes CD44

RT variability.";
RL Nucleic Acids Res. 21:1225-1229(1993).
RN [9]
RP SEQUENCE OF 224-637 FROM N.A. (ISOFORM 9).
RX STRAIN=BALB/c;
RL MEDLINE=93286043; PubMed=8509359;
RA Screation G.R., Bell M.V., Bell J.I., Jackson D.G.,
RT "The identification of a new alternative exon with highly restricted
RT tissue expression in transcripts encoding the mouse Pgp-1 (CD44)
RT homing receptor. Comparison of all 10 variable exons between mouse,
RT human, and rat.";
RL J. Biol. Chem. 268:12235-12238(1993).
RN [10]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS 10 AND 11).
RX STRAIN=Swiss Webster;
RL MEDLINE=96355396; PubMed=8702806; DOI=10.1074/jbc.271.34.20603;
RA Yu Q., Toole B.P.,
RT "A new alternatively spliced exon between v9 and v10 provides a
RT molecular basis for synthesis of soluble CD44.";
RL J. Biol. Chem. 271:20603-20607(1996).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=13;
CC Name=1;
CC IsoId=P15379-14; Sequence=Displayed;
CC Name=2;
CC IsoId=P15379-7; Sequence=VSP_007329;
CC Name=3;
CC IsoId=P15379-8; Sequence=VSP_007330;
CC Name=4; Synonyms=M2;
CC IsoId=P15379-4; Sequence=VSP_007331;
CC Name=5;
CC IsoId=P15379-9; Sequence=VSP_007332;
CC Name=6; Synonyms=M3;
CC IsoId=P15379-5; Sequence=VSP_005326;
CC Name=7; Synonyms=M4;
CC IsoId=P15379-6; Sequence=VSP_005327;
CC Name=8;
CC IsoId=P15379-10; Sequence=VSP_007330, VSP_007334;
CC Name=9;
CC IsoId=P15379-11; Sequence=VSP_007332, VSP_007335;
CC Name=10;
CC IsoId=P15379-12; Sequence=VSP_007336, VSP_007337;
CC Name=11;
CC IsoId=P15379-13; Sequence=VSP_007338, VSP_007339;
CC Name=12; Synonyms=M1;
CC IsoId=P15379-3; Sequence=VSP_005328;
CC Name=13; Synonyms=M0;
CC IsoId=P15379-2; Sequence=VSP_005329, VSP_007333;
CC -!- PTM: N-glycosylated (By similarity).
CC -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which
CC can be more or less sulfated (By similarity).
CC -!- PTM: Phosphorylated; activation of PKC results in the
CC dephosphorylation of Ser-742 (constitutive phosphorylation site),
CC and the phosphorylation of Ser-708 (By similarity).
CC -!- POLYMORPHISM: Two allelic forms of this glycoprotein, PGP-1.1 and
CC PGP-1.2, have been reported. The expressed product is PGP-1.1 (Ly-
CC 24.1).
CC -!- SIMILARITY: Contains 1 Link domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X66084; CAA46883.1; -.

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DR EMBL; X66083; CAA46882.1; -
DR EMBL; X66082; CAA46881.1; -
DR EMBL; X66081; CAA46880.1; -
DR EMBL; M30655; AAA39922.1; -
DR EMBL; M27129; AAA37406.1; -
DR EMBL; M27130; AAA37407.1; -
DR EMBL; AJ251594; CAB61888.1; -
DR EMBL; BC005676; AAH05676.1; -
DR EMBL; AK045226; BAC32269.1; -
DR EMBL; J05163; AAA39923.1; -
DR EMBL; X69724; CAA49380.1; -
DR EMBL; LI3611; AAA37145.1; -

Query Match      18.6%; Score 209.5; DB 1; Length 778;
Best Local Similarity 32.7%; Pred. No. 1.4e-09;
Matches 52; Conservative 25; Mismatches 75; Indels 7; Gaps 3;

QY 4 LVQGSIRAEELSIQVSCRIMGITLVSKKANQQLNFTAEKACRLILGLSLAGKQDVETALK 63
Db 14 LLQLSLAHQQIDILNVTCTRVAGVFHVEKNGRYSISRTEAADLCAAFNSTLPTWDMQKLALS 73
QY 64 ASFETCSYGVGDGFVVISRISPNPKCGKNGVGVLIWKVPVSRQFAAYCYNSSDWTWNSC 123
Db 74 KGFETCRYGFI-EGNVVIPRIHPNAICAAAHHTGVYILVTSNTSHYDTYCFNASAPPEDC 132
QY 124 IPEIITKDPPIENTQTATOTTEFIVSDST-YSVASPYST 161
Db 133 -----TSVTDLPNSFDGVPVTITIVNRDGTTRYSKKGEYRT 166
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Search completed: October 5, 2005, 17:31:52
Job time : 114.256 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 17:16:37 ; Search time 20.5889 Seconds
(without alignments)
1018.766 Million cell updates/sec

Title: US-10-063-510-6_COPY_17_234

Perfect score: 1125

Sequence: 1 TRLLVQGSURABELSIQVSC.....ETEPFVENKAAPKNEAGFG 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : PIR 79.*

1: piri.*

2: piri2.*

3: piri3.*

4: piri4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------|--------------------|
| 1 | 213.5 | 19.0 | 503 | B38745 | cell adhesion mole |
| 2 | 209.5 | 18.6 | 363 | A37009 | CD44 homolog membr |
| 3 | 207 | 18.4 | 362 | A35616 | T-cell surface gly |
| 4 | 203.5 | 18.1 | 362 | A30901 | lymphocyte homing |
| 5 | 202 | 18.0 | 742 | A47195 | lymphocyte homing |
| 6 | 199.5 | 17.7 | 493 | S13530 | CD44E protein, epi |
| 7 | 198.5 | 17.6 | 365 | A34424 | CD44 membrane glyc |
| 8 | 198.5 | 17.6 | 426 | JH0518 | lymphocyte homing |
| 9 | 197 | 17.5 | 361 | JH0417 | cell adhesion mole |
| 10 | 196.5 | 17.5 | 699 | I37369 | epican - human |
| 11 | 196 | 17.4 | 395 | I77371 | CD44R5 - human |
| 12 | 194 | 17.2 | 351 | S45305 | CD44 antigen precu |
| 13 | 194 | 17.2 | 366 | A53286 | cell-surface glyco |
| 14 | 183.5 | 16.3 | 359 | S24240 | lymphocyte surface |
| 15 | 145.5 | 12.9 | 3562 | A47171 | chondroitin sulfat |
| 16 | 145 | 12.9 | 277 | A47135 | hyaluronate-bindin |
| 17 | 144 | 12.8 | 275 | JC6506 | tumor necrosis fac |
| 18 | 143 | 12.7 | 2109 | I50421 | aggrecan precursor |
| 19 | 137 | 12.2 | 276 | A47290 | TSG-6 homolog PS4 |
| 20 | 131.5 | 11.7 | 2124 | A28452 | proteoglycan core |
| 21 | 131 | 11.6 | 2132 | A55182 | aggrecan precursor |
| 22 | 130.5 | 11.6 | 883 | S57653 | brevican precursor |
| 23 | 130.5 | 11.6 | 2415 | A39086 | aggrecan precursor |
| 24 | 128 | 11.4 | 2327 | T42630 | aggrecan - bovine |
| 25 | 127.5 | 11.3 | 883 | S49126 | brevican precursor |
| 26 | 120.5 | 10.7 | 912 | A54423 | brevican precursor |
| 27 | 118 | 10.5 | 1340 | A39808 | proteoglycan core |
| 28 | 116 | 10.3 | 2397 | A55535 | versican precursor |
| 29 | 115 | 10.2 | 370 | S29139 | aggrecan - pig (fr |

versican precursor
versican precursor
brain link protein
versican precursor
neurocan precursor
neurocan precursor
hypothetical prote
proteoglycan link
proteoglycan link
brevican precursor
proteoglycan link
neurocan - mouse
chondroitin sulfat
versican - pig-tai
proteoglycan link
proteoglycan link
hypothetical prote
hypothetical prote
hypothetical prote
brevican precursor
glycoprotein I pre
hypothetical prote
hypothetical prote
hypothetical prote
E2 protein - human
dihydrolipoamide a
96K lysosomal memb
hypothetical prote
salivary glue prot
lysosome-associate
endo-1,4-beta-xyla
probable zinc meta
hypothetical prote
endoglucanase C [E
hypothetical prote
hypothetical prote
hypothetical prote
Ca(2+) -sensing rec
mucin like protein
hypothetical prote
integumentary muc
spasmolysin precu
mucin 5AC (clone J
hypothetical prote
LDL receptor 2 pre
hypothetical prote
nudel protein prec
hypothetical prote
Mutator-like trans
Glucan 1,4-alpha-g
hypothetical prote
hypothetical prote
serine/threonine p
chitinase (EC 3.2.
probable outer mem
hypothetical prote
probable membrane
hypothetical prote
AP2-containing DNA
mucin JUL7 - human
mucin FIM-C.1 - Af
hypothetical prote
mannan endo-1,4-be
amylopullulanase P
xylanase - Caldice
mucin-like glycop
mucin 2 precursor,
mucin - rhesus mac
mucin 5AC (clone J
protein M01E10.2 [

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|-----------------------|-----|------|-----|------|---|--------|--------------------|
| 249 | 74.5 | 6.6 | 1388 | 2 | A53317 | collagen alpha 1(X | 322 | 72.5 | 6.4 | 797 | 1 | VBEX1 | glycoprotein x pre |
| 250 | 74.5 | 6.6 | 1838 | 1 | CGHU4V | collagen alpha 1(V | 323 | 72.5 | 6.4 | 867 | 2 | T45463 | membrane glycoprot |
| 251 | 74.5 | 6.6 | 2688 | 2 | I49477 | alpha-A-crystallin | 324 | 72.5 | 6.4 | 907 | 1 | QOBZ21 | membrane antigen g |
| 252 | 74 | 6.6 | 147 | 2 | S09762 | hypothetical prote | 325 | 72.5 | 6.4 | 930 | 2 | B72537 | hypothetical prote |
| 253 | 74 | 6.6 | 223 | 2 | T21930 | hypothetical prote | 326 | 72.5 | 6.4 | 1021 | 2 | S64506 | protein kinase BUS |
| 254 | 74 | 6.6 | 384 | 2 | T21929 | hypothetical prote | 327 | 72.5 | 6.4 | 1180 | 2 | E86719 | hypothetical prote |
| 255 | 74 | 6.6 | 397 | 2 | E97176 | N-terminal domain | 328 | 72.5 | 6.4 | 1367 | 2 | A59235 | unconventional myo |
| 256 | 74 | 6.6 | 417 | 2 | T20327 | hypothetical prote | 329 | 72.5 | 6.4 | 1365 | 2 | T33216 | hypothetical prote |
| 257 | 74 | 6.6 | 418 | 2 | T16713 | hypothetical prote | 330 | 72 | 6.4 | 159 | 2 | F72758 | hypothetical prote |
| 258 | 74 | 6.6 | 515 | 2 | AD1162 | flagellar motor sw | 331 | 72 | 6.4 | 182 | 2 | T30078 | hypothetical prote |
| 259 | 74 | 6.6 | 518 | 2 | G88961 | protein F59A7.8 [i | 332 | 72 | 6.4 | 199 | 2 | JE0351 | OX40 ligand protei |
| 260 | 74 | 6.6 | 542 | 2 | S64030 | probable membrane | 333 | 72 | 6.4 | 236 | 2 | T03041 | hypothetical prote |
| 261 | 74 | 6.6 | 586 | 2 | S66697 | probable membrane | 334 | 72 | 6.4 | 246 | 2 | PC4397 | mucin 3 T10 - huma |
| 262 | 74 | 6.6 | 606 | 2 | T06292 | hypothetical prote | 335 | 72 | 6.4 | 324 | 2 | S36646 | integrin-associate |
| 263 | 74 | 6.6 | 906 | 2 | G90281 | conserved hypotet | 336 | 72 | 6.4 | 405 | 2 | A60534 | P2B/LAMP-1 precurs |
| 264 | 74 | 6.6 | 1047 | 2 | A55617 | masquerade precurs | 337 | 72 | 6.4 | 481 | 2 | T38149 | pre-mrna splicing |
| 265 | 74 | 6.6 | 2414 | 2 | A54277 | transcription adap | 338 | 72 | 6.4 | 482 | 2 | A44997 | merozoite surface |
| 266 | 73.5 | 6.5 | 263 | 2 | T38003 | hypothetical ser-t | 339 | 72 | 6.4 | 576 | 2 | T38293 | hypothetical serin |
| 267 | 73.5 | 6.5 | 290 | 2 | S66355 | lectin-related sto | 340 | 72 | 6.4 | 592 | 2 | D70863 | hypothetical prote |
| 268 | 73.5 | 6.5 | 358 | 2 | AD2378 | hypothetical prote | 341 | 72 | 6.4 | 688 | 2 | T18263 | S-layer protein - |
| 269 | 73.5 | 6.5 | 371 | 2 | S20075 | promastigote surfa | 342 | 72 | 6.4 | 1176 | 2 | T49482 | hypothetical prote |
| 270 | 73.5 | 6.5 | 447 | 2 | A39321 | mucin - rat (fragm | 343 | 72 | 6.4 | 1203 | 2 | T17415 | mycelial surface a |
| 271 | 73.5 | 6.5 | 451 | 2 | S71754 | cellular hepatitis | 344 | 72 | 6.4 | 1367 | 2 | S51959 | hypothetical prote |
| 272 | 73.5 | 6.5 | 484 | 1 | A24994 | cellulose 1,4-beta | 345 | 72 | 6.4 | 1419 | 2 | T30531 | agglutinin-like ad |
| 273 | 73.5 | 6.5 | 511 | 1 | VBSE1K | glycoprotein C - h | 346 | 72 | 6.4 | 1489 | 2 | T31108 | cyst germination s |
| 274 | 73.5 | 6.5 | 542 | 2 | T19952 | hypothetical prote | 347 | 72 | 6.4 | 1723 | 2 | H86557 | polymorphic membra |
| 275 | 73.5 | 6.5 | 575 | 2 | S29315 | chaperonin 60 - cu | 348 | 72 | 6.4 | 1723 | 2 | E72067 | polymorphic membra |
| 276 | 73.5 | 6.5 | 595 | 2 | A42086 | CD30 antigen precu | 349 | 72 | 6.4 | 1732 | 2 | C81601 | polymorphic membra |
| 277 | 73.5 | 6.5 | 601 | 2 | H90270 | hypothetical prote | 350 | 72 | 6.4 | 2526 | 2 | T20531 | hypothetical prote |
| 278 | 73.5 | 6.5 | 626 | 2 | AB1328 | probable peptidogl | 351 | 72 | 6.4 | 2722 | 2 | T20532 | hypothetical prote |
| 279 | 73.5 | 6.5 | 708 | 2 | F87245 | penicillin-binding | 352 | 72 | 6.4 | 2738 | 2 | E88320 | protein F07A11.6 [|
| 280 | 73.5 | 6.5 | 806 | 2 | E69424 | hypothetical prote | 353 | 72 | 6.4 | 2971 | 2 | T08026 | hypothetical prote |
| 281 | 73.5 | 6.5 | 866 | 2 | T45462 | membrane glycoprot | 354 | 71.5 | 6.4 | 141 | 2 | A38196 | non-structural hyp |
| 282 | 73.5 | 6.5 | 905 | 2 | T02205 | Lu-ECAM-1 protein | 355 | 71.5 | 6.4 | 152 | 2 | T15170 | hypothetical prote |
| 283 | 73.5 | 6.5 | 976 | 2 | A87576 | peptidase, M16 fam | 356 | 71.5 | 6.4 | 152 | 2 | T28759 | hypothetical prote |
| 284 | 73.5 | 6.5 | 989 | 2 | T47503 | hypothetical prote | 357 | 71.5 | 6.4 | 162 | 2 | C84948 | NADH2 dehydrogenas |
| 285 | 73.5 | 6.5 | 1004 | 2 | T38074 | hypothetical prote | 358 | 71.5 | 6.4 | 281 | 2 | T49537 | hypothetical prote |
| 286 | 73.5 | 6.5 | 1016 | 2 | T19006 | ankyrin related pr | 359 | 71.5 | 6.4 | 303 | 2 | AB2149 | hypothetical prote |
| 287 | 73.5 | 6.5 | 2232 | 2 | T34434 | hypothetical prote | 360 | 71.5 | 6.4 | 313 | 2 | AB0734 | probable bacteriop |
| 288 | 73.5 | 6.5 | 3176 | 2 | CGHU3A | collagen alpha 3(V | 361 | 71.5 | 6.4 | 363 | 2 | T25278 | hypothetical prote |
| 289 | 73 | 6.5 | 260 | 2 | IS0109 | gastrulation prote | 362 | 71.5 | 6.4 | 477 | 2 | T32938 | hypothetical prote |
| 290 | 73 | 6.5 | 327 | 2 | S20074 | promastigote surfa | 363 | 71.5 | 6.4 | 496 | 2 | E90181 | hypothetical prote |
| 291 | 73 | 6.5 | 461 | 2 | T51044 | related to spore c | 364 | 71.5 | 6.4 | 499 | 2 | A12449 | hypothetical prote |
| 292 | 73 | 6.5 | 486 | 2 | S66097 | cell-cycle protein | 365 | 71.5 | 6.4 | 540 | 2 | H98086 | chaperonin GroEL [|
| 293 | 73 | 6.5 | 492 | 1 | CHBOA3 | gamma-aminobutyric | 366 | 71.5 | 6.4 | 540 | 2 | G95222 | chaperonin, 60 kDa |
| 294 | 73 | 6.5 | 528 | 2 | S69589 | hypothetical prote | 367 | 71.5 | 6.4 | 675 | 2 | T47378 | probable transposa |
| 295 | 73 | 6.5 | 550 | 2 | C75557 | hypothetical prote | 368 | 71.5 | 6.4 | 755 | 2 | T20950 | hypothetical prote |
| 296 | 73 | 6.5 | 600 | 2 | E72027 | phosphoenolpyruvat | 369 | 71.5 | 6.4 | 822 | 2 | JC4076 | dextranase (EC 3.2 |
| 297 | 73 | 6.5 | 600 | 2 | A86597 | phosphoenolpyruvat | 370 | 71.5 | 6.4 | 882 | 2 | T01168 | hypothetical prote |
| 298 | 73 | 6.5 | 639 | 2 | T13151 | adaptor protein CM | 371 | 71.5 | 6.4 | 1042 | 2 | T48801 | hypothetical prote |
| 299 | 73 | 6.5 | 681 | 2 | S33316 | structural protein CM | 372 | 71.5 | 6.4 | 1166 | 2 | S37692 | probable tumor sup |
| 300 | 73 | 6.5 | 728 | 2 | T20561 | hypothetical prote | 373 | 71.5 | 6.4 | 1557 | 2 | D41214 | protein-tyrosine-p |
| 301 | 73 | 6.5 | 771 | 2 | T34376 | hypothetical prote | 374 | 71.5 | 6.4 | 1630 | 2 | C41214 | protein-tyrosine-p |
| 302 | 73 | 6.5 | 781 | 2 | T49472 | hormone-sensitive | 375 | 71 | 6.3 | 98 | 2 | S53367 | mucin 5AC (clone M |
| 303 | 73 | 6.5 | 814 | 2 | T33140 | hypothetical prote | 376 | 71 | 6.3 | 240 | 2 | T33698 | hypothetical prote |
| 304 | 73 | 6.5 | 825 | 2 | T48431 | hypothetical prote | 377 | 71 | 6.3 | 292 | 2 | S24169 | mucin - rat |
| 305 | 73 | 6.5 | 884 | 2 | AE3166 | ATP-dependent DNA | 378 | 71 | 6.3 | 304 | 2 | T15922 | hypothetical prote |
| 306 | 73 | 6.5 | 918 | 2 | A36337 | membrane glycoprot | 379 | 71 | 6.3 | 343 | 2 | S75435 | hypothetical prote |
| 307 | 73 | 6.5 | 993 | 2 | F97717 | hypothetical prote | 380 | 71 | 6.3 | 349 | 2 | T05857 | hypothetical prote |
| 308 | 73 | 6.5 | 1016 | 2 | T41720 | hypothetical prote | 381 | 71 | 6.3 | 378 | 2 | S00842 | leukosialin precur |
| 309 | 73 | 6.5 | 1235 | 2 | T13710 | protein-tyrosine k | 382 | 71 | 6.3 | 379 | 1 | S71571 | alcohol dehydrogen |
| 310 | 73 | 6.5 | 2179 | 1 | GNNYH4 | genome polypeptide | 383 | 71 | 6.3 | 384 | 2 | A41710 | promastigote surfa |
| 311 | 73 | 6.5 | 2468 | 2 | A83412 | hypothetical prote | 384 | 71 | 6.3 | 410 | 1 | S68153 | cellulase (EC 3.2. |
| 312 | 72.5 | 6.4 | 263 | 2 | I51225 | snail protein - z | 385 | 71 | 6.3 | 415 | 2 | A35560 | lysosomal membrane |
| 313 | 72.5 | 6.4 | 321 | 2 | T25153 | hypothetical prote | 386 | 71 | 6.3 | 416 | 2 | T20448 | hypothetical prote |
| 314 | 72.5 | 6.4 | 382 | 2 | T27058 | hypothetical prote | 387 | 71 | 6.3 | 534 | 2 | G97703 | hypothetical prote |
| 315 | 72.5 | 6.4 | 463 | 1 | A36479 | milk fat globule m | 388 | 71 | 6.3 | 627 | 1 | NBHUIA | platelet glycoprot |
| 316 | 72.5 | 6.4 | 498 | 1 | VGXPLM | surface glycoprote | 389 | 71 | 6.3 | 727 | 2 | A88131 | protein F10G7.9 [i |
| 317 | 72.5 | 6.4 | 560 | 2 | T32661 | hypothetical prote | 390 | 71 | 6.3 | 738 | 2 | I40719 | isocitrate dehydro |
| 318 | 72.5 | 6.4 | 575 | 2 | S39484 | DNA-binding protei | 391 | 71 | 6.3 | 739 | 1 | A34873 | transcription fac |
| 319 | 72.5 | 6.4 | 648 | 2 | PC4395 | mucin 3 - human (f | 392 | 71 | 6.3 | 791 | 2 | T39924 | hypothetical prote |
| 320 | 72.5 | 6.4 | 729 | 2 | G96559 | hypothetical prote | 393 | 71 | 6.3 | 1014 | 1 | A29725 | NAD ADP-ribosyltra |
| 321 | 72.5 | 6.4 | 765 | 1 | T44946 | transducer protein | 394 | 71 | 6.3 | 1241 | 2 | S01827 | period clock prote |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|---------------------|-----|------|-----|-------|---|--------|--------------------|
| 395 | 71 | 6.3 | 1272 | 2 | S26180 | neurofascin - chic | 468 | 69.5 | 6.2 | 558 | 2 | A98199 | translocated intim |
| 396 | 71 | 6.3 | 1367 | 2 | T33819 | hypothetical prote | 469 | 69.5 | 6.2 | 558 | 2 | E86045 | probable transloca |
| 397 | 71 | 6.3 | 1595 | 2 | T31082 | endo-1,4-beta-xyla | 470 | 69.5 | 6.2 | 621 | 2 | T20307 | hypothetical prote |
| 398 | 71 | 6.3 | 1993 | 2 | AF1450 | probable peptidogl | 471 | 69.5 | 6.2 | 640 | 2 | T25367 | hypothetical prote |
| 399 | 70.5 | 6.3 | 118 | 2 | S49913 | cryptogein - Phyto | 472 | 69.5 | 6.2 | 672 | 2 | T20310 | hypothetical prote |
| 400 | 70.5 | 6.3 | 128 | 2 | A35690 | mucin 3 (clone SIB | 473 | 69.5 | 6.2 | 736 | 2 | T19366 | hypothetical prote |
| 401 | 70.5 | 6.3 | 168 | 2 | A31196 | prespore-specific | 474 | 69.5 | 6.2 | 832 | 2 | AF2089 | hypothetical prote |
| 402 | 70.5 | 6.3 | 172 | 2 | F49247 | merozoite surface | 475 | 69.5 | 6.2 | 852 | 2 | T46091 | hypothetical prote |
| 403 | 70.5 | 6.3 | 174 | 2 | E49247 | merozoite surface | 476 | 69.5 | 6.2 | 863 | 2 | T40290 | hypothetical prote |
| 404 | 70.5 | 6.3 | 255 | 2 | I46606 | MHC SLA-DQ alpha c | 477 | 69.5 | 6.2 | 993 | 2 | AE1905 | outer membrane sec |
| 405 | 70.5 | 6.3 | 275 | 2 | T21933 | hypothetical prote | 478 | 69.5 | 6.2 | 1051 | 2 | JC4091 | glycoprotein A - P |
| 406 | 70.5 | 6.3 | 308 | 2 | T29756 | hypothetical prote | 479 | 69.5 | 6.2 | 1071 | 2 | T22327 | hypothetical prote |
| 407 | 70.5 | 6.3 | 321 | 2 | T19259 | hypothetical prote | 480 | 69.5 | 6.2 | 1118 | 2 | A48292 | mucin, tracheobron |
| 408 | 70.5 | 6.3 | 330 | 2 | S28102 | rlx protein - Staph | 481 | 69.5 | 6.2 | 1212 | 2 | T13804 | shs protein - frui |
| 409 | 70.5 | 6.3 | 350 | 2 | AI0139 | UTP-hexose-1-phosp | 482 | 69.5 | 6.2 | 1785 | 2 | A45546 | major merozoite su |
| 410 | 70.5 | 6.3 | 385 | 2 | F70591 | probable kefB prot | 483 | 69.5 | 6.2 | 2717 | 2 | A34203 | DNA-binding protei |
| 411 | 70.5 | 6.3 | 431 | 1 | S35541 | transcription fact | 484 | 69 | 6.1 | 171 | 2 | T31478 | hypothetical prote |
| 412 | 70.5 | 6.3 | 427 | 2 | C88883 | protein JC8.10 (im | 485 | 69 | 6.1 | 217 | 2 | S01358 | salivary glue prot |
| 413 | 70.5 | 6.3 | 431 | 1 | JC2002 | transcription fact | 486 | 69 | 6.1 | 255 | 2 | T22429 | hypothetical prote |
| 414 | 70.5 | 6.3 | 478 | 2 | A32555 | major merozoite su | 487 | 69 | 6.1 | 284 | 2 | S23106 | pria protein - ehi |
| 415 | 70.5 | 6.3 | 496 | 2 | T30976 | hypothetical prote | 488 | 69 | 6.1 | 284 | 2 | T42367 | a-aggutinin core |
| 416 | 70.5 | 6.3 | 534 | 2 | T39903 | serine-rich protei | 489 | 69 | 6.1 | 299 | 2 | S44554 | citrate transport |
| 417 | 70.5 | 6.3 | 562 | 2 | A85042 | hypothetical prote | 490 | 69 | 6.1 | 338 | 2 | F69437 | hypothetical prote |
| 418 | 70.5 | 6.3 | 610 | 2 | S35049 | mucin JERS7 - huma | 491 | 69 | 6.1 | 352 | 2 | S73315 | protoporphyrin IX |
| 419 | 70.5 | 6.3 | 616 | 2 | T29234 | hypothetical prote | 492 | 69 | 6.1 | 382 | 2 | A28067 | lysosomal membrane |
| 420 | 70.5 | 6.3 | 674 | 2 | S74506 | ribonuclease E - S | 493 | 69 | 6.1 | 412 | 1 | AJBORS | argininosuccinate |
| 421 | 70.5 | 6.3 | 893 | 2 | T18271 | hypothetical prote | 494 | 69 | 6.1 | 416 | 2 | T34279 | hypothetical prote |
| 422 | 70.5 | 6.3 | 910 | 1 | S73361 | dnaU homolog prote | 495 | 69 | 6.1 | 420 | 2 | AB2426 | hypothetical prote |
| 423 | 70.5 | 6.3 | 968 | 2 | T00353 | hypothetical prote | 496 | 69 | 6.1 | 483 | 2 | G86902 | dextranucrase (BC |
| 424 | 70.5 | 6.3 | 1032 | 2 | T18293 | guanylate kinase-i | 497 | 69 | 6.1 | 511 | 2 | I50114 | early growth respo |
| 425 | 70.5 | 6.3 | 1123 | 2 | T18270 | hypothetical prote | 498 | 69 | 6.1 | 530 | 2 | S62439 | hypothetical serin |
| 426 | 70.5 | 6.3 | 1131 | 2 | T15787 | hypothetical prote | 499 | 69 | 6.1 | 608 | 2 | A46312 | gag polyprotein - |
| 427 | 70.5 | 6.3 | 1742 | 2 | TL1720 | cellulase (EC 3.2. | 500 | 69 | 6.1 | 652 | 2 | S50210 | surface layer prot |
| 428 | 70.5 | 6.3 | 3054 | 1 | GNEVEV | genome polyprotein | 501 | 69 | 6.1 | 658 | 2 | T41309 | hypothetical threo |
| 429 | 70.5 | 6.3 | 3069 | 2 | H70656 | fatty-acid synthas | 502 | 69 | 6.1 | 670 | 2 | F84540 | hypothetical prote |
| 430 | 70 | 6.2 | 147 | 2 | JC7938 | type II antifreeze | 503 | 69 | 6.1 | 790 | 2 | T34293 | hypothetical prote |
| 431 | 70 | 6.2 | 209 | 2 | AB2218 | hypothetical prote | 504 | 69 | 6.1 | 814 | 2 | T49207 | receptor kinase-li |
| 432 | 70 | 6.2 | 311 | 2 | H96002 | probable sugar kin | 505 | 69 | 6.1 | 850 | 1 | MMHUE4 | erythrocyte membra |
| 433 | 70 | 6.2 | 329 | 2 | S38082 | pathogenesis-relat | 506 | 69 | 6.1 | 854 | 1 | QRHYLD | LDL receptor precu |
| 434 | 70 | 6.2 | 340 | 2 | C90894 | probable LACI-type | 507 | 69 | 6.1 | 1169 | 2 | S38181 | flocculation prote |
| 435 | 70 | 6.2 | 340 | 2 | F85723 | probable LACI-type | 508 | 69 | 6.1 | 1199 | 2 | A40670 | nuclear envelope p |
| 436 | 70 | 6.2 | 340 | 2 | G64905 | sugar-binding prot | 509 | 69 | 6.1 | 1904 | 2 | T13256 | tail-host specific |
| 437 | 70 | 6.2 | 357 | 2 | E72245 | hydrolase, ama/hip | 510 | 69 | 6.1 | 2035 | 2 | A40718 | host cell factor C |
| 438 | 70 | 6.2 | 358 | 2 | A88082 | protein T05A8.7 li | 511 | 69 | 6.1 | 2067 | 2 | A42854 | probable spindle p |
| 439 | 70 | 6.2 | 408 | 2 | A45712 | glycoprotein IIa - | 512 | 69 | 6.1 | 2282 | 2 | T42717 | DNA-binding protei |
| 440 | 70 | 6.2 | 497 | 2 | T51195 | hypothetical prote | 513 | 69 | 6.1 | 2481 | 2 | D50011 | FmB protein limpo |
| 441 | 70 | 6.2 | 542 | 2 | B47022 | chitinase (EC 3.2. | 514 | 69 | 6.1 | 26926 | 1 | I38344 | titin, cardiac mus |
| 442 | 70 | 6.2 | 613 | 2 | B90294 | hypothetical prote | 515 | 68.5 | 6.1 | 204 | 2 | S51232 | gibberellin-respon |
| 443 | 70 | 6.2 | 767 | 1 | JU0474 | glucan 1,4-alpha-g | 516 | 68.5 | 6.1 | 213 | 2 | A86228 | hypothetical prote |
| 444 | 70 | 6.2 | 778 | 1 | ALBYG | glucan 1,4-alpha-g | 517 | 68.5 | 6.1 | 218 | 2 | AH1837 | hypothetical prote |
| 445 | 70 | 6.2 | 835 | 2 | F45140 | cell surface-assoc | 518 | 68.5 | 6.1 | 246 | 2 | S47805 | hypothetical 27.4K |
| 446 | 70 | 6.2 | 1048 | 1 | S61388 | dotA protein - leg | 519 | 68.5 | 6.1 | 246 | 2 | D91186 | probable outer mem |
| 447 | 70 | 6.2 | 1213 | 2 | A41724 | limb deformity (ld | 520 | 68.5 | 6.1 | 246 | 2 | C86033 | probable outer mem |
| 448 | 70 | 6.2 | 1726 | 2 | A39401 | merozoite surface | 521 | 68.5 | 6.1 | 261 | 2 | T30170 | hypothetical prote |
| 449 | 70 | 6.2 | 3507 | 2 | T34513 | hypothetical prote | 522 | 68.5 | 6.1 | 280 | 2 | AE2031 | gamma-tocopherol m |
| 450 | 69.5 | 6.2 | 120 | 1 | M4WL42 | E4 protein - human | 523 | 68.5 | 6.1 | 294 | 2 | AI2016 | hypothetical prote |
| 451 | 69.5 | 6.2 | 124 | 2 | E84613 | hypothetical prote | 524 | 68.5 | 6.1 | 310 | 1 | VAZQ31 | 300K antigen Ag231 |
| 452 | 69.5 | 6.2 | 150 | 2 | T48611 | agp6 protein - Ara | 525 | 68.5 | 6.1 | 318 | 2 | T20063 | hypothetical prote |
| 453 | 69.5 | 6.2 | 172 | 2 | T21753 | hypothetical prote | 526 | 68.5 | 6.1 | 359 | 2 | G70814 | probable far prote |
| 454 | 69.5 | 6.2 | 202 | 2 | AB2378 | hypothetical prote | 527 | 68.5 | 6.1 | 362 | 2 | T01196 | transcription fact |
| 455 | 69.5 | 6.2 | 299 | 2 | G70784 | probable mmp33 pro | 528 | 68.5 | 6.1 | 382 | 2 | T25280 | hypothetical prote |
| 456 | 69.5 | 6.2 | 372 | 2 | T48660 | heat shock protein | 529 | 68.5 | 6.1 | 385 | 2 | H97239 | polyferredoxin (im |
| 457 | 69.5 | 6.2 | 373 | 2 | F81333 | chaperone DnaJ Cj1 | 530 | 68.5 | 6.1 | 420 | 2 | A88962 | protein P59A7.1 li |
| 458 | 69.5 | 6.2 | 400 | 2 | T32705 | hypothetical prote | 531 | 68.5 | 6.1 | 426 | 2 | A35641 | 5-aminimidazole r |
| 459 | 69.5 | 6.2 | 425 | 1 | F0MWGC | gag polyprotein - | 532 | 68.5 | 6.1 | 435 | 2 | C86340 | protein F2D10.28 l |
| 460 | 69.5 | 6.2 | 432 | 2 | T08771 | hypothetical prote | 533 | 68.5 | 6.1 | 435 | 2 | T25350 | hypothetical prote |
| 461 | 69.5 | 6.2 | 458 | 2 | F86433 | protein Ti17H7.5 li | 534 | 68.5 | 6.1 | 498 | 1 | VGXPLA | surface glycoprote |
| 462 | 69.5 | 6.2 | 465 | 2 | S46759 | hypothetical prote | 535 | 68.5 | 6.1 | 500 | 1 | S60929 | probable aldehyde |
| 463 | 69.5 | 6.2 | 476 | 2 | B44997 | merozoite surface | 536 | 68.5 | 6.1 | 507 | 2 | S05542 | hypothetical prote |
| 464 | 69.5 | 6.2 | 514 | 2 | A44100 | cell adhesion mole | 537 | 68.5 | 6.1 | 509 | 2 | T48459 | cytochrome P450-li |
| 465 | 69.5 | 6.2 | 514 | 2 | A31643 | cell adhesion mole | 538 | 68.5 | 6.1 | 514 | 1 | A47692 | fumate hydratase |
| 466 | 69.5 | 6.2 | 519 | 2 | S69989 | unspecific monooxy | 539 | 68.5 | 6.1 | 535 | 2 | B84443 | hypothetical prote |
| 467 | 69.5 | 6.2 | 540 | 1 | F0MVHL | gag polyprotein - | 540 | 68.5 | 6.1 | 553 | 2 | A49364 | 59 protein, brain |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|--------------------|-----|------|-----|------|---|--------|----------------------|
| 541 | 68.5 | 6.1 | 607 | 2 | S63395 | probable membrane | 614 | 67.5 | 6.0 | 391 | 2 | A44063 | paired box transcr |
| 542 | 68.5 | 6.1 | 654 | 2 | T33044 | hypothetical prote | 615 | 67.5 | 6.0 | 399 | 2 | T42242 | hypothetical 44.2K |
| 543 | 68.5 | 6.1 | 659 | 2 | T40383 | hypothetical prote | 616 | 67.5 | 6.0 | 433 | 2 | S37790 | probable serine/th |
| 544 | 68.5 | 6.1 | 690 | 2 | T09483 | Cys-rich protein R | 617 | 67.5 | 6.0 | 435 | 2 | AG1028 | prepilin imported |
| 545 | 68.5 | 6.1 | 700 | 2 | A54641 | interspersed repea | 618 | 67.5 | 6.0 | 476 | 2 | T32032 | hypothetical prote |
| 546 | 68.5 | 6.1 | 721 | 2 | E70766 | hypothetical prote | 619 | 67.5 | 6.0 | 476 | 2 | T27051 | hypothetical prote |
| 547 | 68.5 | 6.1 | 737 | 2 | AG2156 | hypothetical prote | 620 | 67.5 | 6.0 | 493 | 2 | A34130 | gamma-aminobutyric |
| 548 | 68.5 | 6.1 | 795 | 2 | T20609 | hypothetical prote | 621 | 67.5 | 6.0 | 527 | 2 | T28878 | hypothetical prote |
| 549 | 68.5 | 6.1 | 802 | 2 | T21315 | hypothetical prote | 622 | 67.5 | 6.0 | 530 | 2 | T32812 | hypothetical prote |
| 550 | 68.5 | 6.1 | 865 | 2 | AC1966 | hypothetical prote | 623 | 67.5 | 6.0 | 538 | 2 | S65764 | chitinase (EC 3.2. |
| 551 | 68.5 | 6.1 | 942 | 2 | T19553 | hypothetical prote | 624 | 67.5 | 6.0 | 601 | 2 | S56144 | SH3 domain binding |
| 552 | 68.5 | 6.1 | 1200 | 1 | SNP80 | ice nucleation pro | 625 | 67.5 | 6.0 | 642 | 2 | T39607 | fork head protein |
| 553 | 68.5 | 6.1 | 1379 | 2 | T45119 | FIM protein (impor | 626 | 67.5 | 6.0 | 644 | 2 | T75141 | oligopeptide-bind |
| 554 | 68.5 | 6.1 | 1438 | 2 | A48216 | neurexin III-alpha | 627 | 67.5 | 6.0 | 651 | 2 | T21175 | hypothetical prote |
| 555 | 68.5 | 6.1 | 1471 | 2 | B48218 | neurexin III-alpha | 628 | 67.5 | 6.0 | 656 | 1 | A49358 | RNA-binding protei |
| 556 | 68.5 | 6.1 | 1541 | 2 | S46686 | hypothetical prote | 629 | 67.5 | 6.0 | 670 | 2 | T49510 | fibroin-3 related |
| 557 | 68.5 | 6.1 | 3122 | 2 | T17202 | DNA-directed DNA p | 630 | 67.5 | 6.0 | 710 | 2 | A9486 | ABC transporter, b |
| 558 | 68 | 6.0 | 62 | 2 | S53366 | mucin 5AC (Clone M | 631 | 67.5 | 6.0 | 736 | 2 | T41259 | hypothetical prote |
| 559 | 68 | 6.0 | 211 | 2 | H72608 | hypothetical prote | 632 | 67.5 | 6.0 | 749 | 2 | T50397 | probable serine/th |
| 560 | 68 | 6.0 | 248 | 2 | AF1914 | carbon dioxide con | 633 | 67.5 | 6.0 | 792 | 2 | S70305 | hypothetical prote |
| 561 | 68 | 6.0 | 295 | 2 | S50316 | CIN5 protein - yea | 634 | 67.5 | 6.0 | 815 | 2 | C84287 | hypothetical prote |
| 562 | 68 | 6.0 | 301 | 2 | H70644 | hypothetical prote | 635 | 67.5 | 6.0 | 839 | 2 | T41826 | hypothetical prote |
| 563 | 68 | 6.0 | 333 | 2 | T15367 | hypothetical prote | 636 | 67.5 | 6.0 | 872 | 2 | JH0561 | P95orf83 - Bombyx |
| 564 | 68 | 6.0 | 339 | 2 | AH0050 | probable periplasm | 637 | 67.5 | 6.0 | 886 | 2 | T23807 | metabolic glucosyl |
| 565 | 68 | 6.0 | 372 | 2 | T45628 | glycerophosphodias | 638 | 67.5 | 6.0 | 882 | 2 | S29605 | hypothetical prote |
| 566 | 68 | 6.0 | 378 | 2 | S61992 | SLG1 protein - yea | 639 | 67.5 | 6.0 | 901 | 2 | A44825 | glycoprotein 350/2 |
| 567 | 68 | 6.0 | 380 | 1 | S51826 | alcohol dehydrogen | 640 | 67.5 | 6.0 | 971 | 2 | F88448 | phosphoprotein, sy |
| 568 | 68 | 6.0 | 387 | 2 | A56275 | 1,3-propanediol de | 641 | 67.5 | 6.0 | 998 | 2 | S31735 | protein C45G9.10 { |
| 569 | 68 | 6.0 | 388 | 2 | T43019 | probable DNA-bind | 642 | 67.5 | 6.0 | 1051 | 2 | T51904 | NAD ADP-ribosyltra |
| 570 | 68 | 6.0 | 423 | 2 | T45331 | S-locus-specific g | 643 | 67.5 | 6.0 | 1203 | 2 | T04294 | hypothetical prote |
| 571 | 68 | 6.0 | 426 | 2 | T48379 | gene hb protein - | 644 | 67.5 | 6.0 | 1348 | 2 | S27812 | hypothetical prote |
| 572 | 68 | 6.0 | 452 | 2 | T46147 | zinc finger protei | 645 | 67.5 | 6.0 | 1348 | 2 | A43917 | probable epidermal |
| 573 | 68 | 6.0 | 456 | 2 | T38221 | hypothetical serin | 646 | 67.5 | 6.0 | 1633 | 2 | T01879 | probable epidermal |
| 574 | 68 | 6.0 | 479 | 2 | A84588 | probable tyrosine | 647 | 67.5 | 6.0 | 1751 | 2 | A45604 | hypothetical prote |
| 575 | 68 | 6.0 | 500 | 2 | A11913 | apolipoprotein N-a | 648 | 67.5 | 6.0 | 1784 | 2 | T10532 | major blood-stage |
| 576 | 68 | 6.0 | 502 | 2 | T21935 | hypothetical prote | 649 | 67.5 | 6.0 | 1896 | 2 | B72175 | gag-pol polyprotei |
| 577 | 68 | 6.0 | 515 | 2 | B84406 | hypothetical prote | 650 | 67.5 | 6.0 | 1897 | 2 | T28621 | D15R protein - var |
| 578 | 68 | 6.0 | 537 | 1 | FOVMV7 | TRK potassium upta | 651 | 67.5 | 6.0 | 3345 | 2 | T13423 | hypothetical prote |
| 579 | 68 | 6.0 | 530 | 2 | S66744 | gag polyprotein - | 652 | 67 | 6.0 | 149 | 2 | S12913 | hypothetical prote |
| 580 | 68 | 6.0 | 655 | 1 | A55726 | mucin (clone pGM7- | 653 | 67 | 6.0 | 201 | 1 | WNBEHL | cytostatin - fruit f |
| 581 | 68 | 6.0 | 669 | 2 | B70186 | RNA-binding protei | 654 | 67 | 6.0 | 214 | 2 | A46629 | UL4 protein - huma |
| 582 | 68 | 6.0 | 679 | 2 | S64258 | translation elonga | 655 | 67 | 6.0 | 232 | 1 | WMADC2 | mucin 6, gastric (|
| 583 | 68 | 6.0 | 709 | 2 | S51793 | hypothetical prote | 656 | 67 | 6.0 | 232 | 1 | WMADC2 | early E1A 25K prot |
| 584 | 68 | 6.0 | 730 | 2 | A75486 | hypothetical prote | 657 | 67 | 6.0 | 264 | 2 | A49149 | hypothetical prote |
| 585 | 68 | 6.0 | 749 | 2 | B86403 | hypothetical prote | 658 | 67 | 6.0 | 276 | 2 | T51685 | mesoderm developme |
| 586 | 68 | 6.0 | 816 | 2 | S64439 | probable mutator-1 | 659 | 67 | 6.0 | 305 | 2 | T24283 | myb-related trans |
| 587 | 68 | 6.0 | 871 | 2 | T43427 | hypothetical prote | 660 | 67 | 6.0 | 319 | 2 | T43040 | hypothetical prote |
| 588 | 68 | 6.0 | 916 | 2 | T20909 | pobl protein - fis | 661 | 67 | 6.0 | 398 | 2 | AE0975 | hypothetical prote |
| 589 | 68 | 6.0 | 1016 | 1 | J50428 | hypothetical prote | 662 | 67 | 6.0 | 402 | 2 | E86185 | probable racemase |
| 590 | 68 | 6.0 | 1098 | 2 | T08599 | NAD ADP-ribosyltra | 663 | 67 | 6.0 | 412 | 2 | B88736 | hypothetical prote |
| 591 | 68 | 6.0 | 1131 | 2 | T41144 | probable transcrip | 664 | 67 | 6.0 | 426 | 2 | F75394 | protein F33D4.6a { |
| 592 | 68 | 6.0 | 1203 | 2 | T51029 | hypothetical serin | 665 | 67 | 6.0 | 438 | 1 | S70602 | hypothetical prote |
| 593 | 68 | 6.0 | 1204 | 2 | F81158 | related to pathway | 666 | 67 | 6.0 | 441 | 2 | C75076 | cellulose 1,4-beta |
| 594 | 68 | 6.0 | 1275 | 2 | T33369 | exodeoxyribonuclea | 667 | 67 | 6.0 | 443 | 2 | T14916 | heme biosynthesis |
| 595 | 68 | 6.0 | 1390 | 2 | T18883 | hypothetical prote | 668 | 67 | 6.0 | 448 | 2 | G88639 | mitosis-specific c |
| 596 | 68 | 6.0 | 1401 | 2 | T30247 | hypothetical prote | 669 | 67 | 6.0 | 466 | 2 | S45419 | protein C34H4.2 {i |
| 597 | 68 | 6.0 | 1578 | 2 | I48216 | werner syndrome pr | 670 | 67 | 6.0 | 476 | 2 | C39481 | hypothetical prote |
| 598 | 68 | 6.0 | 1711 | 2 | T31337 | neurexin III-alpha | 671 | 67 | 6.0 | 486 | 2 | B39481 | serum response fac |
| 599 | 68 | 6.0 | 2440 | 2 | S39162 | 1,4-beta-glucanase | 672 | 67 | 6.0 | 494 | 1 | A29079 | serum response fac |
| 600 | 68 | 6.0 | 2441 | 2 | S39161 | transcription coac | 673 | 67 | 6.0 | 494 | 1 | A29079 | lymphocyte surface |
| 601 | 68 | 6.0 | 3191 | 2 | T22945 | CREB-binding prote | 674 | 67 | 6.0 | 514 | 2 | H70699 | probable ppp prote |
| 602 | 68 | 6.0 | 3712 | 2 | S18253 | hypothetical prote | 675 | 67 | 6.0 | 536 | 2 | H71563 | hypothetical prote |
| 603 | 67.5 | 6.0 | 150 | 2 | T52587 | laminin alpha-1 ch | 676 | 67 | 6.0 | 549 | 2 | S04845 | Ig heavy chain pre |
| 604 | 67.5 | 6.0 | 159 | 2 | T31598 | probable arabinoga | 677 | 67 | 6.0 | 558 | 2 | S57953 | C4BP protein alpha |
| 605 | 67.5 | 6.0 | 191 | 2 | S38117 | hypothetical prote | 678 | 67 | 6.0 | 579 | 2 | D84137 | methyl-accepting c |
| 606 | 67.5 | 6.0 | 210 | 2 | B88082 | hypothetical prote | 679 | 67 | 6.0 | 581 | 2 | B86408 | F3H9.11 protein - |
| 607 | 67.5 | 6.0 | 256 | 2 | H36857 | protein T05A8.6 {i | 680 | 67 | 6.0 | 588 | 2 | B70618 | probable PE protei |
| 608 | 67.5 | 6.0 | 297 | 2 | S55063 | B26R protein - var | 681 | 67 | 6.0 | 610 | 1 | I46001 | C4b-binding protei |
| 609 | 67.5 | 6.0 | 338 | 2 | S28004 | conserved hypothet | 682 | 67 | 6.0 | 617 | 2 | T15408 | hypothetical prote |
| 610 | 67.5 | 6.0 | 345 | 2 | E88103 | probable cell surf | 683 | 67 | 6.0 | 620 | 2 | A70525 | hypothetical prote |
| 611 | 67.5 | 6.0 | 346 | 2 | T46916 | protein w10G11.5 { | 684 | 67 | 6.0 | 634 | 2 | T49415 | hypothetical prote |
| 612 | 67.5 | 6.0 | 376 | 2 | S22137 | hypothetical prote | 685 | 67 | 6.0 | 636 | 2 | S63131 | probable membrane |
| 613 | 67.5 | 6.0 | 387 | 2 | A86302 | MID2 protein - yea | 686 | 67 | 6.0 | 644 | 2 | F81411 | probable ribonucle |
| | | | | | | hypothetical prote | | | | 650 | 2 | S22835 | alpha-agglutinin - |

| | | | | | | | | | | | | |
|-----|------|------|-----|--------|----------------------|-----|------|-----|------|---|--------|---------------------|
| 687 | 6.0 | 672 | 2 | T32557 | hypothetical prote | 760 | 66.5 | 5.9 | 919 | 2 | T16693 | hypothetical prote |
| 688 | 6.0 | 698 | 1 | JX0202 | long-chain-fatty-a | 761 | 66.5 | 5.9 | 996 | 2 | JE0237 | apolipoprotein E r |
| 689 | 6.0 | 710 | 2 | T21339 | hypothetical prote | 762 | 66.5 | 5.9 | 1059 | 2 | T22545 | hypothetical prote |
| 690 | 6.0 | 723 | 2 | H85092 | hypothetical prote | 763 | 66.5 | 5.9 | 1060 | 2 | T31763 | hypothetical prote |
| 691 | 6.0 | 732 | 2 | T25937 | hypothetical prote | 764 | 66.5 | 5.9 | 1221 | 2 | A10193 | ribonuclease E (EC |
| 692 | 6.0 | 784 | 2 | S26638 | SPR-1 protein - hu | 765 | 66.5 | 5.9 | 1369 | 2 | S70713 | protein-tyrosine k |
| 693 | 6.0 | 824 | 2 | T23923 | hypothetical prote | 766 | 66.5 | 5.9 | 1655 | 2 | T32633 | hypothetical prote |
| 694 | 6.0 | 826 | 2 | G90283 | hypothetical prote | 767 | 66.5 | 5.9 | 1868 | 2 | S48938 | hypothetical prote |
| 695 | 6.0 | 850 | 2 | S56015 | gastric mucin MUC5 | 768 | 66 | 5.9 | 162 | 2 | T02072 | probable glycine c |
| 696 | 6.0 | 855 | 2 | T19405 | hypothetical prote | 769 | 66 | 5.9 | 162 | 2 | A49247 | merozoite surface |
| 697 | 6.0 | 910 | 2 | C69456 | subtilisin sendai | 770 | 66 | 5.9 | 193 | 2 | D72643 | hypothetical prote |
| 698 | 6.0 | 948 | 2 | T11678 | hypothetical prote | 771 | 66 | 5.9 | 253 | 2 | T27279 | hypothetical prote |
| 699 | 6.0 | 1140 | 2 | D88690 | protein F41H10.3 (| 772 | 66 | 5.9 | 255 | 2 | B75309 | hypothetical prote |
| 700 | 6.0 | 1140 | 2 | S73786 | hypothetical prote | 773 | 66 | 5.9 | 256 | 2 | JC2398 | PM33 homolog misma |
| 701 | 6.0 | 1228 | 2 | C98219 | proline dehydratogen | 774 | 66 | 5.9 | 259 | 2 | E82029 | methionyl aminopap |
| 702 | 6.0 | 1228 | 2 | AG3067 | proline dehydratogen | 775 | 66 | 5.9 | 282 | 2 | B90313 | conserved hypothet |
| 703 | 6.0 | 1401 | 2 | T17452 | werner syndrome pr | 776 | 66 | 5.9 | 315 | 2 | S74357 | hypothetical prote |
| 704 | 6.0 | 1630 | 2 | A53577 | ascites sialoglyco | 777 | 66 | 5.9 | 360 | 2 | T33835 | hypothetical prote |
| 705 | 6.0 | 1804 | 2 | H96597 | hypothetical prote | 778 | 66 | 5.9 | 367 | 1 | W2WL11 | E2 protein - human |
| 706 | 6.0 | 1819 | 2 | T32008 | hypothetical prote | 779 | 66 | 5.9 | 369 | 2 | A11079 | conserved hypothet |
| 707 | 6.0 | 1900 | 2 | S45530 | probable 1-phospha | 780 | 66 | 5.9 | 375 | 2 | S36547 | E2 protein - human |
| 708 | 6.0 | 2476 | 2 | T34022 | zonadhesin pig | 781 | 66 | 5.9 | 380 | 1 | S00912 | alcohol dehydrogen |
| 709 | 6.0 | 4377 | 2 | AS5575 | ankyrin 3, long sp | 782 | 66 | 5.9 | 383 | 2 | E96972 | riboflavin biosynt |
| 710 | 66.5 | 5.9 | 128 | T05635 | hypothetical prote | 783 | 66 | 5.9 | 393 | 1 | HVRKCI | 120K lysosomal mem |
| 711 | 66.5 | 5.9 | 148 | S05653 | hypothetical prote | 784 | 66 | 5.9 | 407 | 2 | A30200 | ig mu chain C regi |
| 712 | 66.5 | 5.9 | 149 | E71227 | hypothetical prote | 785 | 66 | 5.9 | 426 | 2 | B53580 | neurexin III beta |
| 713 | 66.5 | 5.9 | 175 | T50094 | hypothetical prote | 786 | 66 | 5.9 | 431 | 2 | G86277 | dermal glycoprotei |
| 714 | 66.5 | 5.9 | 217 | S45446 | hypothetical prote | 787 | 66 | 5.9 | 433 | 2 | T14329 | ADH2 dehydrogenas |
| 715 | 66.5 | 5.9 | 238 | T07921 | probable starch sy | 788 | 66 | 5.9 | 459 | 2 | T17364 | L2 protein - human |
| 716 | 66.5 | 5.9 | 240 | S31573 | hypothetical prote | 789 | 66 | 5.9 | 463 | 1 | P2WL13 | cellulose 1,4-beta |
| 717 | 66.5 | 5.9 | 254 | D88560 | protein F58A4.1 (i | 790 | 66 | 5.9 | 471 | 1 | A38979 | cellulose 1,4-beta |
| 718 | 66.5 | 5.9 | 263 | S01360 | salivary glue prot | 791 | 66 | 5.9 | 471 | 1 | A26160 | hypothetical prote |
| 719 | 66.5 | 5.9 | 319 | A35163 | carbonate dehydrat | 792 | 66 | 5.9 | 482 | 2 | S76376 | hypothetical prote |
| 720 | 66.5 | 5.9 | 327 | H82554 | conserved hypothet | 793 | 66 | 5.9 | 584 | 2 | JC7809 | sulfakinin recepto |
| 721 | 66.5 | 5.9 | 345 | AH0457 | UDP-N-acetylmuram | 794 | 66 | 5.9 | 599 | 2 | G71481 | probable phosphoen |
| 722 | 66.5 | 5.9 | 348 | T37760 | UTP-hexose-1-phosp | 795 | 66 | 5.9 | 611 | 2 | T04510 | hypothetical prote |
| 723 | 66.5 | 5.9 | 348 | AE0594 | galactose-1-phosph | 796 | 66 | 5.9 | 614 | 2 | A43390 | gamma-aminobutyric |
| 724 | 66.5 | 5.9 | 359 | S42787 | serine/threonine-r | 797 | 66 | 5.9 | 627 | 2 | T15969 | hypothetical prote |
| 725 | 66.5 | 5.9 | 369 | E84291 | iron (III) ABC tra | 798 | 66 | 5.9 | 629 | 2 | T27123 | hypothetical prote |
| 726 | 66.5 | 5.9 | 371 | AJMSQ3 | glutamate-ammonia | 799 | 66 | 5.9 | 643 | 2 | H84305 | Htr8 transducer (i |
| 727 | 66.5 | 5.9 | 371 | FOVCS | gag polyprotein - | 800 | 66 | 5.9 | 645 | 2 | T16078 | hypothetical prote |
| 728 | 66.5 | 5.9 | 373 | AJHUQ | glutamate-ammonia | 801 | 66 | 5.9 | 655 | 2 | AD2422 | DNA polymerase III |
| 729 | 66.5 | 5.9 | 385 | T38113 | hypothetical serin | 802 | 66 | 5.9 | 657 | 2 | E96812 | protein F3F9.10 (i |
| 730 | 66.5 | 5.9 | 397 | T22932 | hypothetical prote | 803 | 66 | 5.9 | 657 | 2 | H71422 | hypothetical prote |
| 731 | 66.5 | 5.9 | 413 | S48756 | transcription fact | 804 | 66 | 5.9 | 674 | 2 | G70875 | probable oxidoredu |
| 732 | 66.5 | 5.9 | 452 | T25827 | hypothetical prote | 805 | 66 | 5.9 | 687 | 2 | A49636 | soluble vascular e |
| 733 | 66.5 | 5.9 | 458 | T31631 | hypothetical prote | 806 | 66 | 5.9 | 730 | 2 | A53064 | folded gastrulatio |
| 734 | 66.5 | 5.9 | 461 | D72414 | anthranilate synth | 807 | 66 | 5.9 | 733 | 2 | T01875 | probable long-chai |
| 735 | 66.5 | 5.9 | 506 | AG1864 | hypothetical prote | 808 | 66 | 5.9 | 786 | 1 | A47547 | serine proteinase |
| 736 | 66.5 | 5.9 | 507 | T23375 | hypothetical prote | 809 | 66 | 5.9 | 816 | 2 | A49151 | fibroblast growth |
| 737 | 66.5 | 5.9 | 516 | A31270 | radial spoke prote | 810 | 66 | 5.9 | 897 | 2 | S50550 | SIN1-associated pr |
| 738 | 66.5 | 5.9 | 521 | S69559 | hypothetical prote | 811 | 66 | 5.9 | 978 | 1 | RGBY13 | regulatory protein |
| 739 | 66.5 | 5.9 | 521 | C87472 | hypothetical prote | 812 | 66 | 5.9 | 994 | 1 | KNWVM | nonstructural prot |
| 740 | 66.5 | 5.9 | 527 | T16022 | hypothetical prote | 813 | 66 | 5.9 | 1039 | 2 | T09883 | hypothetical prote |
| 741 | 66.5 | 5.9 | 542 | JN0661 | heat shock protein | 814 | 66 | 5.9 | 1041 | 2 | S55862 | probable membrane |
| 742 | 66.5 | 5.9 | 542 | S32106 | groEL protein - la | 815 | 66 | 5.9 | 1273 | 2 | S58782 | SEC31 protein - ye |
| 743 | 66.5 | 5.9 | 562 | B41035 | chitinase (EC 3.2. | 816 | 66 | 5.9 | 1338 | 2 | S09982 | protein-tyrosine k |
| 744 | 66.5 | 5.9 | 562 | S50371 | chitinase (EC 3.2. | 817 | 66 | 5.9 | 1422 | 2 | T42636 | protein-tyrosine-p |
| 745 | 66.5 | 5.9 | 571 | H97070 | membrane associate | 818 | 66 | 5.9 | 1711 | 2 | AB1283 | peptidoglycan link |
| 746 | 66.5 | 5.9 | 615 | T47395 | hypothetical prote | 819 | 66 | 5.9 | 2271 | 2 | F90073 | hypothetical prote |
| 747 | 66.5 | 5.9 | 637 | T20981 | hypothetical prote | 820 | 66 | 5.9 | 2405 | 2 | T08164 | dynein alpha heavy |
| 748 | 66.5 | 5.9 | 648 | T43337 | polo-like kinase-1 | 821 | 65.5 | 5.8 | 157 | 2 | JP0075 | lectin CEL-IV, C-t |
| 749 | 66.5 | 5.9 | 650 | I49523 | tumor necrosis fac | 822 | 65.5 | 5.8 | 198 | 2 | A40709 | ecdysone receptor |
| 750 | 66.5 | 5.9 | 681 | A45705 | type I transmembra | 823 | 65.5 | 5.8 | 211 | 1 | MUKAD | lysozyme (EC 3.2.1 |
| 751 | 66.5 | 5.9 | 710 | S67098 | probable membrane | 824 | 65.5 | 5.8 | 248 | 2 | T40149 | hypothetical prote |
| 752 | 66.5 | 5.9 | 719 | T23170 | hypothetical prote | 825 | 65.5 | 5.8 | 282 | 2 | T21222 | hypothetical prote |
| 753 | 66.5 | 5.9 | 739 | I56187 | transcription fact | 826 | 65.5 | 5.8 | 287 | 2 | S65765 | chitinase (EC 3.2. |
| 754 | 66.5 | 5.9 | 811 | A41054 | fasciclin II, tran | 827 | 65.5 | 5.8 | 290 | 2 | A43897 | spiculae matrix pro |
| 755 | 66.5 | 5.9 | 843 | S44868 | kinesin heavy chai | 828 | 65.5 | 5.8 | 314 | 2 | D96703 | hypothetical prote |
| 756 | 66.5 | 5.9 | 880 | S44833 | F54H12.5 protein - | 829 | 65.5 | 5.8 | 316 | 2 | G86333 | hypothetical prote |
| 757 | 66.5 | 5.9 | 896 | S46326 | clathrin assembly | 830 | 65.5 | 5.8 | 328 | 2 | S69715 | hypothetical prote |
| 758 | 66.5 | 5.9 | 913 | D82885 | multiple banded an | 831 | 65.5 | 5.8 | 356 | 2 | D86382 | hypothetical prote |
| 759 | 66.5 | 5.9 | 915 | S36327 | clathrin assembly | 832 | 65.5 | 5.8 | 365 | 2 | T26564 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|---------------------|-----|------|-----|------|---|--------|---------------------|
| 833 | 65.5 | 5.8 | 377 | 2 | A48018 | mucin 7 precursor, | 906 | 65 | 5.8 | 633 | 2 | T04835 | probable serine/th |
| 834 | 65.5 | 5.8 | 443 | 2 | C88427 | protein R075.6 [i | 907 | 65 | 5.8 | 674 | 2 | T15524 | hypothetical prote |
| 835 | 65.5 | 5.8 | 459 | 2 | G84752 | En/Spm-like transp | 908 | 65 | 5.8 | 706 | 2 | S33761 | transferrin precu |
| 836 | 65.5 | 5.8 | 460 | 2 | T23955 | hypothetical prote | 909 | 65 | 5.8 | 708 | 2 | T29669 | hypothetical prote |
| 837 | 65.5 | 5.8 | 461 | 2 | T39862 | hypothetical prote | 910 | 65 | 5.8 | 742 | 2 | A42166 | hypothetical prote |
| 838 | 65.5 | 5.8 | 463 | 2 | T15416 | hypothetical prote | 911 | 65 | 5.8 | 770 | 2 | G88445 | protein C46E6.2 [i |
| 839 | 65.5 | 5.8 | 493 | 2 | JC5486 | membrane glycoprot | 912 | 65 | 5.8 | 775 | 1 | WMBE19 | ribonucleoside-dip |
| 840 | 65.5 | 5.8 | 497 | 2 | D81723 | conserved hypotet | 913 | 65 | 5.8 | 786 | 2 | A55501 | cyclin F - human |
| 841 | 65.5 | 5.8 | 516 | 2 | T24644 | hypothetical prote | 914 | 65 | 5.8 | 792 | 2 | F90566 | conserved hypotet |
| 842 | 65.5 | 5.8 | 526 | 2 | C84552 | hypothetical prote | 915 | 65 | 5.8 | 817 | 2 | F86742 | ribonuclease (impo |
| 843 | 65.5 | 5.8 | 540 | 2 | T19956 | hypothetical prote | 916 | 65 | 5.8 | 859 | 2 | T29630 | hypothetical prote |
| 844 | 65.5 | 5.8 | 541 | 2 | T44725 | chaperonin 60K [im | 917 | 65 | 5.8 | 874 | 2 | A10281 | probable insectici |
| 845 | 65.5 | 5.8 | 575 | 2 | S29316 | chaperonin 60 - cu | 918 | 65 | 5.8 | 876 | 2 | T05943 | probable lipoxigen |
| 846 | 65.5 | 5.8 | 575 | 2 | T34280 | hypothetical prote | 919 | 65 | 5.8 | 921 | 2 | A45183 | TBP-associated fac |
| 847 | 65.5 | 5.8 | 588 | 2 | A25902 | 65K antigen - Myco | 920 | 65 | 5.8 | 921 | 2 | A48184 | transcription init |
| 848 | 65.5 | 5.8 | 592 | 2 | S43529 | coiled-coil protei | 921 | 65 | 5.8 | 955 | 2 | F84914 | hypothetical prote |
| 849 | 65.5 | 5.8 | 594 | 2 | S62529 | hypothetical prote | 922 | 65 | 5.8 | 973 | 2 | B86547 | polymorphic outer |
| 850 | 65.5 | 5.8 | 604 | 1 | JP0001 | glucan 1,4-alpha-g | 923 | 65 | 5.8 | 973 | 2 | F27076 | polymorphic outer |
| 851 | 65.5 | 5.8 | 628 | 2 | F84219 | Htr16 transducer [| 924 | 65 | 5.8 | 995 | 2 | C81593 | polymorphic membra |
| 852 | 65.5 | 5.8 | 631 | 2 | T32761 | hypothetical prote | 925 | 65 | 5.8 | 1088 | 1 | IUXLNL | neural cell adhesi |
| 853 | 65.5 | 5.8 | 642 | 1 | T44253 | transducer protein | 926 | 65 | 5.8 | 1095 | 2 | PC1114 | SKDC25 protein - |
| 854 | 65.5 | 5.8 | 649 | 2 | JQ0103 | hypothetical 70K p | 927 | 65 | 5.8 | 1096 | 2 | H86237 | protein F14N23.29 |
| 855 | 65.5 | 5.8 | 667 | 2 | T15710 | hypothetical prote | 928 | 65 | 5.8 | 1097 | 2 | T49187 | hypothetical prote |
| 856 | 65.5 | 5.8 | 679 | 2 | T13703 | hypothetical prote | 929 | 65 | 5.8 | 1124 | 2 | F17119 | hypothetical prote |
| 857 | 65.5 | 5.8 | 713 | 2 | T44447 | neuregulin-3 limpo | 930 | 65 | 5.8 | 1139 | 1 | E64234 | cytadherence-acces |
| 858 | 65.5 | 5.8 | 746 | 2 | G02838 | enhancer-of-zeste | 931 | 65 | 5.8 | 1146 | 2 | S46837 | hypothetical prote |
| 859 | 65.5 | 5.8 | 759 | 2 | T44142 | DR1 protein (impor | 932 | 65 | 5.8 | 1156 | 2 | T43326 | germline RNA helic |
| 860 | 65.5 | 5.8 | 784 | 2 | AH2560 | hypothetical prote | 933 | 65 | 5.8 | 1172 | 2 | T32759 | hypothetical prote |
| 861 | 65.5 | 5.8 | 790 | 1 | FQMVHZ | gag-kit polyprotei | 934 | 65 | 5.8 | 1216 | 2 | B50580 | hypothetical prote |
| 862 | 65.5 | 5.8 | 815 | 2 | H84199 | dihydropterate sy | 935 | 65 | 5.8 | 1314 | 2 | H86327 | hypothetical prote |
| 863 | 65.5 | 5.8 | 821 | 2 | S39983 | eps8 protein - mou | 936 | 65 | 5.8 | 1459 | 2 | T32271 | hypothetical prote |
| 864 | 65.5 | 5.8 | 826 | 2 | T46060 | hypothetical prote | 937 | 65 | 5.8 | 1566 | 2 | T20058 | hypothetical prote |
| 865 | 65.5 | 5.8 | 841 | 2 | B71212 | hypothetical prote | 938 | 65 | 5.8 | 1605 | 2 | T13435 | DNA-directed RNA p |
| 866 | 65.5 | 5.8 | 841 | 2 | F90070 | Clumping factor B | 939 | 65 | 5.8 | 1642 | 2 | T19130 | hypothetical prote |
| 867 | 65.5 | 5.8 | 877 | 2 | T13029 | beta-adaptin homol | 940 | 65 | 5.8 | 1895 | 2 | T15881 | hypothetical prote |
| 868 | 65.5 | 5.8 | 894 | 2 | T23908 | hypothetical prote | 941 | 65 | 5.8 | 1970 | 2 | T03284 | myoblast city prot |
| 869 | 65.5 | 5.8 | 975 | 2 | F97302 | hypothetical prote | 942 | 65 | 5.8 | 2311 | 1 | TVCHSR | kinase-related pro |
| 870 | 65.5 | 5.8 | 1043 | 2 | A27069 | lethal (2) giant 1 | 943 | 64.5 | 5.7 | 69 | 2 | D72852 | actin rearrangemen |
| 871 | 65.5 | 5.8 | 1161 | 2 | S25370 | MSB2 protein - yea | 944 | 64.5 | 5.7 | 117 | 2 | AB0028 | 50S ribosomal prot |
| 872 | 65.5 | 5.8 | 1306 | 2 | S25370 | protein-tyrosine-p | 945 | 64.5 | 5.7 | 134 | 2 | T24968 | hypothetical prote |
| 873 | 65.5 | 5.8 | 1442 | 1 | B48148 | surface layer prot | 946 | 64.5 | 5.7 | 153 | 2 | S67294 | hypothetical prote |
| 874 | 65.5 | 5.8 | 1524 | 2 | S68553 | hypothetical prote | 947 | 64.5 | 5.7 | 204 | 2 | S67295 | probable membrane |
| 875 | 65.5 | 5.8 | 1650 | 2 | S28721 | hypothetical prote | 948 | 64.5 | 5.7 | 220 | 2 | I50588 | fibroblast growth |
| 876 | 65.5 | 5.8 | 1829 | 2 | T24583 | hypothetical prote | 949 | 64.5 | 5.7 | 224 | 2 | G83392 | hypothetical prote |
| 877 | 65.5 | 5.8 | 3124 | 2 | A40020 | collagen alpha 1(X | 950 | 64.5 | 5.7 | 226 | 2 | T28268 | hypothetical prote |
| 878 | 65.5 | 5.8 | 7576 | 2 | T17428 | FK506 polyketide s | 951 | 64.5 | 5.7 | 227 | 2 | T50033 | hypothetical prote |
| 879 | 65 | 5.8 | 179 | 2 | T26929 | hypothetical prote | 952 | 64.5 | 5.7 | 292 | 2 | JC4741 | mosquitoicidal toxi |
| 880 | 65 | 5.8 | 194 | 2 | B72642 | hypothetical prote | 953 | 64.5 | 5.7 | 313 | 2 | A34677 | secretory pathway |
| 881 | 65 | 5.8 | 244 | 2 | D90783 | probable outer mem | 954 | 64.5 | 5.7 | 322 | 2 | AH2192 | hypothetical prote |
| 882 | 65 | 5.8 | 244 | 2 | F85643 | outer membrane pre | 955 | 64.5 | 5.7 | 322 | 2 | AH2192 | hypothetical prote |
| 883 | 65 | 5.8 | 271 | 2 | B96773 | hypothetical prote | 956 | 64.5 | 5.7 | 326 | 2 | S67570 | hypothetical prote |
| 884 | 65 | 5.8 | 275 | 2 | T48436 | hypothetical prote | 957 | 64.5 | 5.7 | 336 | 2 | T15837 | hypothetical prote |
| 885 | 65 | 5.8 | 282 | 2 | T26397 | hypothetical prote | 958 | 64.5 | 5.7 | 341 | 2 | C83578 | hypothetical prote |
| 886 | 65 | 5.8 | 284 | 2 | A97203 | 2-oxoacid ferredox | 959 | 64.5 | 5.7 | 345 | 2 | T12344 | NADH2 dehydrogenas |
| 887 | 65 | 5.8 | 332 | 2 | T31928 | hypothetical prote | 960 | 64.5 | 5.7 | 349 | 2 | T42965 | glycoprotein - ate |
| 888 | 65 | 5.8 | 348 | 2 | AD3264 | electron transfer | 961 | 64.5 | 5.7 | 354 | 2 | S59521 | mucin sac - mouse |
| 889 | 65 | 5.8 | 373 | 2 | AG3191 | amide hydrolase [i | 962 | 64.5 | 5.7 | 378 | 2 | A33271 | manganese peroxida |
| 890 | 65 | 5.8 | 380 | 1 | S53307 | alcohol dehydrogen | 963 | 64.5 | 5.7 | 385 | 2 | AC2857 | conserved hypotet |
| 891 | 65 | 5.8 | 392 | 2 | T49471 | mucin (muc3) relat | 964 | 64.5 | 5.7 | 385 | 2 | A97634 | hypothetical prote |
| 892 | 65 | 5.8 | 393 | 2 | A49008 | paired box transcr | 965 | 64.5 | 5.7 | 397 | 2 | B69378 | probable acyl-CoA |
| 893 | 65 | 5.8 | 402 | 2 | T20595 | hypothetical prote | 966 | 64.5 | 5.7 | 402 | 2 | D69530 | probable acyl-CoA |
| 894 | 65 | 5.8 | 434 | 2 | S62168 | hypothetical prote | 967 | 64.5 | 5.7 | 416 | 2 | S65110 | chitinase (EC 3.2. |
| 895 | 65 | 5.8 | 459 | 2 | T17358 | NADH2 dehydrogenas | 968 | 64.5 | 5.7 | 420 | 1 | AJBYRS | argininosuccinate |
| 896 | 65 | 5.8 | 465 | 2 | T34984 | probable integral | 969 | 64.5 | 5.7 | 424 | 1 | VBEE9 | glycoprotein gp63 |
| 897 | 65 | 5.8 | 473 | 2 | G90401 | flagella-related p | 970 | 64.5 | 5.7 | 425 | 1 | A26431 | nerve growth facto |
| 898 | 65 | 5.8 | 503 | 2 | S63257 | probable membrane | 971 | 64.5 | 5.7 | 446 | 2 | T07907 | hydroxyproline-ric |
| 899 | 65 | 5.8 | 516 | 2 | JE0134 | mannan endo-1,4-be | 972 | 64.5 | 5.7 | 471 | 2 | T15155 | hypothetical prote |
| 900 | 65 | 5.8 | 588 | 2 | JC5013 | 2,4-chlorocatechol | 973 | 64.5 | 5.7 | 485 | 2 | T37550 | hypothetical coile |
| 901 | 65 | 5.8 | 608 | 2 | S05341 | probable reverse t | 974 | 64.5 | 5.7 | 491 | 2 | G86297 | F309.8 protein - A |
| 902 | 65 | 5.8 | 609 | 2 | S36569 | E1 protein - human | 975 | 64.5 | 5.7 | 512 | 2 | E59437 | F02569.2 protein [|
| 903 | 65 | 5.8 | 611 | 2 | E86388 | probable chaperoni | 976 | 64.5 | 5.7 | 519 | 1 | S69988 | unspecific monooxy |
| 904 | 65 | 5.8 | 618 | 2 | A10171 | probable exported | 977 | 64.5 | 5.7 | 532 | 2 | B35621 | spore germination |
| 905 | 65 | 5.8 | 619 | 2 | A43361 | Ets-related transcr | 978 | 64.5 | 5.7 | 568 | 2 | A34891 | ig heavy chain pre |
| | | | 627 | 2 | S37954 | RNA polymerase I t | | | | 568 | 2 | I58106 | gene DMR-N9 protei |

979 64.5 5.7 570 2 H97244 membrane associate
980 64.5 5.7 574 2 E82282 probable chitinase
981 64.5 5.7 577 2 A60501 thrombomodulin pre
982 64.5 5.7 587 2 S21139 amine oxidase (cop
983 64.5 5.7 590 2 S69556 hypothetical prote
984 64.5 5.7 593 2 S49525 glycoprotein G - s
985 64.5 5.7 623 2 A48123 cell cycle regulat
986 64.5 5.7 631 2 H70754 probable abc trans
987 64.5 5.7 648 2 A32576 beta-glucuronidase
988 64.5 5.7 680 2 S26764 major coat protein
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993 64.5 5.7 770 1 S30293 transcription fact
994 64.5 5.7 802 2 T32448 hypothetical prote
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997 64.5 5.7 920 1 PKX2P H+-exporting ATPas
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1003 64.5 5.7 1125 2 B41206 microtubule-associ
1004 64.5 5.7 1152 2 AC1347 probable peptidogl
1005 64.5 5.7 1160 2 A27868 lethal (2) giant l
1006 64.5 5.7 1200 2 T17404 hyalin - sea urchi
1007 64.5 5.7 1205 2 S64819 probable membrane
1008 64.5 5.7 1249 2 A56511 myosin I myoA - Em
1009 64.5 5.7 1277 2 S70306 hypothetical prote
1010 64.5 5.7 1477 2 AG3009 polyketide synthet
1011 64.5 5.7 1489 2 G98274 hypothetical prote
1012 64.5 5.7 1501 2 C84512 hypothetical prote
1013 64.5 5.7 1505 2 S26765 genome retroelem
1014 64.5 5.7 1842 2 T43409 probable fatty-ac
1015 64.5 5.7 1842 2 T38781 fatty acid synthas
1016 64 5.7 131 2 T25705 hypothetical prote
1017 64 5.7 171 2 H86413 hypothetical prote
1018 64 5.7 230 2 T33364 hypothetical prote
1019 64 5.7 234 2 E72456 hypothetical prote
1020 64 5.7 259 2 C81008 methionine aminope
1021 64 5.7 268 2 S63630 acid proteinase (E
1022 64 5.7 279 2 E82689 conserved hypothet
1023 64 5.7 298 2 D95354 probable epimerase
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1030 64 5.7 364 1 EDBESP immediate-early pr
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1032 64 5.7 384 2 S36529 E2 protein - human
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1037 64 5.7 416 2 S68822 neurotensin recept
1038 64 5.7 417 2 S76588 hypothetical prote
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1040 64 5.7 428 2 D86003 hypothetical prote
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1042 64 5.7 438 1 HVRKCS ig mu chain C regl
1043 64 5.7 461 1 HVRKCO ig mu chain C regl
1044 64 5.7 461 2 D96647 hypothetical prote
1045 64 5.7 471 2 S46739 hypothetical prote
1046 64 5.7 473 2 T45954 hypothetical prote
1047 64 5.7 519 2 T45764 hypothetical prote
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1053 64 5.7 562 2 T49386 hypothetical prote
1054 64 5.7 580 2 T20716 hypothetical prote
1055 64 5.7 583 2 S67571 hypothetical prote
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1059 64 5.7 664 2 T48258 kinesin-like prote
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1061 64 5.7 745 2 T03119 hypothetical prote
1062 64 5.7 750 2 T10864 transcription acti
1063 64 5.7 756 2 T27642 hypothetical prote
1064 64 5.7 768 2 A29066 DNA ligase (ATP) (
1065 64 5.7 801 2 A37353 membrane protein 4
1066 64 5.7 825 1 GLHQ beta-glucosidase (
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1072 64 5.7 1280 2 E55031 alkaline amylopull
1073 64 5.7 1282 2 JE0120 glycoprotein A - m
1074 64 5.7 1328 2 T43060 agrin - electric r
1075 64 5.7 1445 1 A48148 protein-tyrosine-p
1076 64 5.7 1547 2 T28657 blackjack protein,
1077 64 5.7 1607 2 T02837 long chain fatty a
1078 64 5.7 1671 2 S71628 sensory transducti
1079 64 5.7 1859 1 A34092 DNA-directed RNA p
1080 64 5.7 1862 2 T29959 DNA-directed RNA p
1081 64 5.7 1870 2 D88486 protein F20H11.2 [i
1082 64 5.7 1975 2 B81192 hemagglutinin/hemo
1083 64 5.7 1995 2 G81044 hemagglutinin/hemo
1084 64 5.7 2055 2 T30259 multiple PDZ domai
1085 64 5.7 2274 1 GNNYEB genome polyprotein
1086 64 5.7 2292 1 GNNYEB capsid polyprotein
1087 64 5.7 2292 1 S55401 capsid polyprotein
1088 64 5.7 2392 2 S20901 titin - rabbit (fr
1089 64 5.7 6805 2 S20901 hypothetical prote
1090 63.5 5.6 101 2 E72458 probable methymal
1091 63.5 5.6 149 2 A71074 NADH2 dehydrogenas
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1096 63.5 5.6 197 2 C49247 merozoite surface
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1099 63.5 5.6 255 2 I47093 MHC OVAR-DQ-ALPHA-
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1101 63.5 5.6 284 2 T28018 hypothetical prote
1102 63.5 5.6 289 2 T41305 outer surface prot
1103 63.5 5.6 296 2 I40258 outer surface prot
1104 63.5 5.6 296 2 I40267 outer surface prot
1105 63.5 5.6 296 2 I40256 outer surface prot
1106 63.5 5.6 296 2 I40250 outer surface prot
1107 63.5 5.6 296 2 I40260 outer surface prot
1108 63.5 5.6 309 2 A00144 hypothetical prote
1109 63.5 5.6 313 2 D71363 conserved hypothet
1110 63.5 5.6 322 2 E82505 Fra-2 - rat
1111 63.5 5.6 327 2 I55459 hypothetical prote
1112 63.5 5.6 341 2 F71042 red-sensitive visu
1113 63.5 5.6 357 2 A37440 hypothetical prote
1114 63.5 5.6 366 2 T27912 glutamate-ammonia
1115 63.5 5.6 373 1 AJMSQ hypothetical prote
1116 63.5 5.6 378 2 A12180 argininosuccinate
1117 63.5 5.6 412 1 AJMSRS argininosuccinate
1118 63.5 5.6 412 1 AJRTRS argininosuccinate
1119 63.5 5.6 423 2 T01559 probable WRKY-type
1120 63.5 5.6 427 2 T00465 hypothetical prote
1121 63.5 5.6 432 2 T25471 inwardly rectifyin
1122 63.5 5.6 445 2 I38521 potassium channel
1123 63.5 5.6 445 2 S45713 inward rectifier p
1124 63.5 5.6 446 2 S66268

| | | | | | | | | | | | | | |
|------|------|-----|------|---|--------|----------------------|------|----|-----|-----|---|--------|--------------------|
| 1125 | 63.5 | 5.6 | 451 | 2 | F97230 | probable maltodext | 1198 | 63 | 5.6 | 139 | 2 | T05847 | hypothetical prote |
| 1126 | 63.5 | 5.6 | 462 | 2 | S05050 | retinoic acid nucl | 1199 | 63 | 5.6 | 154 | 2 | C71162 | hypothetical prote |
| 1127 | 63.5 | 5.6 | 484 | 2 | T20451 | hypothetical prote | 1200 | 63 | 5.6 | 190 | 2 | T26357 | hypothetical prote |
| 1128 | 63.5 | 5.6 | 498 | 2 | H85040 | hypothetical prote | 1201 | 63 | 5.6 | 204 | 2 | AG2437 | hypothetical prote |
| 1129 | 63.5 | 5.6 | 509 | 2 | A35016 | cystathionine gamm | 1202 | 63 | 5.6 | 204 | 2 | S49031 | cadmium-induced pr |
| 1130 | 63.5 | 5.6 | 512 | 2 | S21171 | activin receptor S | 1203 | 63 | 5.6 | 259 | 2 | T09317 | glycoprotein - hum |
| 1131 | 63.5 | 5.6 | 541 | 2 | S40245 | heat shock protein | 1204 | 63 | 5.6 | 266 | 2 | T30919 | hypothetical prote |
| 1132 | 63.5 | 5.6 | 542 | 2 | B86674 | 60 KD chaperonin [| 1205 | 63 | 5.6 | 291 | 2 | G81407 | hypothetical prote |
| 1133 | 63.5 | 5.6 | 546 | 2 | H89780 | hypothetical prote | 1206 | 63 | 5.6 | 292 | 2 | B89807 | exotoxin 9 [import |
| 1134 | 63.5 | 5.6 | 560 | 2 | D83759 | methyl-accepting c | 1207 | 63 | 5.6 | 309 | 2 | E70319 | phosphoribosylanth |
| 1135 | 63.5 | 5.6 | 630 | 2 | A39344 | tumor-associated m | 1208 | 63 | 5.6 | 309 | 2 | T17557 | procyclin homolog |
| 1136 | 63.5 | 5.6 | 631 | 2 | I52257 | episialin - mouse | 1209 | 63 | 5.6 | 321 | 2 | T50966 | hypothetical prote |
| 1137 | 63.5 | 5.6 | 649 | 2 | T04606 | protein kinase hom | 1210 | 63 | 5.6 | 326 | 2 | S15749 | transforming prote |
| 1138 | 63.5 | 5.6 | 651 | 2 | C56653 | membrane glycoprot | 1211 | 63 | 5.6 | 326 | 2 | I48351 | fos-related antige |
| 1139 | 63.5 | 5.6 | 653 | 2 | A13404 | transposase BME112 | 1212 | 63 | 5.6 | 326 | 2 | G69366 | homoserine dehydro |
| 1140 | 63.5 | 5.6 | 675 | 2 | D85065 | receptor protein k | 1213 | 63 | 5.6 | 346 | 2 | H84512 | hypothetical prote |
| 1141 | 63.5 | 5.6 | 688 | 2 | T23108 | hypothetical prote | 1214 | 63 | 5.6 | 346 | 2 | D87097 | conserved hypotet |
| 1142 | 63.5 | 5.6 | 694 | 2 | S68442 | Grb2-associated bi | 1215 | 63 | 5.6 | 348 | 2 | JQ0431 | hypothetical prote |
| 1143 | 63.5 | 5.6 | 699 | 2 | C43674 | US4 protein - huma | 1216 | 63 | 5.6 | 361 | 2 | T19395 | transforming prote |
| 1144 | 63.5 | 5.6 | 702 | 2 | E69498 | hypothetical prote | 1217 | 63 | 5.6 | 371 | 1 | TVXLT1 | transforming prote |
| 1145 | 63.5 | 5.6 | 708 | 2 | H84631 | outer membrane pro | 1218 | 63 | 5.6 | 375 | 2 | T33797 | hypothetical prote |
| 1146 | 63.5 | 5.6 | 713 | 2 | B86315 | F2H15.20 protein - | 1219 | 63 | 5.6 | 376 | 2 | S11558 | probable cell wall |
| 1147 | 63.5 | 5.6 | 761 | 2 | T00940 | hypothetical prote | 1220 | 63 | 5.6 | 380 | 2 | T32944 | hypothetical prote |
| 1148 | 63.5 | 5.6 | 761 | 2 | T03719 | probable thyroid r | 1221 | 63 | 5.6 | 382 | 1 | WZVZ16 | 16 43.5K protein - |
| 1149 | 63.5 | 5.6 | 764 | 2 | A84328 | Htr2 transducer (i | 1222 | 63 | 5.6 | 396 | 1 | C64907 | chloramphenicol re |
| 1150 | 63.5 | 5.6 | 767 | 1 | WMBEP6 | ribonucleoside-dip | 1223 | 63 | 5.6 | 396 | 2 | H85721 | probable resistanc |
| 1151 | 63.5 | 5.6 | 774 | 2 | T22309 | hypothetical prote | 1224 | 63 | 5.6 | 396 | 2 | G90895 | hypothetical prote |
| 1152 | 63.5 | 5.6 | 777 | 2 | C86454 | hypothetical prote | 1225 | 63 | 5.6 | 402 | 2 | S42367 | lag-2 protein - Ca |
| 1153 | 63.5 | 5.6 | 782 | 2 | S04047 | finger protein zfy | 1226 | 63 | 5.6 | 427 | 2 | E83711 | hypothetical prote |
| 1154 | 63.5 | 5.6 | 799 | 2 | H71255 | probable cell divi | 1227 | 63 | 5.6 | 443 | 2 | E82046 | proteinase HslVU, |
| 1155 | 63.5 | 5.6 | 808 | 2 | T23129 | hypothetical prote | 1228 | 63 | 5.6 | 451 | 2 | T15718 | hypothetical prote |
| 1156 | 63.5 | 5.6 | 826 | 2 | T46061 | hypothetical prote | 1229 | 63 | 5.6 | 482 | 2 | A12094 | hypothetical prote |
| 1157 | 63.5 | 5.6 | 854 | 1 | WMBP22 | gene 12 protein - | 1230 | 63 | 5.6 | 486 | 2 | AF1575 | acetaldehyde dehyd |
| 1158 | 63.5 | 5.6 | 861 | 2 | S77409 | hypothetical prote | 1231 | 63 | 5.6 | 486 | 2 | AC1222 | probable permease |
| 1159 | 63.5 | 5.6 | 865 | 2 | A47282 | calcium-binding pr | 1232 | 63 | 5.6 | 487 | 2 | S40820 | hypothetical serin |
| 1160 | 63.5 | 5.6 | 880 | 2 | D89756 | protein T3E7.2b [| 1233 | 63 | 5.6 | 509 | 2 | T50398 | transducin homolog |
| 1161 | 63.5 | 5.6 | 890 | 2 | T21000 | hypothetical prote | 1234 | 63 | 5.6 | 517 | 2 | A49367 | phosphoenolpyruvat |
| 1162 | 63.5 | 5.6 | 937 | 2 | A56517 | nucleoporin Nup98 | 1235 | 63 | 5.6 | 535 | 2 | S18606 | hypothetical prote |
| 1163 | 63.5 | 5.6 | 977 | 2 | S49004 | tyrosine kinase Mp | 1236 | 63 | 5.6 | 535 | 2 | T38244 | and cellulose-bind |
| 1164 | 63.5 | 5.6 | 988 | 2 | I50611 | protein-tyrosine k | 1237 | 63 | 5.6 | 537 | 2 | B97013 | estrogen dependent |
| 1165 | 63.5 | 5.6 | 1009 | 2 | S60248 | NAD ADP-ribosyltra | 1238 | 63 | 5.6 | 539 | 2 | I46470 | K06H7.1 protein - |
| 1166 | 63.5 | 5.6 | 1013 | 1 | S04200 | gag-like protein p | 1239 | 63 | 5.6 | 547 | 2 | S44841 | 71K upper matrix p |
| 1167 | 63.5 | 5.6 | 1043 | 2 | T13172 | hypothetical prote | 1240 | 63 | 5.6 | 559 | 1 | WMBES1 | hypothetical prote |
| 1168 | 63.5 | 5.6 | 1067 | 2 | T30061 | phosphatidylesterase | 1241 | 63 | 5.6 | 564 | 2 | T12550 | methy-accepting c |
| 1169 | 63.5 | 5.6 | 1138 | 2 | S64484 | hypothetical prote | 1242 | 63 | 5.6 | 595 | 2 | B82203 | E1 protein - human |
| 1170 | 63.5 | 5.6 | 1199 | 2 | T15826 | hypothetical prote | 1243 | 63 | 5.6 | 609 | 2 | S36481 | hypothetical prote |
| 1171 | 63.5 | 5.6 | 1208 | 2 | T27822 | hypothetical prote | 1244 | 63 | 5.6 | 609 | 2 | T34371 | calcium-dependent |
| 1172 | 63.5 | 5.6 | 1218 | 2 | AC3580 | 1-pyrroline-5-carb | 1245 | 63 | 5.6 | 611 | 1 | A49082 | hypothetical prote |
| 1173 | 63.5 | 5.6 | 1324 | 2 | S06187 | RNA2 polyprotein - | 1246 | 63 | 5.6 | 611 | 2 | S76211 | indolepyruvate fer |
| 1174 | 63.5 | 5.6 | 1326 | 2 | B56395 | secretory phosphol | 1247 | 63 | 5.6 | 623 | 2 | H69435 | 5'-nucleotidase pr |
| 1175 | 63.5 | 5.6 | 1332 | 2 | T23024 | hypothetical prote | 1248 | 63 | 5.6 | 630 | 2 | A34041 | serotonin receptor |
| 1176 | 63.5 | 5.6 | 1382 | 2 | S70310 | hypothetical prote | 1249 | 63 | 5.6 | 632 | 2 | C98264 | 5'-nucleotidase [i |
| 1177 | 63.5 | 5.6 | 1460 | 2 | T00095 | hypothetical prote | 1250 | 63 | 5.6 | 635 | 2 | T37239 | FUN36 protein - ye |
| 1178 | 63.5 | 5.6 | 1465 | 2 | A56395 | secretory phosphol | 1251 | 63 | 5.6 | 636 | 2 | AF3020 | hypothetical prote |
| 1179 | 63.5 | 5.6 | 1466 | 2 | T17138 | CL1AA protein - ra | 1252 | 63 | 5.6 | 638 | 2 | S36723 | hypothetical prote |
| 1180 | 63.5 | 5.6 | 1467 | 2 | T18411 | latrophilin-1, bra | 1253 | 63 | 5.6 | 640 | 2 | F75114 | hypothetical prote |
| 1181 | 63.5 | 5.6 | 1471 | 2 | T17149 | CL1BA protein - ra | 1254 | 63 | 5.6 | 677 | 2 | T39590 | hypothetical prote |
| 1182 | 63.5 | 5.6 | 1472 | 2 | T18413 | latrophilin-1, bra | 1255 | 63 | 5.6 | 683 | 2 | T37240 | serotonin receptor |
| 1183 | 63.5 | 5.6 | 1475 | 2 | S42718 | nuclear pore compl | 1256 | 63 | 5.6 | 714 | 2 | AF2479 | ABC transporter At |
| 1184 | 63.5 | 5.6 | 1510 | 2 | T17145 | CL1AB protein - ra | 1257 | 63 | 5.6 | 719 | 2 | T47727 | hypothetical prote |
| 1185 | 63.5 | 5.6 | 1515 | 2 | T17156 | CL1BB protein - ra | 1258 | 63 | 5.6 | 722 | 2 | E71403 | hypothetical prote |
| 1186 | 63.5 | 5.6 | 1544 | 2 | T29482 | hypothetical prote | 1259 | 63 | 5.6 | 729 | 2 | T15076 | hypothetical prote |
| 1187 | 63.5 | 5.6 | 1634 | 2 | T26517 | probable membrane | 1260 | 63 | 5.6 | 763 | 2 | T22843 | hypothetical prote |
| 1188 | 63.5 | 5.6 | 1796 | 2 | S65004 | cipa protein - Clo | 1261 | 63 | 5.6 | 776 | 2 | A55448 | An receptor nuclea |
| 1189 | 63.5 | 5.6 | 1854 | 2 | S36859 | adenylate cyclase | 1262 | 63 | 5.6 | 779 | 2 | A57177 | NIMA-like protein |
| 1190 | 63.5 | 5.6 | 2145 | 2 | JC4747 | coagulation factor | 1263 | 63 | 5.6 | 813 | 2 | A72203 | cellobiose-phospho |
| 1191 | 63.5 | 5.6 | 2211 | 1 | KFY05 | enoyl-[acyl-carrie | 1264 | 63 | 5.6 | 838 | 2 | G81444 | molycoprotein-cont |
| 1192 | 63.5 | 5.6 | 2512 | 1 | XYCHFA | protein F21H11.2 [| 1265 | 63 | 5.6 | 843 | 2 | T01438 | hypothetical prote |
| 1193 | 63.5 | 5.6 | 2700 | 2 | D88450 | polyprotein - pars | 1266 | 63 | 5.6 | 862 | 2 | S51493 | major nitrogen reg |
| 1194 | 63.5 | 5.6 | 3027 | 2 | JQ1917 | lg heavy chain V6 | 1267 | 63 | 5.6 | 865 | 2 | B96558 | probable protein k |
| 1195 | 63 | 5.6 | 125 | 2 | S24703 | hypothetical prote | 1268 | 63 | 5.6 | 918 | 1 | PXB11P | H+-exporting ATPas |
| 1196 | 63 | 5.6 | 126 | 2 | S14131 | hypothetical prote | 1269 | 63 | 5.6 | 982 | 2 | T43676 | hunchback-related |
| 1197 | 63 | 5.6 | 135 | 2 | T49996 | AtAGP4 - Arabidops | 1270 | 63 | 5.6 | 986 | 2 | T33135 | hypothetical prote |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|--------|--------------------|------|------|-----|------|---|--------|-----------------------|
| 1271 | 63 | 5.6 | 1002 | 2 | T19226 | hypothetical prote | 1344 | 62.5 | 5.6 | 521 | 2 | C82922 | methionyl-tRNA syn |
| 1272 | 63 | 5.6 | 1028 | 2 | E85089 | probable transposo | 1345 | 62.5 | 5.6 | 545 | 2 | T10662 | aromatic amino-aci |
| 1273 | 63 | 5.6 | 1028 | 2 | C88364 | protein C13B4.1 [i | 1346 | 62.5 | 5.6 | 557 | 2 | JC5487 | cellulase (EC 3.2. |
| 1274 | 63 | 5.6 | 1036 | 2 | B69368 | hypothetical prote | 1347 | 62.5 | 5.6 | 585 | 1 | B70747 | probable serine/th |
| 1275 | 63 | 5.6 | 1065 | 2 | S19482 | hypothetical prote | 1348 | 62.5 | 5.6 | 586 | 2 | D84710 | hypothetical prote |
| 1276 | 63 | 5.6 | 1106 | 2 | T18739 | hypothetical prote | 1349 | 62.5 | 5.6 | 596 | 2 | S61146 | probable membrane |
| 1277 | 63 | 5.6 | 1133 | 2 | T30302 | P-type ATPase - Te | 1350 | 62.5 | 5.6 | 601 | 2 | T34396 | hypothetical prote |
| 1278 | 63 | 5.6 | 1215 | 2 | T43916 | chitinase A [impor | 1351 | 62.5 | 5.6 | 609 | 2 | F87237 | phosphoenolpyruvat |
| 1279 | 63 | 5.6 | 1219 | 2 | H84464 | probable helicase | 1352 | 62.5 | 5.6 | 617 | 2 | A50644 | probable membrane |
| 1280 | 63 | 5.6 | 1279 | 2 | T13613 | hypothetical prote | 1353 | 62.5 | 5.6 | 617 | 2 | A85495 | probable membrane |
| 1281 | 63 | 5.6 | 1320 | 1 | S66279 | proline dehydrogen | 1354 | 62.5 | 5.6 | 621 | 1 | YRNC | monophenol monooxy |
| 1282 | 63 | 5.6 | 1320 | 2 | AE0633 | proline dehydrogen | 1355 | 62.5 | 5.6 | 626 | 2 | S53871 | Pmel 17 protein - |
| 1283 | 63 | 5.6 | 1636 | 2 | S60403 | probable membrane | 1356 | 62.5 | 5.6 | 647 | 2 | S26386 | transcription fact |
| 1284 | 63 | 5.6 | 1817 | 2 | T34249 | hypothetical prote | 1357 | 62.5 | 5.6 | 653 | 1 | E86787 | hypothetical prote |
| 1285 | 63 | 5.6 | 1820 | 2 | S71853 | genome polyprotein | 1358 | 62.5 | 5.6 | 671 | 1 | VCWCE | env polyprotein - |
| 1286 | 63 | 5.6 | 1902 | 2 | C97702 | cell surface antiq | 1359 | 62.5 | 5.6 | 697 | 2 | E96752 | hypothetical prote |
| 1287 | 63 | 5.6 | 1972 | 2 | S68176 | TOM protein - huma | 1360 | 62.5 | 5.6 | 706 | 2 | T49700 | related to AP-1-li |
| 1288 | 63 | 5.6 | 2628 | 2 | T28651 | hemagglutinin A - | 1361 | 62.5 | 5.6 | 722 | 2 | T37970 | probable G2-specif |
| 1289 | 63 | 5.6 | 2697 | 2 | T25444 | hypothetical prote | 1362 | 62.5 | 5.6 | 725 | 2 | JC1300 | endo-beta-1,4-gluc |
| 1290 | 63 | 5.6 | 3066 | 1 | JQ1662 | genome polyprotein | 1363 | 62.5 | 5.6 | 728 | 2 | F72693 | probable phosphos |
| 1291 | 63 | 5.6 | 3163 | 1 | JQ1895 | genome polyprotein | 1364 | 62.5 | 5.6 | 761 | 2 | A96810 | probable Mutator-1 |
| 1292 | 63 | 5.6 | 6420 | 2 | T30283 | polyketide synthas | 1365 | 62.5 | 5.6 | 761 | 2 | A81985 | probable secretin NWA |
| 1293 | 62.5 | 5.6 | 123 | 2 | B75546 | hypothetical prote | 1366 | 62.5 | 5.6 | 823 | 2 | G90848 | probable exonuclea |
| 1294 | 62.5 | 5.6 | 130 | 2 | T12478 | hypothetical prote | 1367 | 62.5 | 5.6 | 823 | 2 | F90914 | hypothetical prote |
| 1295 | 62.5 | 5.6 | 139 | 2 | G98226 | hypothetical prote | 1368 | 62.5 | 5.6 | 823 | 2 | E85706 | probable exonuclea |
| 1296 | 62.5 | 5.6 | 139 | 2 | A13059 | hypothetical prote | 1369 | 62.5 | 5.6 | 853 | 2 | H70939 | probable nirB prot |
| 1297 | 62.5 | 5.6 | 142 | 2 | G84194 | hypothetical prote | 1370 | 62.5 | 5.6 | 873 | 2 | B41054 | fasciclin II Pf-li |
| 1298 | 62.5 | 5.6 | 147 | 2 | T34803 | hypothetical prote | 1371 | 62.5 | 5.6 | 874 | 2 | AC2287 | hypothetical prote |
| 1299 | 62.5 | 5.6 | 157 | 2 | S36784 | mucin - rat (fragm | 1372 | 62.5 | 5.6 | 887 | 2 | G88484 | protein F23F12.8 [|
| 1300 | 62.5 | 5.6 | 177 | 2 | G75285 | hypothetical prote | 1373 | 62.5 | 5.6 | 893 | 2 | A47550 | bride of sevenless |
| 1301 | 62.5 | 5.6 | 198 | 2 | S48994 | hypothetical prote | 1374 | 62.5 | 5.6 | 899 | 2 | C84765 | hypothetical prote |
| 1302 | 62.5 | 5.6 | 210 | 2 | S53300 | self-incompatibili | 1375 | 62.5 | 5.6 | 903 | 2 | T00074 | hypothetical prote |
| 1303 | 62.5 | 5.6 | 219 | 2 | F65018 | hypothetical prote | 1376 | 62.5 | 5.6 | 907 | 2 | T04820 | aconitate hydratase |
| 1304 | 62.5 | 5.6 | 220 | 2 | AC2961 | thiamin-phosphate | 1377 | 62.5 | 5.6 | 929 | 2 | JC6124 | diacylglycerol kin |
| 1305 | 62.5 | 5.6 | 234 | 2 | T35448 | hypothetical prote | 1378 | 62.5 | 5.6 | 955 | 4 | C40045 | probable transcrip |
| 1306 | 62.5 | 5.6 | 238 | 2 | C98322 | probable thiamin b | 1379 | 62.5 | 5.6 | 968 | 2 | S46992 | protein p130 - rat |
| 1307 | 62.5 | 5.6 | 245 | 2 | S43565 | R01H10.4 protein (| 1380 | 62.5 | 5.6 | 988 | 1 | S35362 | protein kinase C (|
| 1308 | 62.5 | 5.6 | 252 | 2 | T04739 | hypothetical prote | 1381 | 62.5 | 5.6 | 1018 | 2 | T40253 | hypothetical prote |
| 1309 | 62.5 | 5.6 | 257 | 2 | C84890 | hypothetical prote | 1382 | 62.5 | 5.6 | 1033 | 2 | I48775 | Smcx protein (esca |
| 1310 | 62.5 | 5.6 | 277 | 2 | H97266 | mind family ATPase | 1383 | 62.5 | 5.6 | 1117 | 2 | T19727 | hypothetical prote |
| 1311 | 62.5 | 5.6 | 287 | 2 | S45662 | histone H1 - tomat | 1384 | 62.5 | 5.6 | 1197 | 2 | D86317 | protein F15H18.21 |
| 1312 | 62.5 | 5.6 | 289 | 2 | T52354 | hypothetical prote | 1385 | 62.5 | 5.6 | 1203 | 2 | H87687 | helicase, Uvrp/Rep |
| 1313 | 62.5 | 5.6 | 299 | 2 | F84810 | hypothetical prote | 1386 | 62.5 | 5.6 | 1302 | 2 | T23236 | hypothetical prote |
| 1314 | 62.5 | 5.6 | 304 | 2 | H86332 | T20H2-26 protein - | 1387 | 62.5 | 5.6 | 1309 | 1 | BVBVD9 | hypothetical prote |
| 1315 | 62.5 | 5.6 | 306 | 2 | T48715 | hypothetical prote | 1388 | 62.5 | 5.6 | 1337 | 2 | T30291 | RAD9 protein - yea |
| 1316 | 62.5 | 5.6 | 314 | 2 | B75588 | Frah-related prote | 1389 | 62.5 | 5.6 | 1337 | 2 | JC5502 | dextranase - Strept |
| 1317 | 62.5 | 5.6 | 329 | 2 | T43012 | conserved hypothet | 1390 | 62.5 | 5.6 | 1560 | 2 | I54361 | G-protein signalin |
| 1318 | 62.5 | 5.6 | 343 | 2 | F95915 | probable sugar ABC | 1391 | 62.5 | 5.6 | 1577 | 2 | T18396 | SMCX protein - hum |
| 1319 | 62.5 | 5.6 | 348 | 2 | C85578 | galactose-1-phosph | 1392 | 62.5 | 5.6 | 1729 | 2 | T30858 | glucosyltransferas |
| 1320 | 62.5 | 5.6 | 348 | 2 | B90727 | galactose-1-phosph | 1393 | 62.5 | 5.6 | 1784 | 2 | A49420 | erythrocyte membra |
| 1321 | 62.5 | 5.6 | 356 | 2 | A32945 | GTP-binding protei | 1394 | 62.5 | 5.6 | 1802 | 2 | S69703 | tuberosus sclerosi |
| 1322 | 62.5 | 5.6 | 359 | 2 | T31821 | hypothetical prote | 1395 | 62.5 | 5.6 | 1872 | 2 | T00339 | HKR1 protein precu |
| 1323 | 62.5 | 5.6 | 364 | 2 | T16837 | hypothetical prote | 1396 | 62.5 | 5.6 | 2054 | 2 | T46612 | hypothetical prote |
| 1324 | 62.5 | 5.6 | 372 | 2 | T23680 | hypothetical prote | 1397 | 62.5 | 5.6 | 2090 | 2 | S26058 | multi PDZ domain p |
| 1325 | 62.5 | 5.6 | 385 | 2 | JC7783 | hypothetical prote | 1398 | 62.5 | 5.6 | 2114 | 2 | E96505 | probable transform |
| 1326 | 62.5 | 5.6 | 389 | 2 | A38302 | RAD 23B protein - | 1399 | 62.5 | 5.6 | 2366 | 2 | S10317 | hypothetical prote |
| 1327 | 62.5 | 5.6 | 391 | 2 | JEC193 | pepsin (EC 3.4.23. | 1400 | 62.5 | 5.6 | 2367 | 2 | S70172 | toxin B - Clostrid |
| 1328 | 62.5 | 5.6 | 393 | 2 | T33103 | tumor suppressor p | 1401 | 62.5 | 5.6 | 3002 | 2 | A47221 | toxin B - Clostrid |
| 1329 | 62.5 | 5.6 | 396 | 2 | S54999 | lin-1 protein - Ca | 1402 | 62.5 | 5.6 | 3033 | 1 | JQ1303 | fibrillin 1 precur |
| 1330 | 62.5 | 5.6 | 396 | 2 | PC4236 | ubiquinol-cytochro | 1403 | 62.5 | 5.6 | 3343 | 2 | S44887 | genome polyprotein |
| 1331 | 62.5 | 5.6 | 398 | 1 | W2WL42 | trans-cinnamate 4- | 1404 | 62.5 | 5.6 | 5107 | 2 | T29144 | ZK112.7 protein - |
| 1332 | 62.5 | 5.6 | 412 | 2 | T50944 | E2 protein - human | 1405 | 62 | 5.6 | 125 | 2 | E90350 | partial CDS - Caen |
| 1333 | 62.5 | 5.6 | 426 | 2 | T50948 | P-selectin glycopo | 1406 | 62 | 5.5 | 165 | 1 | KTHUB | hypothetical prote |
| 1334 | 62.5 | 5.6 | 428 | 1 | Q4ECAD | damx protein (arob | 1407 | 62 | 5.5 | 170 | 2 | E84257 | chorigonadotropin |
| 1335 | 62.5 | 5.6 | 433 | 2 | MHRB | origin recognition | 1408 | 62 | 5.5 | 174 | 2 | AH1979 | flagellin A2 precu |
| 1336 | 62.5 | 5.6 | 458 | 1 | MHRB | Ig mu chain C regi | 1409 | 62 | 5.5 | 181 | 2 | T31481 | hypothetical prote |
| 1337 | 62.5 | 5.6 | 462 | 1 | A29491 | retinoic acid rece | 1410 | 62 | 5.5 | 189 | 2 | G70512 | hypothetical prote |
| 1338 | 62.5 | 5.6 | 479 | 1 | MHRBM | Ig mu chain C regi | 1411 | 62 | 5.5 | 192 | 2 | T51463 | probable lppK prot |
| 1339 | 62.5 | 5.6 | 493 | 2 | S73752 | hypothetical prote | 1412 | 62 | 5.5 | 194 | 1 | B28944 | hypothetical prote |
| 1340 | 62.5 | 5.6 | 503 | 2 | T37119 | probable membrane- | 1413 | 62 | 5.5 | 197 | 2 | F72356 | flagellin A2 precu |
| 1341 | 62.5 | 5.6 | 513 | 2 | S11439 | cellulose 1,4-beta | 1414 | 62 | 5.5 | 197 | 2 | B49247 | hypothetical prote |
| 1342 | 62.5 | 5.6 | 513 | 2 | S50915 | SIN3 protein-bindi | 1415 | 62 | 5.5 | 222 | 2 | T16381 | merozoite surface |
| 1343 | 62.5 | 5.6 | 518 | 2 | T33196 | hypothetical prote | 1416 | 62 | 5.5 | 250 | 2 | D71710 | hypothetical prote |

S13530
CD44E protein, epithelial - human
C:Species: Homo sapiens (man)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: S13530
R:Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B.
EMBO J. 10, 343-348, 1991
A>Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with different cytoplasmic domains
A:Reference number: S13530; MUID:91122041; PMID:1991450
A:Accession: S13530
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <STA>
A:Cross-references: EMBL:X55150; NID:g29800; PIDN:CAA38951.1; PID:g29801
C:Keywords: transmembrane protein

Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.5e-10;
Matches 66; Conservative 39; Mismatches 100; Indels 75; Gaps 8;

QY 9 LRAEELSIQVSCRIMGITLVSKKANQQLNFTAEKACRLGLSLAGKQOVETALKASPET 68
DB 17 LSLAQIDLNITCFAGVHFVXKNGRYSISRTEADLCQAFNSTLPTMDQMKLALSKGFETCRY 83
QY 69 CSYGVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 124
DB 77 CRYGFI-EGHVVIPRIHPNSICAAANTGVYILTNTS-QYDTYCFNASAPPEEDCTSVTD 134
QY 125 -----PELIITKDPINFNTQTATQTE-----FI 147
DB 135 LNAFDGPTITIVNRDGRYVQKGEYRNPEDVPSNPTDDVSGSSERSSTGGYI 194
QY 148 -----VSDST-----YSVASPYSTIPAPTTTPAPASTSPRKKILIC 185
DB 195 FYTESVHPIDPESDPIWTDSTDRIPRTNMDSSHSTLTLOPTANPTGLVEDLDRGLPSM 254
QY 186 VTEVMEVETMTETETEPFVENK-----AAFKNEAAG 216
DB 255 LTQQ-SNSQSFSTSEGLEEDKHPTTSLTSSNRNDVTG 293

RESULT 7
A34424
CD44 membrane glycoprotein precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 01-Dec-2000
C:Accession: A34424; A34907
R:Nottenburg, C.; Rees, G.; St. John, T.
Proc. Natl. Acad. Sci. U.S.A. 86, 8521-8525, 1989
A>Title: Isolation of mouse CD44 cDNA: structural features are distinct from the primate
A:Reference number: A34424; MUID:90046829; PMID:2682651
A:Accession: A34424
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-365 <NOT>
A:Cross-references: GB:M27130; NID:g192530; PIDN:AAA37407.1; PID:g309161
R:Wolfe, E.J.; Gause, W.C.; Pelfrey, C.M.; Holland, S.M.; Steinberg, A.D.; August, J.T.
J. Biol. Chem. 265, 341-347, 1990
A>Title: The cDNA sequence of mouse Pgp-1 and homology to human CD44 cell surface antigen
A:Reference number: A34907; MUID:90094420; PMID:2403559
A:Accession: A34907
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 8-195,'G', 197-365 <WOL>
A:Cross-references: GB:J05163; NID:g200334; PIDN:AAA39923.1; PID:g200335
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; Glycoprotein; membrane protein

Query Match 17.6%; Score 198.5; DB 2; Length 365;
Best Local Similarity 31.8%; Pred. No. 8.1e-10;
Matches 48; Conservative 24; Mismatches 72; Indels 7; Gaps 3;

QY 12 BELSIQVSCRIMGITLVSKKANQQLNFTAEKACRLGLSLAGKQOVETALKASPETCSY 71

DB 24 QQIDLNVTCRYAGVHFVXKNGRYSISRTEADLCQAFNSTLPTMDQMKLALSKGFETCRY 83
QY 72 GWVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCIPEIITTK 131
DB 84 GFI-EGHVVIPRIHPNAICAAANTGVYILTNTSHYDTYCFNASAPPEEDC-----TSV 137
QY 132 DFINFNTQTATQTEFIVSDST-YSVASPYST 161
DB 138 TDLNPSFDGPTITIVNRDGRYVQKGEYR 168

RESULT 8
JH0518
Lymphocyte homing receptor CD44, splice form CD44R1 - human
N:Alternate names: cell adhesion molecule core protein CD44E, keratinocyte; cell surface
N:Contains: lymphocyte homing receptor CD44, splice form CD44R1; lymphocyte homing receptor
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: JH0518; JH0519; PH0859; A39209; A42402; C42402; A53029; S16147
R:Dougherty, G.J.; Lansford, P.M.; Cooper, D.L.; Humphries, R.K.
J. Exp. Med. 174, 1-5, 1991
A>Title: Molecular cloning of CD44R1 and CD44R2, two novel isoforms of the human CD44 ly
A:Reference number: JH0518; MUID:91277598; PMID:2056274
A:Accession: JH0518
A:Molecule type: mRNA
A:Residues: 1-426 <DOU>
A:Cross-references: UNIPROT:Q9UCB0
A:Experimental source: lymphocytes, cell line KGIA
A:Accession: JH0519
A:Molecule type: mRNA
A:Residues: 1-223,288-426 <DO2>
A:Experimental source: lymphocyte, cell line KGIA
R:Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Data,
Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A>Title: The complex CD44 transcriptional unit: alternative splicing of three internal
A:Reference number: PH0859; MUID:92134271; PMID:1734871
A:Accession: PH0859
A:Molecule type: DNA
A:Residues: 223-357 <COO>
R:Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G.
J. Cell Biol. 113, 207-221, 1991
A>Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfat
A:Reference number: A39209; MUID:91177958; PMID:2007624
A:Accession: A39209
A:Molecule type: mRNA
A:Residues: 184-376 <BRO>
A:Cross-references: GB:X55938; NID:g29802; PIDN:CAA39404.1; PID:g930047
R:Jackson, D.G.; Buckley, J.; Bell, J.I.
J. Biol. Chem. 267, 4732-4739, 1992
A>Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by in
A:Reference number: A42402; MUID:92165834; PMID:1537855
A:Accession: A42402
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 217-223,288-359 <JAC>
A>Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIP:83965)
A>Note: variant B
A:Accession: C42402
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 217-320 <JAJ2>
A>Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIP:83969)
R:Shepley, M.P.; Racaniello, V.R.
J. Virol. 68, 1301-1308, 1994
A>Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocy
A:Reference number: A53029; MUID:94149816; PMID:7508992
A:Accession: A53029
A>Status: preliminary
A:Molecule type: protein
A:Residues: 67-76,'X',78-89 <SHE>
C:Genetics:

A:Reference number: I57483; MUID:93356912; PMID:8352881
A:Accession: I77371
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-395 <RES>
A:Cross-references: GB:S66400; NID:G435697; PIDN:AAB27919.1; PID:G435700
A:Gene: GDB:CD44
A:Cross-references: GDB:I20739; OMIM:107269
A:Map position: 11pter-11p13
A:Introns: 257/1
C:Superfamily: human cell adhesion protein CD44

Query Match 17.4%; Score 196; DB 2; Length 395;
Best Local Similarity 30.9%; Pred. No. 1.5e-09;
Matches 54; Conservative 23; Mismatches 84; Indels 14; Gaps 5;

QY 9 LRAEELSIQVSCRMGITLVSKKANQQLNFTKEACRLLGLSLAGKQDVETALKASPT 68
DB 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGFET 76
QY 69 CSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNCSICEII 128
DB 77 CRYGFI-EGHVVIPRIHPNSICANNVTGVILTSNTS-QYDYCFNASAPPEDC----- 129
QY 129 TTKDPINFNTQTATQTFEIVSDST-YSVASPYSTIPA-----PTTTPAPASTS 176
DB 130 TSVTDLNAPDFGPTITIVNRDGRYVQKGEYRTNPEDIVPSNPTDDVSSGSS 184

RESULT 12
S45305
C:Title: Antigen precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 20-Oct-1994 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S45305
R:Milde, K.F.; Alejandro, R.; Mintz, D.H.; Pastori, R.L.
Biochim. Biophys. Acta 1218, 112-114, 1994
A:Title: Molecular cloning of the canine CD44 antigen cDNA.
A:Reference number: S45305; MUID:94250687; PMID:7514890
A:Accession: S45305
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-351 <MIL>
A:Cross-references: UNIPROT:Q28284; EMBL:Z27115; NID:G473226; PIDN:CAA81630.1; PID:G47322
C:Superfamily: human cell adhesion protein CD44

Query Match 17.2%; Score 194; DB 2; Length 351;
Best Local Similarity 30.3%; Pred. No. 1.9e-09;
Matches 53; Conservative 25; Mismatches 83; Indels 14; Gaps 5;

QY 9 LRAEELSIQVSCRMGITLVSKKANQQLNFTKEACRLLGLSLAGKQDVETALKASPT 68
DB 10 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMERALSIGFET 69
QY 69 CSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNCSICEII 128
DB 70 CRYGFI-EGHVVIPRIQPNALCAANHGTGYI-LISNTSQDYDYCFNASAPPEDC----- 122
QY 129 TTKDPINFNTQTATQTFEIVSDST-YSVASPYSTIPA-----PTTTPAPASTS 176
DB 123 TSVTHLPNAPDFGPTITIVNRDGRYVQKGEYRTNPEDINPSNPTDDVSSGSS 177

RESULT 13
A53286
N:Alternate names: CD44 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A:Accession: A53286; S22123
R:Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991

A:Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A:Reference number: A53286; MUID:92017904; PMID:1922105
A:Accession: A53286
A:Molecule type: mRNA
A:Residues: 1-366 <ROS>
A:Cross-references: UNIPROT:Q29423; EMBL:X62881; NID:G186; PIDN:CAA44675.1; PID:G187
A:Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
F:274-294/Domain: transmembrane #status predicted <TMW>
F:25,57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 17.2%; Score 194; DB 2; Length 366;
Best Local Similarity 29.9%; Pred. No. 2e-09;
Matches 56; Conservative 27; Mismatches 86; Indels 18; Gaps 6;

QY 4 LVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTKEACRLLGLSLAGKQDVETALK 63
DB 14 LVQSL--AQIDLNITCRFAGVFHVEKNGRYSISKTEAADLCKAFNSTLPTMAQMEARN 71
QY 64 ASFTCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSC 123
DB 72 IGFETCRYGFI-EGHVVIPRIHPNSICANNVTGVILTSNTS-QYDYTCFNASAPPEDC 129
QY 124 IPEILTKDPIENTQTATQTFEIVSDST-YSVASPYSTIP-----APTTPPAPAS 174
DB 130 -----TSVTDLPNAPFGPTITIVNRDGRYTKKGEYRTNPEDINPSVSPSPDDEMS 184
QY 175 TSIPRRK 181
DB 185 SGSPSER 191

RESULT 14
S24240
Lymphocyte surface antigen CD44 precursor - horse
C:Species: Equus caballus (domestic horse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: I46245; S24240
R:Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, W.; But
Immunogenetics 37, 474-477, 1993
A:Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A:Reference number: I46245; MUID:93170897; PMID:8436424
A:Accession: I46245
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-359 <TA2>
A:Cross-references: UNIPROT:Q05078; EMBL:X66862; NID:G1059; PIDN:CAA47331.1; PID:G1060
C:Superfamily: human cell adhesion protein CD44
C:Keywords: surface antigen; transmembrane protein

Query Match 16.3%; Score 183.5; DB 2; Length 359;
Best Local Similarity 29.4%; Pred. No. 1.6e-08;
Matches 50; Conservative 24; Mismatches 87; Indels 9; Gaps 5;

QY 9 LRAEELSIQVSCRMGITLVSKKANQQLNFTKEACRLLGLSLAGKQDVETALKASPT 68
DB 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMKALNIGFET 76
QY 69 CSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNCSICEII 128
DB 77 CRIGFI-EGHVVIPPIHPNSICANNVTGVILTSNTS-QYDYTCFNASAPPEDC----- 129
QY 129 TTKDPINFNTQTATQTFEIVSDST-YSVASPYSTIPAPTTTPPAPASTSI 177
DB 130 TSVTDLNAPFGPTITIVNRDGRYTKKGEYRTNP-EDINPSTADDDV 178

RESULT 15
A47171
chondroitin sulfate proteoglycan PG-M core protein - chicken

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 17:27:34 ; Search time 92.8519 Seconds
(without alignments)
974.620 Million cell updates/sec

Perfect score: 1125
Sequence: 1 TRLVQSLRAEELSIQVSC.....ETEPVENKAAPKNEAGFG 218

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Published Applications AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| Sequence 2665, Ap | US-10-264-237-2665 | 322 | 15 |
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| Sequence 1047, Ap | US-10-741-600-1047 | 668 | 17 |
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| Sequence 1282, Ap | US-10-473-127-1282 | 742 | 16 |
| Sequence 1319, Ap | US-10-473-127-1319 | 742 | 16 |
| Sequence 1054, Ap | US-10-741-600-1054 | 742 | 17 |
| Sequence 545, App | US-10-287-436A-545 | 742 | 18 |
| Sequence 1236, Ap | US-10-287-436A-1236 | 742 | 18 |
| Sequence 1284, Ap | US-10-473-127-1284 | 675 | 16 |
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| Sequence 16, Appl | US-09-983-000A-16 | 742 | 10 |
| Sequence 206, App | US-10-116-275-206 | 742 | 15 |
| Sequence 1, Appl | US-10-663-244-1 | 742 | 16 |
| Sequence 338, App | US-10-741-601-338 | 742 | 16 |
| Sequence 339, App | US-10-741-601-339 | 742 | 16 |
| Sequence 1286, Ap | US-10-473-127-1286 | 742 | 16 |
| Sequence 1311, Ap | US-10-473-127-1311 | 742 | 16 |
| Sequence 40, Appl | US-10-600-880-40 | 742 | 17 |
| Sequence 1046, Ap | US-10-741-600-1046 | 742 | 17 |
| Sequence 1049, Ap | US-10-741-600-1049 | 742 | 17 |
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| Sequence 1292, Ap | US-10-473-127-1292 | 361 | 16 |
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| 305 | 197 | 17.5 | 361 | 16 | US-10-473-127-1304 | Sequence 1304, Ap | 378 | 127.5 | 11.3 | 649 | 14 | US-10-188-495-63 | Sequence 63, Appl |
| 306 | 197 | 17.5 | 361 | 16 | US-10-473-127-1309 | Sequence 1309, Ap | 379 | 127.5 | 11.3 | 649 | 16 | US-10-741-790-333 | Sequence 333, App |
| 307 | 197 | 17.5 | 361 | 16 | US-10-473-127-1310 | Sequence 1310, Ap | 380 | 127.5 | 11.3 | 671 | 10 | US-09-759-1308-331 | Sequence 331, App |
| 308 | 197 | 17.5 | 361 | 17 | US-10-483-029-255 | Sequence 255, App | 381 | 127.5 | 11.3 | 671 | 10 | US-09-983-000A-14 | Sequence 14, Appl |
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| 311 | 197 | 17.5 | 436 | 16 | US-10-473-127-1308 | Sequence 1308, Ap | 384 | 127.5 | 11.3 | 671 | 16 | US-10-741-790-331 | Sequence 331, App |
| 312 | 197 | 17.5 | 719 | 16 | US-10-473-127-1270 | Sequence 1270, Ap | 385 | 127.5 | 11.3 | 671 | 17 | US-10-652-981-14 | Sequence 14, Appl |
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| 320 | 196.5 | 17.5 | 700 | 14 | US-10-012-969C-2 | Sequence 2, Appli | 499 | 127.5 | 11.3 | 911 | 15 | US-10-453-420-8 | Sequence 8, Appli |
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| 322 | 196 | 17.4 | 294 | 16 | US-10-473-127-1290 | Sequence 1290, Ap | 501 | 127.5 | 11.3 | 911 | 15 | US-10-312-352-24 | Sequence 24, Appl |
| 323 | 196 | 17.4 | 294 | 16 | US-10-473-127-1312 | Sequence 1312, Ap | 502 | 127.5 | 11.3 | 911 | 17 | US-10-936-626-89 | Sequence 89, Appl |
| 324 | 196 | 17.4 | 361 | 16 | US-10-663-244-3 | Sequence 3, Appli | 503 | 127.5 | 11.3 | 911 | 17 | US-10-938-061-89 | Sequence 89, Appl |
| 325 | 196 | 17.4 | 361 | 16 | US-10-741-601-340 | Sequence 340, App | 504 | 127 | 11.3 | 277 | 15 | US-10-295-027-294 | Sequence 294, App |
| 326 | 196 | 17.4 | 361 | 16 | US-10-473-127-1288 | Sequence 1288, Ap | 505 | 127 | 11.3 | 277 | 15 | US-10-755-889-118 | Sequence 118, App |
| 327 | 196 | 17.4 | 361 | 17 | US-10-741-600-1048 | Sequence 1048, Ap | 506 | 124 | 11.0 | 482 | 15 | US-10-104-047-3794 | Sequence 3794, Ap |
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| 331 | 196 | 17.4 | 425 | 16 | US-10-741-601-337 | Sequence 337, App | 510 | 123 | 10.9 | 2212 | 15 | US-10-028-248A-43 | Sequence 43, Appl |
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| 348 | 183 | 16.3 | 112 | 17 | US-10-487-620-10 | Sequence 10, Appl | 1118 | 121 | 10.8 | 528 | 14 | US-10-189-123-71 | Sequence 71, Appl |
| 349 | 182 | 16.2 | 112 | 17 | US-10-487-620-4 | Sequence 4, Appli | 1119 | 121 | 10.8 | 528 | 14 | US-10-188-495-71 | Sequence 71, Appl |
| 350 | 181 | 16.1 | 112 | 17 | US-10-487-620-12 | Sequence 12, Appl | 1120 | 121 | 10.8 | 528 | 16 | US-10-741-790-341 | Sequence 341, App |
| 351 | 175.5 | 15.6 | 920 | 18 | US-10-450-763-47426 | Sequence 47426, A | 1121 | 121 | 10.8 | 528 | 17 | US-10-314-942-20 | Sequence 20, Appl |
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| 353 | 161 | 14.3 | 90 | 9 | US-09-799-118-3 | Sequence 3, Appli | 1123 | 119 | 10.6 | 457 | 10 | US-09-969-730-110 | Sequence 110, App |
| 354 | 153.5 | 13.6 | 90 | 10 | US-09-927-463-8 | Sequence 8, Appli | 1124 | 119 | 10.6 | 457 | 15 | US-10-621-363-110 | Sequence 110, App |
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| 357 | 148.5 | 13.2 | 80 | 17 | US-10-487-620-23 | Sequence 23, Appl | 1127 | 118.5 | 10.5 | 3396 | 16 | US-10-788-792-170 | Sequence 170, App |
| 358 | 145 | 12.9 | 277 | 9 | US-09-799-118-2 | Sequence 2, Appli | 1128 | 118.5 | 10.5 | 3396 | 17 | US-10-741-600-1172 | Sequence 1172, Ap |
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| 360 | 145 | 12.9 | 277 | 15 | US-10-295-027-292 | Sequence 292, App | 1130 | 118.5 | 10.5 | 3396 | 18 | US-10-631-467-773 | Sequence 773, App |
| 361 | 145 | 12.9 | 277 | 15 | US-10-295-027-1237 | Sequence 1237, Ap | 1131 | 116 | 10.3 | 2397 | 18 | US-10-631-467-1518 | Sequence 1518, Ap |
| 362 | 145 | 12.9 | 277 | 16 | US-10-723-860-4326 | Sequence 4326, Ap | 1132 | 113.5 | 10.1 | 97 | 9 | US-09-799-118-5 | Sequence 5, Appli |
| 363 | 145 | 12.9 | 2626 | 15 | US-10-634-574-4 | Sequence 4, Appli | 1133 | 112.5 | 10.0 | 287 | 9 | US-09-764-853-576 | Sequence 576, App |
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| 366 | 131.5 | 11.7 | 883 | 15 | US-10-453-420-3 | Sequence 3, Appli | 1136 | 112 | 10.0 | 897 | 15 | US-10-028-248A-211 | Sequence 211, App |
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| 368 | 130.5 | 11.6 | 883 | 14 | US-10-189-123-72 | Sequence 72, Appl | 1138 | 112 | 10.0 | 897 | 15 | US-10-107-782-211 | Sequence 211, App |
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| 1147 | 111 | 9.9 | 655 | 16 | US-10-270-253-2 | Sequence 2, Appl | 1220 | 94.5 | 8.4 | 1795 | 20 | US-11-097-143-36210 | Sequence 36210, A |
| 1148 | 111 | 9.9 | 655 | 17 | US-10-741-600-1174 | Sequence 1174, Ap | 1221 | 93.5 | 8.3 | 258 | 9 | US-09-764-853-840 | Sequence 840, App |
| 1149 | 111 | 9.9 | 2409 | 14 | US-10-177-293-90 | Sequence 90, Appl | 1222 | 93.5 | 8.3 | 258 | 14 | US-10-091-438-205 | Sequence 205, App |
| 1150 | 111 | 9.9 | 2409 | 17 | US-10-741-600-1175 | Sequence 1175, Ap | 1223 | 93.5 | 8.3 | 261 | 9 | US-09-764-853-669 | Sequence 669, App |
| 1151 | 111 | 9.9 | 2409 | 17 | US-10-741-600-1177 | Sequence 1177, Ap | 1224 | 93.5 | 8.3 | 261 | 14 | US-10-091-438-144 | Sequence 144, App |
| 1152 | 111 | 9.9 | 2409 | 17 | US-10-482-029-194 | Sequence 194, App | 1225 | 92.5 | 8.2 | 40 | 17 | US-10-487-620-26 | Sequence 26, Appl |
| 1153 | 111 | 9.9 | 2409 | 17 | US-10-852-335A-184 | Sequence 184, App | 1226 | 91.5 | 8.1 | 166 | 9 | US-09-764-853-777 | Sequence 777, App |
| 1154 | 110 | 9.8 | 2675 | 15 | US-10-028-248A-2 | Sequence 2, Appl | 1227 | 91.5 | 8.1 | 166 | 14 | US-10-091-438-181 | Sequence 181, App |
| 1155 | 110 | 9.8 | 2675 | 15 | US-10-107-782-2 | Sequence 2, Appl | 1228 | 91.5 | 8.1 | 1126 | 20 | US-11-097-143-35952 | Sequence 35952, A |
| 1156 | 109.5 | 9.7 | 1357 | 18 | US-10-698-130-22 | Sequence 22, Appl | 1229 | 90.5 | 8.0 | 505 | 15 | US-10-442-017-17 | Sequence 17, Appl |
| 1157 | 109 | 9.7 | 1069 | 15 | US-10-028-248A-39 | Sequence 39, Appl | 1230 | 90.5 | 8.0 | 1976 | 20 | US-11-097-143-35049 | Sequence 35049, A |
| 1158 | 109 | 9.7 | 1069 | 15 | US-10-107-782-39 | Sequence 39, Appl | 1231 | 90 | 8.0 | 402 | 15 | US-10-282-122A-64209 | Sequence 64209, A |
| 1159 | 109 | 9.7 | 1321 | 14 | US-10-241-220-82 | Sequence 82, Appl | 1232 | 90 | 8.0 | 1103 | 15 | US-10-369-493-3228 | Sequence 3228, Ap |
| 1160 | 109 | 9.7 | 1321 | 15 | US-10-295-027-262 | Sequence 262, App | 1233 | 89 | 7.9 | 307 | 20 | US-11-097-143-24429 | Sequence 24429, A |
| 1161 | 109 | 9.7 | 1321 | 16 | US-10-408-765A-1421 | Sequence 1421, Ap | 1234 | 89 | 7.9 | 416 | 15 | US-10-371-525-26 | Sequence 26, Appl |
| 1162 | 109 | 9.7 | 1321 | 16 | US-10-872-972-82 | Sequence 82, Appl | 1235 | 89 | 7.9 | 416 | 15 | US-10-371-069-36 | Sequence 26, Appl |
| 1163 | 109 | 9.7 | 1321 | 16 | US-10-872-991-82 | Sequence 82, Appl | 1236 | 89 | 7.9 | 416 | 15 | US-10-371-645-26 | Sequence 26, Appl |
| 1164 | 109 | 9.7 | 1321 | 18 | US-10-698-130-18 | Sequence 18, Appl | 1237 | 89 | 7.9 | 416 | 15 | US-10-371-260-26 | Sequence 26, Appl |
| 1165 | 108 | 9.6 | 322 | 15 | US-10-120-907A-32 | Sequence 32, Appl | 1238 | 89 | 7.9 | 416 | 16 | US-10-684-422-68 | Sequence 68, Appl |
| 1166 | 108 | 9.6 | 322 | 15 | US-10-120-907A-33 | Sequence 33, Appl | 1239 | 89 | 7.9 | 416 | 18 | US-10-287-436A-533 | Sequence 533, App |
| 1167 | 108 | 9.6 | 354 | 15 | US-10-120-907A-3 | Sequence 3, Appl | 1240 | 89 | 7.9 | 416 | 18 | US-10-287-436A-1224 | Sequence 1224, Ap |
| 1168 | 108 | 9.6 | 354 | 15 | US-10-120-907A-7 | Sequence 7, Appl | 1241 | 89 | 7.9 | 1441 | 16 | US-10-437-963-138354 | Sequence 138354, Sequence 138279 |
| 1169 | 108 | 9.6 | 354 | 15 | US-10-120-907A-9 | Sequence 9, Appl | 1242 | 89 | 7.9 | 2588 | 16 | US-10-437-963-138279 | Sequence 138279, Sequence 138279 |
| 1170 | 108 | 9.6 | 354 | 15 | US-10-120-907A-11 | Sequence 11, Appl | 1243 | 87.5 | 7.8 | 536 | 14 | US-10-218-743-21 | Sequence 21, Appl |
| 1171 | 108 | 9.6 | 354 | 15 | US-10-120-907A-13 | Sequence 13, Appl | 1244 | 87.5 | 7.8 | 536 | 14 | US-10-218-743-18 | Sequence 18, Appl |
| 1172 | 108 | 9.6 | 354 | 15 | US-10-120-907A-15 | Sequence 15, Appl | 1245 | 87.5 | 7.8 | 555 | 14 | US-10-218-743-18 | Sequence 18, Appl |
| 1173 | 108 | 9.6 | 354 | 15 | US-10-120-907A-17 | Sequence 17, Appl | 1246 | 87.5 | 7.8 | 1085 | 14 | US-10-159-339-10 | Sequence 10, Appl |
| 1174 | 108 | 9.6 | 354 | 15 | US-10-120-907A-19 | Sequence 19, Appl | 1247 | 87.5 | 7.8 | 1085 | 15 | US-10-041-615-108 | Sequence 108, App |
| 1175 | 108 | 9.6 | 354 | 15 | US-10-120-907A-21 | Sequence 21, Appl | 1248 | 87.5 | 7.8 | 1085 | 15 | US-10-436-715-21 | Sequence 21, Appl |
| 1176 | 108 | 9.6 | 354 | 15 | US-10-120-907A-23 | Sequence 23, Appl | 1249 | 87.5 | 7.8 | 1085 | 15 | US-10-436-715-21 | Sequence 21, Appl |
| 1177 | 108 | 9.6 | 354 | 15 | US-10-120-907A-24 | Sequence 24, Appl | 1250 | 87 | 7.7 | 288 | 9 | US-09-216-393-341 | Sequence 341, App |
| 1178 | 108 | 9.6 | 354 | 15 | US-10-120-907A-28 | Sequence 28, Appl | 1251 | 87 | 7.7 | 288 | 9 | US-09-216-393-341 | Sequence 341, App |
| 1179 | 108 | 9.6 | 354 | 15 | US-10-120-907A-29 | Sequence 29, Appl | 1252 | 87 | 7.7 | 288 | 14 | US-10-321-856-344 | Sequence 344, App |
| 1180 | 108 | 9.6 | 354 | 15 | US-10-120-907A-30 | Sequence 30, Appl | 1253 | 87 | 7.7 | 288 | 14 | US-10-321-856-344 | Sequence 344, App |
| 1181 | 108 | 9.6 | 354 | 15 | US-10-120-907A-36 | Sequence 36, Appl | 1254 | 86.5 | 7.7 | 245 | 16 | US-10-425-115-334180 | Sequence 334180, Sequence 58, Appl |
| 1182 | 108 | 9.6 | 354 | 15 | US-10-120-907A-38 | Sequence 38, Appl | 1255 | 86.5 | 7.7 | 585 | 17 | US-10-868-381-58 | Sequence 58, Appl |
| 1183 | 108 | 9.6 | 354 | 15 | US-10-120-907A-42 | Sequence 42, Appl | 1256 | 85.5 | 7.6 | 652 | 16 | US-10-467-490-5 | Sequence 5, Appl |
| 1184 | 108 | 9.6 | 354 | 15 | US-10-120-907A-64 | Sequence 64, Appl | 1257 | 85.5 | 7.6 | 841 | 16 | US-10-467-490-2 | Sequence 2, Appl |
| 1185 | 108 | 9.6 | 354 | 15 | US-10-120-907A-66 | Sequence 66, Appl | 1258 | 85.5 | 7.6 | 977 | 16 | US-10-467-490-3 | Sequence 3, Appl |
| 1186 | 108 | 9.6 | 354 | 18 | US-10-754-473-19 | Sequence 19, Appl | 1259 | 85.5 | 7.6 | 1367 | 9 | US-09-801-368-108 | Sequence 108, App |
| 1187 | 108 | 9.6 | 354 | 18 | US-10-754-473-22 | Sequence 22, Appl | 1260 | 85.5 | 7.6 | 1799 | 10 | US-09-965-738-299 | Sequence 299, App |
| 1188 | 108 | 9.6 | 721 | 15 | US-10-120-907A-5 | Sequence 5, Appl | 1261 | 85.5 | 7.6 | 1799 | 10 | US-09-965-738-149 | Sequence 149, App |
| 1189 | 108 | 9.6 | 721 | 15 | US-10-120-907A-25 | Sequence 25, Appl | 1262 | 85.5 | 7.6 | 1821 | 10 | US-09-965-738-82 | Sequence 82, Appl |
| 1190 | 108 | 9.6 | 721 | 15 | US-10-120-907A-43 | Sequence 43, Appl | 1263 | 85.5 | 7.6 | 5877 | 14 | US-10-142-515-11 | Sequence 11, Appl |
| 1191 | 108 | 9.6 | 721 | 15 | US-10-120-907A-65 | Sequence 65, Appl | 1264 | 85.5 | 7.6 | 5935 | 14 | US-10-243-243A-8 | Sequence 8, Appl |
| 1192 | 108 | 9.6 | 721 | 15 | US-10-120-907A-67 | Sequence 67, Appl | 1265 | 85.5 | 7.6 | 11721 | 10 | US-09-965-738-162 | Sequence 162, App |
| 1193 | 107 | 9.5 | 93 | 14 | US-10-133-172-5 | Sequence 5, Appl | 1266 | 85.5 | 7.6 | 22152 | 16 | US-10-715-066-5 | Sequence 5, Appl |
| 1194 | 107 | 9.5 | 315 | 18 | US-10-667-723-4 | Sequence 4, Appl | 1267 | 85 | 7.6 | 569 | 15 | US-10-282-122A-60442 | Sequence 60442, A |
| 1195 | 107 | 9.5 | 339 | 18 | US-10-754-473-21 | Sequence 21, Appl | 1268 | 85 | 7.6 | 627 | 15 | US-10-369-493-18499 | Sequence 18499, A |
| 1196 | 107 | 9.5 | 354 | 15 | US-10-120-907A-39 | Sequence 39, Appl | 1269 | 85 | 7.6 | 631 | 9 | US-09-841-132-325 | Sequence 325, App |
| 1197 | 107 | 9.5 | 355 | 15 | US-10-120-907A-31 | Sequence 31, Appl | 1270 | 85 | 7.6 | 631 | 16 | US-10-872-155-325 | Sequence 325, App |
| 1198 | 107 | 9.5 | 355 | 18 | US-10-754-473-20 | Sequence 20, Appl | 1271 | 85 | 7.6 | 664 | 17 | US-10-197-220-168 | Sequence 168, App |
| 1199 | 107 | 9.5 | 1268 | 18 | US-10-698-130-24 | Sequence 24, Appl | 1272 | 85 | 7.6 | 1016 | 10 | US-09-841-260-95 | Sequence 95, Appl |
| 1200 | 107 | 9.5 | 2420 | 15 | US-10-028-248A-4 | Sequence 4, Appl | 1273 | 85 | 7.6 | 1016 | 13 | US-10-007-693-95 | Sequence 95, Appl |
| 1201 | 107 | 9.5 | 2420 | 15 | US-10-107-782-4 | Sequence 4, Appl | 1274 | 85 | 7.6 | 1016 | 16 | US-10-467-534-41 | Sequence 41, Appl |
| 1202 | 105.5 | 9.4 | 341 | 10 | US-09-948-820-48 | Sequence 48, Appl | 1275 | 85 | 7.6 | 1016 | 16 | US-10-782-058-95 | Sequence 95, Appl |
| 1203 | 105.5 | 9.4 | 341 | 16 | US-10-613-076-48 | Sequence 48, Appl | 1276 | 85 | 7.6 | 1016 | 17 | US-10-197-220-95 | Sequence 95, Appl |
| 1204 | 105 | 9.3 | 354 | 15 | US-10-120-907A-37 | Sequence 37, Appl | 1277 | 85 | 7.6 | 1016 | 17 | US-10-498-327-95 | Sequence 95, Appl |
| 1205 | 105 | 9.3 | 354 | 18 | US-10-754-473-18 | Sequence 18, Appl | 1278 | 85 | 7.6 | 1049 | 20 | US-11-097-143-7953 | Sequence 7953, Ap |
| 1206 | 104 | 9.2 | 98 | 9 | US-09-799-118-4 | Sequence 4, Appl | 1279 | 84.5 | 7.5 | 427 | 15 | US-10-434-599-191566 | Sequence 191566, Sequence 122189, |
| 1207 | 104 | 9.2 | 139 | 16 | US-10-741-601-342 | Sequence 342, App | 1280 | 84.5 | 7.5 | 479 | 16 | US-10-437-963-122189 | Sequence 122189, Sequence 20, Appl |
| 1208 | 104 | 9.2 | 139 | 16 | US-10-473-127-2037 | Sequence 2037, Ap | 1281 | 84.5 | 7.5 | 2234 | 15 | US-10-612-090-20 | Sequence 20, Appl |
| 1209 | 104 | 9.2 | 139 | 16 | US-10-473-127-2040 | Sequence 2040, Ap | 1282 | 84 | 7.5 | 330 | 20 | US-11-037-143-5586 | Sequence 5586, Ap |
| 1210 | 104 | 9.2 | 139 | 17 | US-10-741-600-1050 | Sequence 1050, Ap | 1283 | 84 | 7.5 | 330 | 17 | US-10-732-923-5372 | Sequence 5372, Ap |
| 1211 | 101.5 | 9.0 | 380 | 15 | US-10-369-493-6206 | Sequence 6206, Ap | 1284 | 83.5 | 7.4 | 357 | 15 | US-10-425-114-56835 | Sequence 56835, A |
| 1212 | 100.5 | 8.9 | 402 | 15 | US-10-343-953-2 | Sequence 2, Appl | 1285 | 83.5 | 7.4 | 357 | 15 | US-10-425-115-267262 | Sequence 267262, Sequence 14, Appl |
| 1213 | 100.5 | 8.9 | 402 | 15 | US-10-257-174-47 | Sequence 47, Appl | 1286 | 83.5 | 7.4 | 393 | 9 | US-09-846-500B-14 | Sequence 14, Appl |
| 1214 | 99.5 | 8.8 | 402 | 16 | US-10-481-698-17 | Sequence 17, Appl | 1287 | 83.5 | 7.4 | 551 | 9 | US-09-764-853-657 | Sequence 657, App |
| 1215 | 99 | 8.8 | 201 | 15 | US-10-120-907A-40 | Sequence 40, Appl | 1288 | 83.5 | 7.4 | 591 | 16 | US-10-437-963-161046 | Sequence 161046, Sequence 14, Appl |
| 1216 | 99 | 8.8 | 201 | 15 | US-10-120-907A-41 | Sequence 41, Appl | 1289 | 83.5 | 7.4 | 615 | 15 | US-10-239-818-14 | Sequence 14, Appl |
| 1217 | 99 | 8.8 | 1428 | 20 | US-11-097-143-37923 | Sequence 37923, A | 1290 | 83.5 | 7.4 | 4123 | 14 | US-10-213-509-5 | Sequence 5, Appl |

| | | | | | | | | | | | | | |
|------|------|-----|------|----|----------------------|--------------------|------|------|-----|------|----|----------------------|--------------------|
| 1291 | 83.5 | 7.4 | 4219 | 15 | US-10-085-198-2 | Sequence 2, Appli | 1364 | 79.5 | 7.1 | 985 | 10 | US-09-994-064-6 | Sequence 6, Appli |
| 1292 | 83.5 | 7.4 | 5179 | 9 | US-09-922-217-1068 | Sequence 1068, Ap | 1365 | 79.5 | 7.1 | 985 | 10 | US-09-994-064-66 | Sequence 66, Appl |
| 1293 | 83.5 | 7.4 | 5179 | 9 | US-09-833-263-1068 | Sequence 1068, Ap | 1366 | 79.5 | 7.1 | 985 | 11 | US-09-993-777-6 | Sequence 6, Appli |
| 1294 | 83.5 | 7.4 | 5179 | 13 | US-10-025-380-1068 | Sequence 1068, Ap | 1367 | 79.5 | 7.1 | 985 | 11 | US-09-993-777-66 | Sequence 66, Appli |
| 1295 | 83.5 | 7.4 | 5179 | 16 | US-10-734-564-121 | Sequence 121, App | 1368 | 79.5 | 7.1 | 985 | 16 | US-10-836-383-6 | Sequence 66, Appl |
| 1296 | 83 | 7.4 | 471 | 20 | US-11-097-143-12147 | Sequence 12147, A | 1369 | 79.5 | 7.1 | 985 | 16 | US-10-836-383-66 | Sequence 148212, |
| 1297 | 83 | 7.4 | 605 | 9 | US-09-801-368-428 | Sequence 428, App | 1370 | 79.5 | 7.1 | 1216 | 16 | US-10-437-963-148212 | Sequence 526, App |
| 1298 | 83 | 7.4 | 605 | 9 | US-10-369-493-32016 | Sequence 22016, A | 1371 | 79.5 | 7.1 | 1403 | 14 | US-10-225-567A-526 | Sequence 71, Appl |
| 1299 | 83 | 7.4 | 662 | 15 | US-10-425-115-230245 | Sequence 230245, A | 1372 | 79.5 | 7.1 | 1403 | 15 | US-10-331-496A-71 | Sequence 152, Ap |
| 1300 | 82.5 | 7.3 | 825 | 15 | US-10-369-493-32501 | Sequence 2501, A | 1373 | 79.5 | 7.1 | 1441 | 17 | US-10-732-923-1652 | Sequence 1652, Ap |
| 1301 | 82.5 | 7.3 | 843 | 20 | US-11-097-143-39828 | Sequence 39828, A | 1374 | 79.5 | 7.1 | 1441 | 17 | US-10-732-923-1653 | Sequence 1653, Ap |
| 1302 | 82.5 | 7.3 | 1371 | 20 | US-11-097-143-33825 | Sequence 33825, A | 1375 | 79.5 | 7.1 | 1459 | 15 | US-10-188-186-100 | Sequence 100, App |
| 1303 | 82 | 7.3 | 89 | 9 | US-09-864-761-42220 | Sequence 42220, A | 1376 | 79.5 | 7.1 | 1486 | 20 | US-11-097-143-4767 | Sequence 4767, Ap |
| 1304 | 82 | 7.3 | 339 | 20 | US-11-097-143-30054 | Sequence 30054, A | 1377 | 79 | 7.0 | 162 | 16 | US-10-437-963-145598 | Sequence 145598, A |
| 1305 | 82 | 7.3 | 349 | 15 | US-10-425-114-38370 | Sequence 38370, A | 1378 | 79 | 7.0 | 195 | 20 | US-11-097-143-34818 | Sequence 34818, A |
| 1306 | 82 | 7.3 | 477 | 16 | US-10-723-860-897 | Sequence 897, App | 1379 | 79 | 7.0 | 323 | 15 | US-10-425-114-59856 | Sequence 59856, A |
| 1307 | 82 | 7.3 | 477 | 18 | US-10-756-149-4935 | Sequence 897, App | 1380 | 79 | 7.0 | 352 | 14 | US-09-934-455-118 | Sequence 118, App |
| 1308 | 82 | 7.3 | 553 | 9 | US-09-888-224-2 | Sequence 4935, Ap | 1381 | 79 | 7.0 | 352 | 14 | US-10-278-173-110 | Sequence 110, App |
| 1309 | 82 | 7.3 | 637 | 15 | US-10-094-749-2621 | Sequence 2, Appli | 1382 | 79 | 7.0 | 352 | 15 | US-10-225-066A-112 | Sequence 112, App |
| 1310 | 82 | 7.3 | 1099 | 17 | US-10-732-923-8770 | Sequence 2621, Ap | 1383 | 79 | 7.0 | 352 | 15 | US-10-225-067-20 | Sequence 20, Appl |
| 1311 | 82 | 7.3 | 1489 | 16 | US-10-437-963-138442 | Sequence 8770, Ap | 1384 | 79 | 7.0 | 352 | 15 | US-10-374-780A-2052 | Sequence 2052, Ap |
| 1312 | 82 | 7.3 | 1671 | 15 | US-10-187-975-18 | Sequence 18, Appl | 1385 | 79 | 7.0 | 352 | 15 | US-10-412-699B-450 | Sequence 450, App |
| 1313 | 81.5 | 7.2 | 186 | 16 | US-10-437-963-186467 | Sequence 186467, A | 1386 | 79 | 7.0 | 352 | 15 | US-10-225-066A-112 | Sequence 112, App |
| 1314 | 81.5 | 7.2 | 346 | 15 | US-10-416-328-6 | Sequence 6, Appli | 1387 | 79 | 7.0 | 425 | 16 | US-10-425-115-227109 | Sequence 227109, A |
| 1315 | 81.5 | 7.2 | 346 | 15 | US-10-432-290-11 | Sequence 11, Appl | 1388 | 79 | 7.0 | 629 | 20 | US-11-097-143-5313 | Sequence 5313, Ap |
| 1316 | 81.5 | 7.2 | 346 | 17 | US-10-498-778-6 | Sequence 6, Appli | 1389 | 79 | 7.0 | 629 | 20 | US-11-097-143-29106 | Sequence 29106, A |
| 1317 | 81.5 | 7.2 | 352 | 15 | US-10-424-599-195846 | Sequence 6, Appli | 1390 | 79 | 7.0 | 820 | 16 | US-10-437-963-155777 | Sequence 155777, A |
| 1318 | 81.5 | 7.2 | 386 | 15 | US-10-282-122A-51488 | Sequence 195846, A | 1391 | 79 | 7.0 | 1605 | 17 | US-10-732-923-18432 | Sequence 18432, A |
| 1319 | 81.5 | 7.2 | 792 | 9 | US-09-802-207-27 | Sequence 51488, A | 1392 | 79 | 7.0 | 2156 | 17 | US-10-732-923-18431 | Sequence 18431, A |
| 1320 | 81.5 | 7.2 | 800 | 14 | US-10-029-386-32198 | Sequence 27, Appl | 1393 | 79 | 7.0 | 2616 | 20 | US-11-097-143-21459 | Sequence 21459, A |
| 1321 | 81.5 | 7.2 | 929 | 15 | US-10-425-114-59344 | Sequence 32198, A | 1394 | 78.5 | 7.0 | 133 | 15 | US-10-424-599-161524 | Sequence 161524, A |
| 1322 | 81.5 | 7.2 | 957 | 9 | US-09-922-217-1065 | Sequence 59344, A | 1395 | 78.5 | 7.0 | 252 | 17 | US-10-868-381-36 | Sequence 36, Appl |
| 1323 | 81.5 | 7.2 | 957 | 9 | US-09-833-263-1065 | Sequence 1065, Ap | 1396 | 78.5 | 7.0 | 569 | 15 | US-10-108-260A-4361 | Sequence 4361, Ap |
| 1324 | 81.5 | 7.2 | 957 | 13 | US-10-025-380-1065 | Sequence 1065, Ap | 1397 | 78.5 | 7.0 | 585 | 17 | US-10-868-381-56 | Sequence 56, Appl |
| 1325 | 81.5 | 7.2 | 1354 | 20 | US-10-097-143-36711 | Sequence 36711, A | 1398 | 78.5 | 7.0 | 585 | 17 | US-10-868-381-57 | Sequence 57, Appl |
| 1326 | 81.5 | 7.2 | 1500 | 16 | US-10-437-963-118360 | Sequence 118360, A | 1399 | 78.5 | 7.0 | 586 | 17 | US-10-635-211-2 | Sequence 2, Appli |
| 1327 | 81 | 7.2 | 260 | 15 | US-10-460-512-3 | Sequence 3, Appli | 1400 | 78.5 | 7.0 | 590 | 10 | US-09-957-187-12 | Sequence 12, Appl |
| 1328 | 81 | 7.2 | 260 | 16 | US-10-897-911-3 | Sequence 3, Appli | 1401 | 78.5 | 7.0 | 590 | 20 | US-11-058-709-12 | Sequence 12, Appl |
| 1329 | 81 | 7.2 | 260 | 17 | US-10-898-615-3 | Sequence 3, Appli | 1402 | 78.5 | 7.0 | 652 | 16 | US-10-425-115-301014 | Sequence 301014, A |
| 1330 | 81 | 7.2 | 294 | 20 | US-11-097-143-21039 | Sequence 21039, A | 1403 | 78.5 | 7.0 | 653 | 16 | US-09-957-187-10 | Sequence 10, Appl |
| 1331 | 81 | 7.2 | 746 | 14 | US-10-156-761-14411 | Sequence 21039, A | 1404 | 78.5 | 7.0 | 653 | 20 | US-11-058-709-10 | Sequence 10, Appl |
| 1332 | 81 | 7.2 | 1128 | 15 | US-10-369-493-22484 | Sequence 14411, A | 1405 | 78.5 | 7.0 | 1478 | 14 | US-10-240-154-10 | Sequence 10, Appl |
| 1333 | 81 | 7.2 | 1537 | 9 | US-09-801-368-104 | Sequence 22484, A | 1406 | 78.5 | 7.0 | 1595 | 17 | US-10-484-218-20 | Sequence 20, Appl |
| 1334 | 81 | 7.2 | 1537 | 15 | US-10-369-493-1398 | Sequence 104, App | 1407 | 78.5 | 7.0 | 1891 | 16 | US-10-437-963-194977 | Sequence 194977, A |
| 1335 | 81 | 7.2 | 1537 | 17 | US-10-324-035-17 | Sequence 1398, Ap | 1408 | 78.5 | 7.0 | 2040 | 20 | US-11-097-143-18441 | Sequence 18441, A |
| 1336 | 81 | 7.2 | 1609 | 15 | US-10-369-493-1535 | Sequence 17, Appl | 1409 | 78.5 | 7.0 | 5374 | 15 | US-10-028-248A-75 | Sequence 75, Appl |
| 1337 | 81 | 7.2 | 2977 | 20 | US-11-097-143-35232 | Sequence 1535, Ap | 1410 | 78.5 | 7.0 | 5374 | 15 | US-10-107-782-75 | Sequence 75, Appl |
| 1338 | 80.5 | 7.2 | 323 | 15 | US-10-282-122A-54172 | Sequence 35232, A | 1411 | 78 | 6.9 | 184 | 15 | US-10-425-114-44214 | Sequence 44214, A |
| 1339 | 80.5 | 7.2 | 769 | 16 | US-10-437-963-119061 | Sequence 54172, A | 1412 | 78 | 6.9 | 268 | 10 | US-09-820-649-118 | Sequence 118, App |
| 1340 | 80.5 | 7.2 | 901 | 16 | US-10-425-115-323903 | Sequence 119061, A | 1413 | 78 | 6.9 | 268 | 14 | US-10-160-162-118 | Sequence 118, App |
| 1341 | 80.5 | 7.2 | 1167 | 20 | US-11-097-143-63 | Sequence 323903, A | 1414 | 78 | 6.9 | 268 | 17 | US-10-936-773-118 | Sequence 118, App |
| 1342 | 80 | 7.1 | 89 | 9 | US-09-867-550-32 | Sequence 63, Appl | 1415 | 78 | 6.9 | 293 | 14 | US-10-080-170-340 | Sequence 340, App |
| 1343 | 80 | 7.1 | 169 | 15 | US-10-425-114-42832 | Sequence 32, Appl | 1416 | 78 | 6.9 | 293 | 16 | US-10-080-170-340 | Sequence 340, App |
| 1344 | 80 | 7.1 | 284 | 15 | US-10-424-599-150965 | Sequence 42832, A | 1417 | 78 | 6.9 | 293 | 16 | US-10-468-356-340 | Sequence 340, App |
| 1345 | 80 | 7.1 | 365 | 15 | US-10-425-114-64809 | Sequence 150965, A | 1418 | 78 | 6.9 | 400 | 14 | US-10-300-819-2 | Sequence 2, Appli |
| 1346 | 80 | 7.1 | 390 | 17 | US-10-732-923-20210 | Sequence 64809, A | 1419 | 78 | 6.9 | 508 | 16 | US-10-437-963-155768 | Sequence 155768, A |
| 1347 | 80 | 7.1 | 449 | 20 | US-11-097-143-25305 | Sequence 20210, A | 1420 | 78 | 6.9 | 536 | 15 | US-10-424-599-245648 | Sequence 245648, A |
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| 154 | 78.5 | 7.0 | 130 | 3 | US-08-700-651-9 | Sequence 9, Appl | 236 | 73.5 | 6.5 | 138 | 3 | US-08-928-361B-15 | Sequence 15, Appl |
| 155 | 78.5 | 7.0 | 130 | 3 | US-08-928-361B-14 | Sequence 14, Appl | 237 | 73.5 | 6.5 | 138 | 4 | US-09-588-995A-15 | Sequence 15, Appl |
| 156 | 78.5 | 7.0 | 130 | 4 | US-09-588-995A-14 | Sequence 14, Appl | 238 | 73.5 | 6.5 | 251 | 4 | US-09-949-016-11174 | Sequence 11174, A |
| 157 | 78.5 | 7.0 | 322 | 4 | US-09-248-796A-23680 | Sequence 23680, A | 239 | 73.5 | 6.5 | 251 | 4 | US-09-248-796A-23216 | Sequence 23216, A |
| 158 | 78.5 | 7.0 | 507 | 4 | US-09-949-016-8889 | Sequence 8889, Ap | 240 | 73.5 | 6.5 | 427 | 2 | US-08-282-197C-53 | Sequence 53, Appl |
| 159 | 78.5 | 7.0 | 507 | 4 | US-09-949-016-8897 | Sequence 8897, Ap | 241 | 73.5 | 6.5 | 451 | 5 | PCT-US95-09941-2 | Sequence 2, Appl |
| 160 | 78.5 | 7.0 | 590 | 4 | US-09-520-781-12 | Sequence 12, Appl | 242 | 73.5 | 6.5 | 451 | 5 | PCT-US95-09941-2 | Sequence 2, Appl |
| 161 | 78.5 | 7.0 | 653 | 4 | US-09-520-781-10 | Sequence 10, Appl | 243 | 73.5 | 6.5 | 570 | 4 | US-09-565-501A-104 | Sequence 104, App |
| 162 | 78.5 | 7.0 | 685 | 4 | US-09-248-796A-20197 | Sequence 20197, A | 244 | 73.5 | 6.5 | 570 | 4 | US-09-639-206A-104 | Sequence 104, App |
| 163 | 78 | 6.9 | 261 | 4 | US-09-248-796A-14279 | Sequence 14279, A | 245 | 73.5 | 6.5 | 570 | 4 | US-09-874-923-104 | Sequence 104, App |
| 164 | 77.5 | 6.9 | 346 | 2 | US-08-687-702-36 | Sequence 36, Appl | 246 | 73.5 | 6.5 | 595 | 2 | US-08-232-087A-2 | Sequence 2, Appl |
| 165 | 77.5 | 6.9 | 497 | 3 | US-09-377-557-10 | Sequence 10, Appl | 247 | 73.5 | 6.5 | 595 | 3 | US-09-006-353A-9 | Sequence 9, Appl |
| 166 | 77.5 | 6.9 | 514 | 3 | US-08-738-168B-15 | Sequence 15, Appl | 248 | 73.5 | 6.5 | 595 | 4 | US-09-573-986-9 | Sequence 9, Appl |
| 167 | 77.5 | 6.9 | 562 | 2 | US-09-687-702-1 | Sequence 1, Appl | 249 | 73.5 | 6.5 | 595 | 4 | US-09-949-016-6048 | Sequence 6048, Ap |
| 168 | 77.5 | 6.9 | 673 | 4 | US-09-949-016-7388 | Sequence 7388, Ap | 250 | 73.5 | 6.5 | 642 | 4 | US-09-949-016-8043 | Sequence 8043, Ap |
| 169 | 77 | 6.8 | 249 | 3 | US-08-700-651-15 | Sequence 15, Appl | 251 | 73.5 | 6.5 | 646 | 4 | US-09-902-540-12044 | Sequence 12044, A |
| 170 | 77 | 6.8 | 249 | 3 | US-08-928-361B-20 | Sequence 20, Appl | 252 | 73.5 | 6.5 | 780 | 4 | US-09-248-796A-16702 | Sequence 16702, A |
| 171 | 77 | 6.8 | 249 | 4 | US-09-588-995A-20 | Sequence 20, Appl | 253 | 73.5 | 6.5 | 795 | 3 | US-09-193-562D-11 | Sequence 11, Appl |
| 172 | 77 | 6.8 | 714 | 4 | US-09-949-016-7038 | Sequence 7038, Ap | 254 | 73.5 | 6.5 | 795 | 3 | US-10-055-412B-11 | Sequence 11, Appl |
| 173 | 77 | 6.8 | 750 | 3 | US-09-165-239A-4 | Sequence 4, Appl | 255 | 73.5 | 6.5 | 821 | 3 | US-09-193-562D-12 | Sequence 12, Appl |
| 174 | 77 | 6.8 | 2123 | 3 | US-08-968-685A-10 | Sequence 10, Appl | 256 | 73.5 | 6.5 | 821 | 4 | US-10-055-412B-12 | Sequence 12, Appl |
| 175 | 76.5 | 6.8 | 134 | 4 | US-09-248-796A-27317 | Sequence 27317, A | 257 | 73.5 | 6.5 | 905 | 3 | US-09-193-562D-2 | Sequence 2, Appl |
| 176 | 76.5 | 6.8 | 303 | 4 | US-09-248-796A-14269 | Sequence 14269, A | 258 | 73.5 | 6.5 | 905 | 4 | US-10-055-412B-2 | Sequence 2, Appl |
| 177 | 76.5 | 6.8 | 348 | 3 | US-09-216-295-16 | Sequence 16, Appl | 259 | 73.5 | 6.5 | 1101 | 4 | US-09-561-709B-5 | Sequence 5, Appl |
| 178 | 76.5 | 6.8 | 348 | 4 | US-09-632-570-16 | Sequence 16, Appl | 260 | 73.5 | 6.5 | 1761 | 4 | US-09-561-709B-1 | Sequence 1, Appl |
| 179 | 76.5 | 6.8 | 348 | 4 | US-09-632-575-46 | Sequence 46, Appl | 261 | 73 | 6.5 | 155 | 4 | US-09-252-991A-22634 | Sequence 22634, A |
| 180 | 76.5 | 6.8 | 452 | 4 | US-09-248-796A-16219 | Sequence 16219, A | 262 | 73 | 6.5 | 162 | 3 | US-08-700-651-13 | Sequence 13, Appl |
| 181 | 76 | 6.8 | 321 | 4 | US-09-248-796A-20146 | Sequence 20146, A | 263 | 73 | 6.5 | 332 | 4 | US-09-313-942-10 | Sequence 10, Appl |
| 182 | 76 | 6.8 | 334 | 4 | US-09-197-970B-7 | Sequence 7, Appl | 264 | 73 | 6.5 | 488 | 2 | US-08-593-455B-5 | Sequence 5, Appl |
| 183 | 76 | 6.8 | 380 | 3 | US-09-134-001C-4558 | Sequence 4558, Ap | 265 | 73 | 6.5 | 488 | 3 | US-09-069-781B-5 | Sequence 5, Appl |
| 184 | 76 | 6.8 | 1426 | 3 | US-09-136-574A-43 | Sequence 43, Appl | 266 | 73 | 6.5 | 488 | 3 | US-09-137-132-5 | Sequence 5, Appl |
| 185 | 75.5 | 6.7 | 348 | 1 | US-08-035-392-2 | Sequence 2, Appl | 267 | 73 | 6.5 | 488 | 3 | US-08-864-564A-5 | Sequence 5, Appl |
| 186 | 75.5 | 6.7 | 348 | 1 | US-08-511A-2 | Sequence 2, Appl | 268 | 73 | 6.5 | 488 | 4 | US-09-094-410-5 | Sequence 5, Appl |
| 187 | 75.5 | 6.7 | 430 | 1 | US-08-035-392A-2 | Sequence 4, Appl | 269 | 73 | 6.5 | 488 | 4 | US-08-708-123D-5 | Sequence 5, Appl |
| 188 | 75.5 | 6.7 | 430 | 1 | US-08-504-511A-4 | Sequence 4, Appl | 270 | 73 | 6.5 | 488 | 4 | US-08-583-153A-5 | Sequence 5, Appl |
| 189 | 75.5 | 6.7 | 453 | 4 | US-09-230-225B-4 | Sequence 4, Appl | 271 | 73 | 6.5 | 488 | 4 | US-08-638-524B-5 | Sequence 5, Appl |
| 190 | 75.5 | 6.7 | 468 | 2 | US-08-959-011-3 | Sequence 3, Appl | 272 | 73 | 6.5 | 579 | 4 | US-09-198-452A-918 | Sequence 918, App |
| 191 | 75.5 | 6.7 | 478 | 4 | US-09-345-473B-51 | Sequence 51, Appl | 273 | 73 | 6.5 | 606 | 4 | US-09-438-185A-853 | Sequence 853, App |
| 201 | 75.5 | 6.7 | 511 | 1 | US-08-220-151-17 | Sequence 17, Appl | 274 | 73 | 6.5 | 624 | 4 | US-09-877-730-24 | Sequence 24, Appl |

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|-----|------|-----|------|---|----------------------|-------------------|-----|------|-----|------|---|----------------------|-------------------|
| 275 | 73 | 6.5 | 639 | 4 | US-09-949-016-6812 | Sequence 6812, Ap | 348 | 72 | 6.4 | 1404 | 4 | US-10-164-595-78 | Sequence 78, Appl |
| 276 | 73 | 6.5 | 652 | 4 | US-09-949-016-7323 | Sequence 7323, Ap | 349 | 72 | 6.4 | 1404 | 4 | US-09-298-970A-1 | Sequence 1, Appli |
| 277 | 73 | 6.5 | 658 | 4 | US-08-825-558-4 | Sequence 4, Appli | 350 | 72 | 6.4 | 1411 | 4 | US-09-949-016-10827 | Sequence 10827, A |
| 278 | 73 | 6.5 | 658 | 3 | US-09-312-611-4 | Sequence 4, Appli | 351 | 72 | 6.4 | 1693 | 3 | US-08-840-316-1 | Sequence 1, Appli |
| 279 | 73 | 6.5 | 708 | 1 | US-07-797-556-2 | Sequence 2, Appli | 352 | 72 | 6.4 | 1693 | 3 | US-08-809-523-1 | Sequence 1, Appli |
| 280 | 73 | 6.5 | 708 | 1 | US-08-308-881-2 | Sequence 2, Appli | 353 | 72 | 6.4 | 1693 | 3 | US-08-471-971-1 | Sequence 1, Appli |
| 281 | 73 | 6.5 | 708 | 2 | US-09-058-263-2 | Sequence 2, Appli | 354 | 72 | 6.4 | 1693 | 4 | US-09-402-776-1 | Sequence 1, Appli |
| 282 | 73 | 6.5 | 708 | 2 | US-09-059-099-2 | Sequence 2, Appli | 355 | 72 | 6.4 | 1693 | 4 | US-08-470-246-1 | Sequence 1, Appli |
| 283 | 73 | 6.5 | 708 | 3 | US-09-058-264-2 | Sequence 2, Appli | 356 | 72 | 6.4 | 1693 | 4 | US-08-316-765-1 | Sequence 1, Appli |
| 284 | 73 | 6.5 | 708 | 4 | US-09-455-962-2 | Sequence 2, Appli | 357 | 72 | 6.4 | 1693 | 4 | US-09-724-475-1 | Sequence 1, Appli |
| 285 | 73 | 6.5 | 708 | 5 | PCT-US95-06530-2 | Sequence 2, Appli | 358 | 72 | 6.4 | 1693 | 5 | PCT-US93-08849A-1 | Sequence 1, Appli |
| 286 | 73 | 6.5 | 712 | 4 | US-09-877-730-22 | Sequence 22, Appl | 359 | 72 | 6.4 | 1693 | 5 | PCT-US93-08849-1 | Sequence 1, Appli |
| 287 | 73 | 6.5 | 733 | 4 | US-08-877-730-28 | Sequence 28, Appl | 360 | 72 | 6.4 | 1744 | 4 | US-09-438-185A-542 | Sequence 542, App |
| 288 | 73 | 6.5 | 852 | 4 | US-09-206-551-19 | Sequence 19, Appl | 361 | 72 | 6.4 | 1876 | 4 | US-09-418-710-71 | Sequence 70, Appl |
| 289 | 73 | 6.5 | 859 | 4 | US-09-313-942-7 | Sequence 7, Appli | 362 | 72 | 6.4 | 1876 | 4 | US-09-839-479-70 | Sequence 13, Appl |
| 290 | 73 | 6.5 | 918 | 2 | US-08-825-558-6 | Sequence 6, Appli | 363 | 72 | 6.4 | 1878 | 4 | US-09-418-710-13 | Sequence 13, Appl |
| 291 | 73 | 6.5 | 918 | 3 | US-09-312-611-6 | Sequence 3, Appli | 364 | 72 | 6.4 | 1878 | 4 | US-09-839-479-13 | Sequence 13, Appl |
| 292 | 73 | 6.5 | 918 | 4 | US-09-853-180B-3 | Sequence 3, Appli | 365 | 71.5 | 6.4 | 1335 | 4 | US-09-252-991A-17514 | Sequence 17514, A |
| 293 | 73 | 6.5 | 951 | 4 | US-09-313-942-9 | Sequence 9, Appli | 366 | 71.5 | 6.4 | 232 | 4 | US-09-333-809-217 | Sequence 217, App |
| 294 | 73 | 6.5 | 991 | 4 | US-09-877-730-12 | Sequence 12, Appl | 367 | 71.5 | 6.4 | 232 | 4 | US-09-746-311B-366 | Sequence 366, App |
| 295 | 73 | 6.5 | 1069 | 4 | US-09-877-730-2 | Sequence 2, Appli | 368 | 71.5 | 6.4 | 240 | 4 | US-09-107-532A-4430 | Sequence 4430, Ap |
| 296 | 73 | 6.5 | 1072 | 4 | US-09-877-730-18 | Sequence 18, Appl | 369 | 71.5 | 6.4 | 321 | 4 | US-09-107-433-4282 | Sequence 4282, Ap |
| 297 | 73 | 6.5 | 1150 | 4 | US-09-877-730-8 | Sequence 8, Appli | 370 | 71.5 | 6.4 | 386 | 4 | US-09-248-796A-18312 | Sequence 18312, A |
| 298 | 73 | 6.5 | 1158 | 4 | US-09-313-942-26 | Sequence 26, Appl | 371 | 71.5 | 6.4 | 442 | 2 | US-08-687-553-6 | Sequence 6, Appli |
| 299 | 73 | 6.5 | 1168 | 4 | US-09-313-942-24 | Sequence 24, Appl | 372 | 71.5 | 6.4 | 442 | 4 | US-09-401-415-6 | Sequence 6, Appli |
| 300 | 73 | 6.5 | 1312 | 3 | US-09-345-882-29 | Sequence 29, Appl | 373 | 71.5 | 6.4 | 529 | 4 | US-09-248-796A-20186 | Sequence 20186, A |
| 301 | 73 | 6.5 | 2736 | 4 | US-09-252-991A-30227 | Sequence 30227, A | 374 | 71.5 | 6.4 | 540 | 4 | US-09-583-110-3685 | Sequence 3685, Ap |
| 302 | 72.5 | 6.4 | 150 | 3 | US-08-928-361B-18 | Sequence 18, Appl | 375 | 71.5 | 6.4 | 595 | 1 | US-08-225-989-2 | Sequence 2, Appli |
| 303 | 72.5 | 6.4 | 150 | 4 | US-09-588-995A-18 | Sequence 18, Appl | 376 | 71.5 | 6.4 | 595 | 1 | US-08-570-923-2 | Sequence 2, Appli |
| 304 | 72.5 | 6.4 | 185 | 4 | US-09-248-796A-18311 | Sequence 18311, A | 377 | 71.5 | 6.4 | 595 | 1 | US-08-580-014-2 | Sequence 2, Appli |
| 305 | 72.5 | 6.4 | 233 | 4 | US-09-496-320-5 | Sequence 5, Appli | 378 | 71.5 | 6.4 | 595 | 3 | US-09-079-785-2 | Sequence 2, Appli |
| 306 | 72.5 | 6.4 | 328 | 4 | US-09-489-039A-12803 | Sequence 12803, A | 379 | 71.5 | 6.4 | 595 | 4 | US-09-921-667-6 | Sequence 6, Appli |
| 307 | 72.5 | 6.4 | 463 | 1 | US-08-162-402B-9 | Sequence 9, Appli | 380 | 71.5 | 6.4 | 641 | 4 | US-09-613-303-51 | Sequence 51, Appl |
| 308 | 72.5 | 6.4 | 841 | 4 | US-09-949-016-9669 | Sequence 11, Appl | 381 | 71.5 | 6.4 | 641 | 4 | US-10-267-311-51 | Sequence 51, Appl |
| 309 | 72.5 | 6.4 | 878 | 4 | US-09-556-706B-2 | Sequence 2, Appli | 382 | 71.5 | 6.4 | 641 | 4 | US-10-267-311-51 | Sequence 51, Appl |
| 310 | 72.5 | 6.4 | 878 | 4 | US-09-724-418A-2 | Sequence 2, Appli | 383 | 71.5 | 6.4 | 903 | 3 | US-09-193-562D-46 | Sequence 46, Appl |
| 311 | 72.5 | 6.4 | 907 | 3 | US-08-783-774-2 | Sequence 2, Appli | 384 | 71.5 | 6.4 | 903 | 4 | US-09-623-624-18 | Sequence 18, Appl |
| 312 | 72.5 | 6.4 | 907 | 3 | US-08-783-774-2 | Sequence 2, Appli | 385 | 71.5 | 6.4 | 903 | 4 | US-10-055-412B-46 | Sequence 46, Appl |
| 313 | 72.5 | 6.4 | 907 | 4 | US-09-328-599A-1 | Sequence 1, Appli | 386 | 71.5 | 6.4 | 903 | 4 | US-10-270-595-18 | Sequence 18, Appl |
| 314 | 72.5 | 6.4 | 907 | 5 | PCT-US95-04611A-19 | Sequence 19, Appl | 387 | 71.5 | 6.4 | 1013 | 3 | US-08-860-886-2 | Sequence 2, Appli |
| 315 | 72 | 6.4 | 279 | 4 | US-09-248-796A-16859 | Sequence 16859, A | 388 | 71.5 | 6.4 | 1224 | 4 | US-09-607-510-2 | Sequence 2, Appli |
| 316 | 72 | 6.4 | 300 | 4 | US-09-254-465A-10 | Sequence 10, Appl | 389 | 71.5 | 6.4 | 1751 | 3 | US-09-136-574A-44 | Sequence 44, Appl |
| 317 | 72 | 6.4 | 300 | 4 | US-09-397-243D-12 | Sequence 12, Appl | 390 | 71 | 6.3 | 169 | 4 | US-09-252-991A-32019 | Sequence 32019, A |
| 318 | 72 | 6.4 | 300 | 4 | US-09-953-499-10 | Sequence 10, Appl | 391 | 71 | 6.3 | 189 | 4 | US-09-270-767-39457 | Sequence 39457, A |
| 319 | 72 | 6.4 | 489 | 4 | US-09-545-814-29 | Sequence 29, Appl | 392 | 71 | 6.3 | 216 | 4 | US-09-270-767-54674 | Sequence 54674, A |
| 320 | 72 | 6.4 | 557 | 4 | US-09-248-796A-26892 | Sequence 26892, A | 393 | 71 | 6.3 | 216 | 4 | US-09-248-796A-25076 | Sequence 25076, A |
| 321 | 72 | 6.4 | 559 | 4 | US-09-545-814-14 | Sequence 14, Appl | 394 | 71 | 6.3 | 230 | 4 | US-09-328-352-7443 | Sequence 7443, Ap |
| 322 | 72 | 6.4 | 583 | 4 | US-09-545-814-2 | Sequence 2, Appli | 395 | 71 | 6.3 | 230 | 4 | US-09-248-796A-22910 | Sequence 22910, A |
| 323 | 72 | 6.4 | 583 | 4 | US-09-545-814-5 | Sequence 5, Appli | 396 | 71 | 6.3 | 251 | 4 | US-09-248-796A-20695 | Sequence 20695, A |
| 324 | 72 | 6.4 | 609 | 4 | US-09-198-452A-579 | Sequence 579, App | 397 | 71 | 6.3 | 610 | 1 | US-07-821-717B-6 | Sequence 6, Appli |
| 325 | 72 | 6.4 | 635 | 4 | US-09-545-814-32 | Sequence 32, Appl | 398 | 71 | 6.3 | 610 | 1 | US-08-119-262B-6 | Sequence 6, Appli |
| 326 | 72 | 6.4 | 785 | 3 | US-08-374-077C-3 | Sequence 3, Appli | 399 | 71 | 6.3 | 610 | 1 | US-08-135-929A-11 | Sequence 11, Appl |
| 327 | 72 | 6.4 | 785 | 3 | US-08-895-590-3 | Sequence 3, Appli | 400 | 71 | 6.3 | 610 | 1 | US-08-234-265A-11 | Sequence 11, Appl |
| 328 | 72 | 6.4 | 785 | 4 | US-09-539-879A-3 | Sequence 3, Appli | 401 | 71 | 6.3 | 1014 | 3 | US-09-078-347A-3 | Sequence 3, Appli |
| 329 | 72 | 6.4 | 941 | 4 | US-07-757-022B-14 | Sequence 14, Appl | 402 | 71 | 6.3 | 1014 | 3 | US-09-596-248D-25 | Sequence 25, Appl |
| 330 | 72 | 6.4 | 1022 | 4 | US-07-757-022B-84 | Sequence 84, Appl | 403 | 71 | 6.3 | 1063 | 4 | US-09-596-248D-47 | Sequence 47, Appl |
| 331 | 72 | 6.4 | 1038 | 4 | US-07-757-022B-74 | Sequence 74, Appl | 404 | 70.5 | 6.3 | 153 | 4 | US-09-252-991A-17880 | Sequence 17880, A |
| 332 | 72 | 6.4 | 1049 | 4 | US-07-757-022B-58 | Sequence 58, Appl | 405 | 70.5 | 6.3 | 173 | 4 | US-09-107-532A-4115 | Sequence 4115, Ap |
| 333 | 72 | 6.4 | 1129 | 4 | US-09-023-905A-2 | Sequence 2, Appli | 406 | 70.5 | 6.3 | 198 | 4 | US-09-489-039A-9988 | Sequence 9988, Ap |
| 334 | 72 | 6.4 | 1404 | 4 | US-07-757-022B-104 | Sequence 104, App | 407 | 70.5 | 6.3 | 213 | 4 | US-09-538-092-1255 | Sequence 1255, Ap |
| 335 | 72 | 6.4 | 1203 | 3 | US-09-351-200-2 | Sequence 2, Appli | 408 | 70.5 | 6.3 | 232 | 4 | US-09-333-809-214 | Sequence 214, App |
| 336 | 72 | 6.4 | 1270 | 4 | US-07-757-022B-44 | Sequence 44, Appl | 409 | 70.5 | 6.3 | 232 | 4 | US-09-333-809-216 | Sequence 216, App |
| 337 | 72 | 6.4 | 1311 | 4 | US-07-757-022B-42 | Sequence 42, Appl | 410 | 70.5 | 6.3 | 232 | 4 | US-09-333-809-216 | Sequence 216, App |
| 338 | 72 | 6.4 | 1313 | 4 | US-07-757-022B-142 | Sequence 142, App | 411 | 70.5 | 6.3 | 232 | 4 | US-09-746-311B-363 | Sequence 363, App |
| 339 | 72 | 6.4 | 1314 | 4 | US-07-757-022B-50 | Sequence 50, Appl | 412 | 70.5 | 6.3 | 232 | 4 | US-09-746-311B-364 | Sequence 364, App |
| 340 | 72 | 6.4 | 1320 | 4 | US-07-757-022B-46 | Sequence 46, Appl | 413 | 70.5 | 6.3 | 232 | 4 | US-09-746-311B-365 | Sequence 365, App |
| 341 | 72 | 6.4 | 1320 | 4 | US-07-757-022B-60 | Sequence 60, Appl | 414 | 70.5 | 6.3 | 292 | 1 | US-08-286-888B-6 | Sequence 6, Appli |
| 342 | 72 | 6.4 | 1320 | 4 | US-10-164-595-58 | Sequence 58, Appl | 415 | 70.5 | 6.3 | 319 | 4 | US-09-270-767-44343 | Sequence 44343, A |
| 343 | 72 | 6.4 | 1354 | 4 | US-07-757-022B-48 | Sequence 48, Appl | 416 | 70.5 | 6.3 | 330 | 4 | US-09-248-796A-14853 | Sequence 14853, A |
| 344 | 72 | 6.4 | 1361 | 4 | US-07-757-022B-40 | Sequence 40, Appl | 417 | 70.5 | 6.3 | 401 | 4 | US-09-949-016-7956 | Sequence 7956, Ap |
| 345 | 72 | 6.4 | 1363 | 4 | US-07-757-022B-52 | Sequence 52, Appl | 418 | 70.5 | 6.3 | 441 | 4 | US-09-248-796A-20171 | Sequence 20171, A |
| 346 | 72 | 6.4 | 1404 | 4 | US-07-757-022B-2 | Sequence 2, Appli | 419 | 70.5 | 6.3 | 591 | 4 | US-09-270-767-32687 | Sequence 32687, A |
| 347 | 72 | 6.4 | 1404 | 4 | US-07-757-022B-62 | Sequence 62, Appl | 420 | 70.5 | 6.3 | 591 | 4 | US-09-270-767-47904 | Sequence 47904, A |

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| 421 | 70.5 | 6.3 | 639 | 4 | US-09-252-991A-24474 | Sequence 24474, A | 494 | 67.5 | 6.0 | 140 | 4 | US-09-270-787-42846 | Sequence 42846, A |
| 422 | 70 | 6.2 | 232 | 4 | US-09-252-991A-27628 | Sequence 27628, A | 495 | 67.5 | 6.0 | 159 | 4 | US-09-252-991A-20138 | Sequence 20138, A |
| 423 | 70 | 6.2 | 340 | 4 | US-09-492-709A-26252 | Sequence 26252, App | 496 | 67.5 | 6.0 | 218 | 1 | US-08-463-115-92 | Sequence 92, Appl |
| 424 | 70 | 6.2 | 722 | 4 | US-09-252-991A-26452 | Sequence 26452, A | 497 | 67.5 | 6.0 | 218 | 1 | US-08-463-388-92 | Sequence 92, Appl |
| 425 | 69.5 | 6.2 | 51 | 4 | US-09-902-540-15148 | Sequence 15148, A | 498 | 67.5 | 6.0 | 284 | 4 | US-09-270-767-46344 | Sequence 46344, A |
| 426 | 69.5 | 6.2 | 139 | 4 | US-09-248-796A-14268 | Sequence 14268, A | 499 | 67.5 | 6.0 | 291 | 4 | US-09-248-796A-14273 | Sequence 14273, A |
| 427 | 69.5 | 6.2 | 300 | 4 | US-09-248-796A-16245 | Sequence 16245, A | 500 | 67.5 | 6.0 | 312 | 4 | US-10-101-464A-930 | Sequence 930, App |
| 428 | 69.5 | 6.2 | 360 | 4 | US-09-489-039A-9383 | Sequence 9383, Ap | 501 | 67.5 | 6.0 | 338 | 4 | US-09-538-092-144 | Sequence 144, App |
| 429 | 69.5 | 6.2 | 398 | 4 | US-09-248-796A-14978 | Sequence 14978, A | 502 | 67.5 | 6.0 | 362 | 1 | US-08-437-027-21 | Sequence 21, Appl |
| 430 | 69.5 | 6.2 | 401 | 4 | US-09-270-767-44680 | Sequence 44680, A | 503 | 67.5 | 6.0 | 365 | 1 | US-08-437-027-20 | Sequence 20, Appl |
| 431 | 69.5 | 6.2 | 462 | 6 | 5171671-2 | Patent No. 5171671 | 504 | 67.5 | 6.0 | 383 | 4 | US-09-107-532A-5105 | Sequence 5105, Ap |
| 432 | 69.5 | 6.2 | 462 | 6 | 5171671-2 | Patent No. 5171671 | 505 | 67.5 | 6.0 | 394 | 4 | US-09-949-016-9565 | Sequence 9565, Ap |
| 433 | 69.5 | 6.2 | 554 | 4 | US-09-599-360B-78 | Sequence 78, Appl | 506 | 67.5 | 6.0 | 427 | 4 | US-09-328-352-5205 | Sequence 5205, Ap |
| 434 | 69.5 | 6.2 | 559 | 4 | US-09-543-681A-7241 | Sequence 7241, Ap | 507 | 67.5 | 6.0 | 428 | 4 | US-09-489-039A-10901 | Sequence 10901, A |
| 435 | 69.5 | 6.2 | 643 | 4 | US-09-248-796A-18427 | Sequence 18427, A | 508 | 67.5 | 6.0 | 498 | 4 | US-09-718-096-26 | Sequence 26, Appl |
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| 444 | 69 | 6.1 | 237 | 4 | US-09-721-908-4 | Sequence 4, Appli | 517 | 67.5 | 6.0 | 656 | 2 | US-08-214-564A-4 | Sequence 4, Appli |
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| 456 | 69 | 6.1 | 845 | 3 | US-08-804-439A-94 | Sequence 94, Appl | 529 | 67 | 6.0 | 387 | 4 | US-09-570-778A-7 | Sequence 7, Appli |
| 457 | 69 | 6.1 | 1650 | 4 | US-09-720-229-94 | Sequence 21798, A | 530 | 67 | 6.0 | 387 | 4 | US-09-570-778A-8 | Sequence 8, Appli |
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| 460 | 69 | 6.1 | 2035 | 5 | US-08-393-703-5 | Sequence 5, Appli | 533 | 67 | 6.0 | 387 | 4 | US-09-991-138-7 | Sequence 7, Appli |
| 461 | 69 | 6.1 | 2035 | 5 | US-08-393-703-5 | Sequence 5, Appli | 534 | 67 | 6.0 | 387 | 4 | US-09-991-138-8 | Sequence 8, Appli |
| 462 | 69 | 6.1 | 2035 | 5 | US-08-393-703-5 | Sequence 5, Appli | 535 | 67 | 6.0 | 387 | 4 | US-09-991-138-9 | Sequence 9, Appli |
| 463 | 69 | 6.1 | 2045 | 4 | US-09-949-016-10491 | Sequence 10491, A | 536 | 67 | 6.0 | 387 | 4 | US-10-037-677A-4 | Sequence 4, Appli |
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| 466 | 68.5 | 6.1 | 351 | 4 | US-09-248-796A-23675 | Sequence 23675, A | 539 | 67 | 6.0 | 387 | 4 | US-09-949-016-8822 | Sequence 2, Appli |
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| 469 | 68.5 | 6.1 | 498 | 4 | US-09-718-096-4 | Sequence 4, Appli | 542 | 67 | 6.0 | 416 | 4 | US-09-949-016-6158 | Sequence 6158, Ap |
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| 471 | 68.5 | 6.1 | 680 | 2 | US-08-674-351-2 | Sequence 2, Appli | 544 | 67 | 6.0 | 510 | 4 | US-09-949-016-10170 | Sequence 10170, A |
| 472 | 68.5 | 6.1 | 697 | 4 | US-09-270-767-41650 | Sequence 41650, A | 545 | 67 | 6.0 | 543 | 4 | US-08-480-917-2 | Sequence 2, Appli |
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| 474 | 68.5 | 6.1 | 827 | 4 | US-09-248-796A-17307 | Sequence 17307, A | 547 | 67 | 6.0 | 650 | 4 | US-08-781-891-206 | Sequence 206, App |
| 475 | 68 | 6.0 | 147 | 4 | US-09-252-991A-21137 | Sequence 21137, A | 548 | 67 | 6.0 | 699 | 4 | US-09-618-166-206 | Sequence 206, App |
| 476 | 68 | 6.0 | 155 | 4 | US-10-101-464A-573 | Sequence 573, App | 549 | 67 | 6.0 | 702 | 4 | US-09-538-092-564 | Sequence 564, App |
| 477 | 68 | 6.0 | 204 | 4 | US-09-252-991A-29026 | Sequence 29026, A | 550 | 67 | 6.0 | 702 | 4 | US-08-276-967-2 | Sequence 2, Appli |
| 478 | 68 | 6.0 | 270 | 4 | US-09-134-000C-3553 | Sequence 3553, Ap | 551 | 67 | 6.0 | 784 | 4 | US-09-949-016-11476 | Sequence 11476, A |
| 479 | 68 | 6.0 | 372 | 4 | US-09-489-039A-13193 | Sequence 13193, A | 552 | 67 | 6.0 | 786 | 4 | US-09-538-092-1254 | Sequence 1254, Ap |
| 480 | 68 | 6.0 | 387 | 4 | US-09-570-778A-11 | Sequence 11, Appl | 553 | 67 | 6.0 | 915 | 2 | US-09-949-016-10170 | Sequence 10170, A |
| 481 | 68 | 6.0 | 387 | 4 | US-09-991-138-11 | Sequence 11, Appl | 554 | 67 | 6.0 | 915 | 3 | US-08-917-2 | Sequence 2, Appli |
| 482 | 68 | 6.0 | 843 | 4 | US-09-252-991A-32668 | Sequence 32668, A | 555 | 67 | 6.0 | 915 | 3 | US-08-138-716-2 | Sequence 2, Appli |
| 483 | 68 | 6.0 | 873 | 1 | US-08-571-758-6 | Sequence 6, Appli | 556 | 67 | 6.0 | 1401 | 3 | US-08-988-242-2 | Sequence 2, Appli |
| 484 | 68 | 6.0 | 873 | 1 | US-08-909-984A-6 | Sequence 6, Appli | 557 | 67 | 6.0 | 1401 | 3 | US-08-781-891-206 | Sequence 206, App |
| 485 | 68 | 6.0 | 873 | 1 | US-08-909-983-6 | Sequence 6, Appli | 558 | 67 | 6.0 | 1900 | 4 | US-09-618-166-206 | Sequence 206, App |
| 486 | 68 | 6.0 | 1401 | 3 | US-09-127-670-6 | Sequence 6, Appli | 559 | 67 | 6.0 | 2476 | 2 | US-09-538-092-564 | Sequence 564, App |
| 487 | 68 | 6.0 | 1675 | 4 | US-09-540-236-1994 | Sequence 1994, Ap | 560 | 67 | 6.0 | 4377 | 4 | US-08-276-967-2 | Sequence 2, Appli |
| 488 | 68 | 6.0 | 2441 | 1 | US-08-194-468-2 | Sequence 2, Appli | 561 | 66.5 | 5.9 | 91 | 3 | US-09-949-016-6978 | Sequence 6978, Ap |
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| 493 | 68 | 6.0 | 2442 | 4 | US-09-538-092-1370 | Sequence 1370, Ap | 566 | 66.5 | 5.9 | 239 | 4 | US-08-745-404-4 | Sequence 4, Appli |
| | | | | | | | | | | | | US-09-248-796A-21096 | Sequence 21096, A |

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|-----|------|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|--------------------|
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| 570 | 66.5 | 5.9 | 374 | 4 | US-09-489-847-166 | Sequence 166, App | 661 | 65.5 | 5.8 | 145 | 4 | US-09-252-991A-31617 | Sequence 31617, A |
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| 585 | 66.5 | 5.9 | 516 | 3 | US-08-745-404-2 | Sequence 2, Appl | 666 | 65.5 | 5.8 | 202 | 4 | US-09-252-991A-32054 | Sequence 32054, A |
| 586 | 66.5 | 5.9 | 516 | 3 | US-09-320-774-8 | Sequence 8, Appl | 667 | 65.5 | 5.8 | 214 | 4 | US-08-722-570-2 | Sequence 2, Appl |
| 587 | 66.5 | 5.9 | 527 | 2 | US-08-762-106-9 | Sequence 9, Appl | 668 | 65.5 | 5.8 | 214 | 4 | US-08-932-411A-2 | Sequence 2, Appl |
| 588 | 66.5 | 5.9 | 527 | 3 | US-08-762-106-9 | Sequence 9, Appl | 669 | 65.5 | 5.8 | 280 | 4 | US-09-248-796A-18704 | Sequence 18704, A |
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| 596 | 66.5 | 5.9 | 815 | 4 | US-09-914-259-18 | Sequence 18, Appl | 677 | 65.5 | 5.8 | 448 | 4 | US-09-520-781-32 | Sequence 32, Appl |
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| 620 | 66 | 5.9 | 540 | 4 | US-09-468-041-3 | Sequence 3, Appl | 701 | 65.5 | 5.8 | 872 | 3 | US-09-196-466-3 | Sequence 3, Appl |
| 621 | 66 | 5.9 | 540 | 5 | PCT-US94-06362-3 | Sequence 3, Appl | 702 | 65.5 | 5.8 | 872 | 4 | US-09-669-459A-3 | Sequence 3, Appl |
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| 624 | 66 | 5.9 | 584 | 4 | US-09-693-746-22 | Sequence 22, Appl | 705 | 65.5 | 5.8 | 1442 | 2 | US-08-015-986A-3 | Sequence 3, Appl |
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| 651 | 66 | 5.9 | 1564 | 4 | US-10-144-198-4 | Sequence 4, Appl | 723 | 65 | 5.8 | 557 | 4 | US-09-773-877B-14 | Sequence 14, Appl |
| 652 | 66 | 5.9 | 1619 | 4 | US-09-328-352-7347 | Sequence 7347, App | 724 | 65 | 5.8 | 567 | 4 | US-09-773-877B-20 | Sequence 20, Appl |
| 653 | 66 | 5.9 | 2169 | 4 | US-09-949-016-6930 | Sequence 6930, App | 725 | 65 | 5.8 | 630 | 4 | US-09-485-529-8 | Sequence 8, Appl |
| 654 | 66 | 5.9 | 3123 | 4 | US-09-949-016-10933 | Sequence 10933, A | 726 | 65 | 5.8 | 692 | 3 | US-09-003-574-31 | Sequence 31, Appl |
| 655 | 65.5 | 5.8 | 101 | 4 | US-09-270-767-44082 | Sequence 44082, A | 727 | 65 | 5.8 | 692 | 3 | US-09-003-570-31 | Sequence 31, Appl |
| 656 | 65.5 | 5.8 | 103 | 4 | US-09-107-532A-4889 | Sequence 4889, App | 728 | 65 | 5.8 | 692 | 4 | US-09-864-541A-31 | Sequence 31, Appl |
| 657 | 65.5 | 5.8 | 128 | 4 | US-09-270-767-38128 | Sequence 38128, A | 729 | 65 | 5.8 | 724 | 4 | US-09-949-016-9953 | Sequence 9953, App |
| | | | | | | | 730 | 65 | 5.8 | 883 | 4 | US-09-489-039A-12755 | Sequence 12755, A |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|----------------------|-------------------|-----|------|-----|------|---|----------------------|-------------------|
| 731 | 65 | 5.8 | 921 | 1 | US-08-188-582-2 | Sequence 2, Appli | 804 | 64 | 5.7 | 547 | 4 | US-09-489-039A-13843 | Sequence 13843, A |
| 732 | 65 | 5.8 | 921 | 1 | US-08-646-715-2 | Sequence 2, Appli | 805 | 64 | 5.7 | 562 | 4 | US-09-538-092-779 | Sequence 779, App |
| 733 | 65 | 5.8 | 921 | 4 | US-09-430-723-2 | Sequence 2, Appli | 806 | 64 | 5.7 | 574 | 4 | US-09-248-786A-16162 | Sequence 16162, A |
| 734 | 65 | 5.8 | 999 | 4 | US-09-438-185A-455 | Sequence 455, App | 807 | 64 | 5.7 | 588 | 4 | US-09-248-796A-20295 | Sequence 20295, A |
| 735 | 65 | 5.8 | 1833 | 4 | US-08-621-944A-4 | Sequence 4, Appli | 808 | 64 | 5.7 | 614 | 1 | US-08-291-299-7 | Sequence 7, Appli |
| 736 | 65 | 5.8 | 1833 | 4 | US-08-945-567D-4 | Sequence 4, Appli | 809 | 64 | 5.7 | 614 | 5 | PCT-US95-10579-7 | Sequence 7, Appli |
| 737 | 65 | 5.8 | 1992 | 4 | US-08-621-944A-3 | Sequence 3, Appli | 810 | 64 | 5.7 | 636 | 4 | US-09-949-016-11656 | Sequence 11656, A |
| 738 | 65 | 5.8 | 1992 | 4 | US-08-945-567D-3 | Sequence 3, Appli | 811 | 64 | 5.7 | 638 | 3 | US-09-376-781-6 | Sequence 6, Appli |
| 739 | 64.5 | 5.7 | 94 | 4 | US-09-621-976-5361 | Sequence 5361, Ap | 812 | 64 | 5.7 | 639 | 4 | US-09-248-796A-20583 | Sequence 20583, A |
| 740 | 64.5 | 5.7 | 127 | 4 | US-09-252-991A-26303 | Sequence 26303, A | 813 | 64 | 5.7 | 687 | 4 | US-09-248-796A-23026 | Sequence 23026, A |
| 741 | 64.5 | 5.7 | 133 | 4 | US-09-252-991A-24089 | Sequence 24089, A | 814 | 64 | 5.7 | 693 | 4 | US-09-248-796A-26890 | Sequence 26890, A |
| 742 | 64.5 | 5.7 | 203 | 4 | US-09-059-625-85 | Sequence 85, Appl | 815 | 64 | 5.7 | 728 | 4 | US-09-949-016-8296 | Sequence 8296, Ap |
| 743 | 64.5 | 5.7 | 279 | 3 | US-08-397-411-13 | Sequence 13, Appl | 816 | 64 | 5.7 | 737 | 1 | US-08-188-582-16 | Sequence 16, Appl |
| 744 | 64.5 | 5.7 | 349 | 4 | US-09-270-767-44336 | Sequence 44336, A | 817 | 64 | 5.7 | 737 | 1 | US-08-646-715-16 | Sequence 16, Appl |
| 745 | 64.5 | 5.7 | 391 | 4 | US-09-200-090-4 | Sequence 4, Appli | 818 | 64 | 5.7 | 740 | 4 | US-09-949-016-10931 | Sequence 10931, A |
| 746 | 64.5 | 5.7 | 394 | 4 | US-09-252-991A-28045 | Sequence 28045, A | 819 | 64 | 5.7 | 750 | 3 | US-09-185-160-14 | Sequence 14, Appl |
| 747 | 64.5 | 5.7 | 407 | 4 | US-09-972-784-3 | Sequence 3, Appli | 820 | 64 | 5.7 | 750 | 4 | US-09-508-824-12 | Sequence 12, Appl |
| 748 | 64.5 | 5.7 | 420 | 4 | US-09-538-092-703 | Sequence 703, App | 821 | 64 | 5.7 | 854 | 4 | US-09-590-304-7 | Sequence 7, Appli |
| 749 | 64.5 | 5.7 | 425 | 4 | US-09-748-537-14 | Sequence 14, Appl | 822 | 64 | 5.7 | 897 | 4 | US-09-590-304-2 | Sequence 2, Appli |
| 750 | 64.5 | 5.7 | 491 | 4 | US-09-107-532A-6115 | Sequence 6115, Ap | 823 | 64 | 5.7 | 923 | 4 | US-09-825-147-2 | Sequence 2, Appli |
| 751 | 64.5 | 5.7 | 553 | 4 | US-09-949-016-10648 | Sequence 10648, A | 824 | 64 | 5.7 | 932 | 4 | US-09-813-148-2 | Sequence 2, Appli |
| 752 | 64.5 | 5.7 | 566 | 4 | US-09-513-783A-142 | Sequence 142, App | 825 | 64 | 5.7 | 999 | 4 | US-09-747-371-2 | Sequence 2, Appli |
| 753 | 64.5 | 5.7 | 566 | 4 | US-09-430-656-142 | Sequence 142, App | 826 | 64 | 5.7 | 1330 | 4 | US-09-543-681A-8057 | Sequence 8057, Ap |
| 754 | 64.5 | 5.7 | 571 | 4 | US-09-252-991A-30957 | Sequence 30957, A | 827 | 64 | 5.7 | 1380 | 4 | US-09-949-016-11688 | Sequence 11688, A |
| 755 | 64.5 | 5.7 | 630 | 4 | US-09-520-781-30 | Sequence 30, Appl | 828 | 64 | 5.7 | 1445 | 2 | US-08-015-986A-2 | Sequence 2, Appli |
| 756 | 64.5 | 5.7 | 638 | 1 | US-08-463-262A-11 | Sequence 11, Appl | 829 | 64 | 5.7 | 1574 | 4 | US-08-446-363-2 | Sequence 2, Appli |
| 757 | 64.5 | 5.7 | 638 | 1 | US-08-463-989-11 | Sequence 11, Appl | 830 | 64 | 5.7 | 1574 | 4 | US-09-302-626B-179 | Sequence 179, App |
| 758 | 64.5 | 5.7 | 638 | 3 | US-09-003-574-11 | Sequence 11, Appl | 831 | 64 | 5.7 | 1978 | 4 | US-09-302-626B-60 | Sequence 60, Appl |
| 759 | 64.5 | 5.7 | 638 | 3 | US-09-003-570-11 | Sequence 11, Appl | 832 | 64 | 5.7 | 2781 | 4 | US-09-698-295-10 | Sequence 10, Appl |
| 760 | 64.5 | 5.7 | 638 | 4 | US-09-864-541A-11 | Sequence 11, Appl | 833 | 64 | 5.7 | 2907 | 4 | US-09-698-295-1 | Sequence 1, Appli |
| 761 | 64.5 | 5.7 | 648 | 4 | US-09-715-858-4 | Sequence 4, Appli | 834 | 63.5 | 5.6 | 83 | 4 | US-09-252-991A-21499 | Sequence 21499, A |
| 762 | 64.5 | 5.7 | 659 | 4 | US-09-562-737-14 | Sequence 14, Appl | 835 | 63.5 | 5.6 | 179 | 4 | US-09-252-991A-26797 | Sequence 26797, A |
| 763 | 64.5 | 5.7 | 669 | 4 | US-09-107-532A-5532 | Sequence 5532, Ap | 836 | 63.5 | 5.6 | 210 | 4 | US-09-270-767-33951 | Sequence 33951, A |
| 764 | 64.5 | 5.7 | 712 | 4 | US-09-949-016-10600 | Sequence 10600, A | 837 | 63.5 | 5.6 | 210 | 4 | US-09-270-767-48168 | Sequence 48168, A |
| 765 | 64.5 | 5.7 | 763 | 4 | US-09-949-016-10382 | Sequence 10382, A | 838 | 63.5 | 5.6 | 216 | 4 | US-09-107-532A-4916 | Sequence 4916, Ap |
| 766 | 64.5 | 5.7 | 793 | 4 | US-09-270-767-42801 | Sequence 42801, A | 839 | 63.5 | 5.6 | 264 | 1 | US-08-463-115-93 | Sequence 93, Appl |
| 767 | 64.5 | 5.7 | 812 | 4 | US-09-513-783A-6 | Sequence 6, Appli | 840 | 63.5 | 5.6 | 264 | 1 | US-08-465-388-93 | Sequence 93, Appl |
| 768 | 64.5 | 5.7 | 812 | 4 | US-09-513-783A-6 | Sequence 6, Appli | 841 | 63.5 | 5.6 | 319 | 3 | US-08-832-399-2 | Sequence 2, Appli |
| 769 | 64.5 | 5.7 | 812 | 4 | US-09-430-656-4 | Sequence 4, Appli | 842 | 63.5 | 5.6 | 319 | 3 | US-09-372-498-2 | Sequence 2, Appli |
| 770 | 64.5 | 5.7 | 812 | 4 | US-09-430-656-6 | Sequence 6, Appli | 843 | 63.5 | 5.6 | 347 | 4 | US-09-252-991A-19498 | Sequence 19498, A |
| 771 | 64.5 | 5.7 | 919 | 4 | US-09-949-016-6954 | Sequence 6954, Ap | 844 | 63.5 | 5.6 | 384 | 4 | US-09-248-786A-15499 | Sequence 15499, A |
| 772 | 64.5 | 5.7 | 939 | 4 | US-09-520-781-4 | Sequence 4, Appli | 845 | 63.5 | 5.6 | 384 | 4 | US-10-029-180-50 | Sequence 50, Appl |
| 773 | 64.5 | 5.7 | 994 | 4 | US-09-248-796A-15273 | Sequence 15273, A | 846 | 63.5 | 5.6 | 399 | 1 | US-08-414-926A-5 | Sequence 5, Appli |
| 774 | 64.5 | 5.7 | 1039 | 4 | US-09-902-540-13739 | Sequence 13739, A | 847 | 63.5 | 5.6 | 399 | 3 | US-08-926-922-5 | Sequence 5, Appli |
| 775 | 64.5 | 5.7 | 1056 | 4 | US-09-513-783A-32 | Sequence 32, Appl | 848 | 63.5 | 5.6 | 399 | 3 | US-09-253-682-5 | Sequence 5, Appli |
| 776 | 64.5 | 5.7 | 1056 | 4 | US-09-430-656-32 | Sequence 32, Appl | 849 | 63.5 | 5.6 | 399 | 3 | US-09-527-687-5 | Sequence 5, Appli |
| 777 | 64.5 | 5.7 | 1125 | 4 | US-09-513-783A-152 | Sequence 152, App | 850 | 63.5 | 5.6 | 410 | 3 | US-09-892-100-5 | Sequence 2, Appli |
| 778 | 64.5 | 5.7 | 1125 | 4 | US-09-430-656-152 | Sequence 152, App | 851 | 63.5 | 5.6 | 410 | 3 | US-08-858-876A-2 | Sequence 2, Appli |
| 779 | 64.5 | 5.7 | 1140 | 4 | US-09-538-092-647 | Sequence 647, App | 852 | 63.5 | 5.6 | 410 | 3 | US-09-472-880-2 | Sequence 2, Appli |
| 780 | 64.5 | 5.7 | 1310 | 4 | US-09-170-496D-290 | Sequence 290, App | 853 | 63.5 | 5.6 | 428 | 4 | US-09-826-509-537 | Sequence 537, App |
| 781 | 64.5 | 5.7 | 1310 | 4 | US-09-364-425B-55 | Sequence 55, Appl | 854 | 63.5 | 5.6 | 428 | 4 | US-09-134-000C-6457 | Sequence 6457, Ap |
| 782 | 64.5 | 5.7 | 1481 | 4 | US-09-231-899-70 | Sequence 70, Appl | 855 | 63.5 | 5.6 | 447 | 1 | US-08-450-360-4 | Sequence 4, Appli |
| 783 | 64.5 | 5.7 | 1610 | 4 | US-09-513-783A-22 | Sequence 22, Appl | 856 | 63.5 | 5.6 | 459 | 4 | US-09-691-220-4 | Sequence 4, Appli |
| 784 | 64.5 | 5.7 | 1610 | 4 | US-09-430-656-22 | Sequence 22, Appl | 857 | 63.5 | 5.6 | 465 | 3 | US-08-845-258-30 | Sequence 30, Appl |
| 785 | 64 | 5.7 | 134 | 4 | US-09-270-767-40850 | Sequence 40850, A | 858 | 63.5 | 5.6 | 465 | 3 | US-08-990-571-30 | Sequence 30, Appl |
| 786 | 64 | 5.7 | 134 | 4 | US-09-270-767-56066 | Sequence 56066, A | 859 | 63.5 | 5.6 | 465 | 3 | US-08-723-142A-30 | Sequence 30, Appl |
| 787 | 64 | 5.7 | 152 | 4 | US-09-252-991A-19284 | Sequence 19284, A | 860 | 63.5 | 5.6 | 465 | 4 | US-09-528-784A-30 | Sequence 30, Appl |
| 788 | 64 | 5.7 | 176 | 4 | US-09-252-991A-21933 | Sequence 21933, A | 861 | 63.5 | 5.6 | 465 | 4 | US-09-569-098A-30 | Sequence 30, Appl |
| 789 | 64 | 5.7 | 198 | 4 | US-09-252-991A-18773 | Sequence 18773, A | 862 | 63.5 | 5.6 | 468 | 3 | US-08-802-805D-21 | Sequence 21, Appl |
| 790 | 64 | 5.7 | 198 | 4 | US-09-248-796A-19318 | Sequence 19318, A | 863 | 63.5 | 5.6 | 468 | 4 | US-08-837-199A-4 | Sequence 4, Appli |
| 791 | 64 | 5.7 | 219 | 1 | US-08-463-115-91 | Sequence 91, Appl | 864 | 63.5 | 5.6 | 468 | 4 | US-08-860-370-2 | Sequence 2, Appli |
| 792 | 64 | 5.7 | 219 | 1 | US-08-465-388-91 | Sequence 91, Appl | 865 | 63.5 | 5.6 | 468 | 4 | US-09-187-906-2 | Sequence 2, Appli |
| 793 | 64 | 5.7 | 206 | 4 | US-09-302-540-9859 | Sequence 9859, Ap | 866 | 63.5 | 5.6 | 468 | 4 | US-08-861-990-1 | Sequence 1, Appli |
| 794 | 64 | 5.7 | 341 | 4 | US-09-252-991A-26208 | Sequence 26208, A | 867 | 63.5 | 5.6 | 468 | 4 | US-09-388-316C-21 | Sequence 21, Appl |
| 795 | 64 | 5.7 | 354 | 4 | US-09-949-016-10392 | Sequence 10392, A | 868 | 63.5 | 5.6 | 486 | 1 | US-08-450-360-2 | Sequence 2, Appli |
| 796 | 64 | 5.7 | 380 | 4 | US-09-248-796A-19662 | Sequence 19662, A | 869 | 63.5 | 5.6 | 486 | 4 | US-09-134-000C-4392 | Sequence 4392, Ap |
| 797 | 64 | 5.7 | 415 | 4 | US-09-743-742B-6 | Sequence 6, Appli | 870 | 63.5 | 5.6 | 545 | 4 | US-09-134-000C-4559 | Sequence 4559, Ap |
| 798 | 64 | 5.7 | 416 | 3 | US-08-858-876A-4 | Sequence 4, Appli | 871 | 63.5 | 5.6 | 613 | 4 | US-09-248-796A-17277 | Sequence 17277, A |
| 799 | 64 | 5.7 | 416 | 3 | US-09-472-880-4 | Sequence 4, Appli | 872 | 63.5 | 5.6 | 623 | 4 | US-09-485-529-7 | Sequence 7, Appli |
| 800 | 64 | 5.7 | 501 | 4 | US-09-248-796A-14118 | Sequence 14118, A | 873 | 63.5 | 5.6 | 658 | 4 | US-09-248-796A-17674 | Sequence 17674, A |
| 801 | 64 | 5.7 | 511 | 4 | US-09-248-796A-14125 | Sequence 14125, A | 874 | 63.5 | 5.6 | 689 | 4 | US-09-248-796A-15264 | Sequence 15264, A |
| 802 | 64 | 5.7 | 525 | 4 | US-09-107-532A-5095 | Sequence 5095, Ap | 875 | 63.5 | 5.6 | 691 | 4 | US-09-949-016-10422 | Sequence 10422, A |
| 803 | 64 | 5.7 | 529 | 4 | US-09-248-796A-16703 | Sequence 16703, A | 876 | 63.5 | 5.6 | 694 | 2 | US-08-701-240-2 | Sequence 2, Appli |

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|-----|------|-----|------|---|----------------------|--------------------|------|------|-----|------|---|----------------------|-------------------|
| 877 | 63.5 | 5.6 | 694 | 3 | US-09-138-236-2 | Sequence 2, Appli | 950 | 63 | 5.6 | 977 | 4 | US-09-248-796A-15579 | Sequence 15579, A |
| 878 | 63.5 | 5.6 | 699 | 4 | US-10-237-551-143 | Sequence 143, App | 951 | 63 | 5.6 | 1065 | 4 | US-09-538-092-84 | Sequence 84, Appl |
| 879 | 63.5 | 5.6 | 700 | 4 | US-10-237-551-254 | Sequence 254, App | 952 | 63 | 5.6 | 1557 | 4 | US-09-410-551B-27 | Sequence 27, Appl |
| 880 | 63.5 | 5.6 | 708 | 4 | US-09-336-115C-2 | Sequence 2, Appli | 953 | 63 | 5.6 | 1574 | 4 | US-09-940-316B-27 | Sequence 27, Appl |
| 881 | 63.5 | 5.6 | 918 | 4 | US-09-200-650B-1 | Sequence 1, Appli | 954 | 63 | 5.6 | 1574 | 4 | US-09-410-551B-25 | Sequence 25, Appl |
| 882 | 63.5 | 5.6 | 973 | 1 | US-08-162-809-10 | Sequence 10, Appl | 955 | 63 | 5.6 | 1574 | 4 | US-09-940-316B-25 | Sequence 25, Appl |
| 883 | 63.5 | 5.6 | 978 | 1 | US-08-162-809-14 | Sequence 14, Appl | 956 | 63 | 5.6 | 1578 | 4 | US-09-410-551B-31 | Sequence 31, Appl |
| 884 | 63.5 | 5.6 | 1009 | 2 | US-08-357-642A-1 | Sequence 1, Appli | 957 | 63 | 5.6 | 1578 | 4 | US-09-940-316B-31 | Sequence 31, Appl |
| 885 | 63.5 | 5.6 | 1009 | 2 | US-08-357-642A-1 | Sequence 1, Appli | 957 | 63 | 5.6 | 1578 | 4 | US-09-940-316B-31 | Sequence 31, Appl |
| 886 | 63.5 | 5.6 | 1014 | 4 | US-09-949-016-11533 | Sequence 11533, A | 958 | 63 | 5.6 | 1588 | 4 | US-09-410-551B-29 | Sequence 29, Appl |
| 887 | 63.5 | 5.6 | 1036 | 4 | US-09-902-540-14218 | Sequence 14218, A | 959 | 63 | 5.6 | 1588 | 4 | US-09-410-551B-29 | Sequence 29, Appl |
| 888 | 63.5 | 5.6 | 1132 | 4 | US-09-528-784A-87 | Sequence 87, Appl | 960 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 889 | 63.5 | 5.6 | 1132 | 4 | US-09-528-784A-87 | Sequence 87, Appl | 961 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 890 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 891 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 892 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 893 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 894 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 895 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 896 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 897 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 898 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 899 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 900 | 63.5 | 5.6 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl | 962 | 63 | 5.6 | 1605 | 4 | US-09-410-551B-33 | Sequence 33, Appl |
| 901 | 63 | 5.6 | 126 | 1 | US-08-450-360-12 | Sequence 12, Appl | 974 | 62.5 | 5.6 | 3392 | 4 | US-09-328-991A-21266 | Sequence 21266, A |
| 902 | 63 | 5.6 | 128 | 3 | US-08-845-258-41 | Sequence 41, Appl | 975 | 62.5 | 5.6 | 98 | 4 | US-09-252-991A-21266 | Sequence 21266, A |
| 903 | 63 | 5.6 | 128 | 3 | US-08-990-571-41 | Sequence 41, Appl | 976 | 62.5 | 5.6 | 99 | 4 | US-09-270-767-59460 | Sequence 59460, A |
| 904 | 63 | 5.6 | 128 | 3 | US-08-723-142A-41 | Sequence 41, Appl | 977 | 62.5 | 5.6 | 159 | 4 | US-09-248-796A-12631 | Sequence 12631, A |
| 905 | 63 | 5.6 | 128 | 3 | US-09-528-784A-41 | Sequence 41, Appl | 978 | 62.5 | 5.6 | 170 | 4 | US-09-252-991A-28860 | Sequence 28860, A |
| 906 | 63 | 5.6 | 128 | 3 | US-09-528-784A-41 | Sequence 41, Appl | 978 | 62.5 | 5.6 | 170 | 4 | US-09-252-991A-28860 | Sequence 28860, A |
| 907 | 63 | 5.6 | 128 | 3 | US-09-528-784A-41 | Sequence 41, Appl | 978 | 62.5 | 5.6 | 170 | 4 | US-09-252-991A-28860 | Sequence 28860, A |
| 908 | 63 | 5.6 | 131 | 4 | US-09-252-991A-23872 | Sequence 23872, A | 980 | 62.5 | 5.6 | 171 | 4 | US-09-248-796A-19229 | Sequence 19229, A |
| 909 | 63 | 5.6 | 143 | 4 | US-09-252-991A-25829 | Sequence 25829, A | 981 | 62.5 | 5.6 | 171 | 4 | US-09-248-796A-19229 | Sequence 19229, A |
| 910 | 63 | 5.6 | 157 | 4 | US-09-270-767-59757 | Sequence 59757, A | 982 | 62.5 | 5.6 | 204 | 4 | US-09-252-991A-24939 | Sequence 24939, A |
| 911 | 63 | 5.6 | 161 | 4 | US-09-252-991A-27097 | Sequence 27097, A | 983 | 62.5 | 5.6 | 252 | 4 | US-09-270-767-43125 | Sequence 43125, A |
| 912 | 63 | 5.6 | 178 | 4 | US-09-252-991A-20280 | Sequence 20280, A | 984 | 62.5 | 5.6 | 252 | 4 | US-09-270-767-43125 | Sequence 43125, A |
| 913 | 63 | 5.6 | 182 | 4 | US-09-489-035A-3823 | Sequence 3823, Ap | 985 | 62.5 | 5.6 | 325 | 1 | US-08-233-788A-55 | Sequence 15102, A |
| 914 | 63 | 5.6 | 191 | 1 | US-08-253-155A-39 | Sequence 39, Appl | 986 | 62.5 | 5.6 | 331 | 3 | US-08-808-720-5 | Sequence 55, Appl |
| 915 | 63 | 5.6 | 204 | 4 | US-09-252-991A-20995 | Sequence 20995, A | 987 | 62.5 | 5.6 | 331 | 3 | US-08-808-720-5 | Sequence 55, Appl |
| 916 | 63 | 5.6 | 204 | 4 | US-09-248-796A-16962 | Sequence 16962, A | 988 | 62.5 | 5.6 | 336 | 4 | US-09-467-638-5 | Sequence 18342, A |
| 917 | 63 | 5.6 | 213 | 4 | US-09-949-016-6681 | Sequence 6681, Ap | 989 | 62.5 | 5.6 | 342 | 4 | US-09-543-681A-5179 | Sequence 5179, Ap |
| 918 | 63 | 5.6 | 221 | 4 | US-09-489-035A-7778 | Sequence 7778, Ap | 990 | 62.5 | 5.6 | 362 | 1 | US-08-415-751-5 | Sequence 5, Appli |
| 919 | 63 | 5.6 | 248 | 4 | US-09-533-023-22 | Sequence 22, Appl | 991 | 62.5 | 5.6 | 362 | 1 | US-08-415-751-5 | Sequence 5, Appli |
| 920 | 63 | 5.6 | 291 | 6 | 5194600-2 | Patent No. 5194600 | 992 | 62.5 | 5.6 | 366 | 4 | US-09-248-796A-21767 | Sequence 21767, A |
| 921 | 63 | 5.6 | 302 | 4 | US-09-252-991A-21231 | Sequence 21231, A | 993 | 62.5 | 5.6 | 367 | 3 | US-09-378-088A-54 | Sequence 54, Appl |
| 922 | 63 | 5.6 | 306 | 3 | US-09-189-060B-68 | Sequence 68, Appl | 994 | 62.5 | 5.6 | 367 | 3 | US-09-378-088A-54 | Sequence 54, Appl |
| 923 | 63 | 5.6 | 309 | 4 | US-09-248-796A-25339 | Sequence 25339, A | 995 | 62.5 | 5.6 | 371 | 3 | US-09-643-596B-64 | Sequence 64, Appl |
| 924 | 63 | 5.6 | 316 | 4 | US-09-248-796A-25802 | Sequence 25802, A | 996 | 62.5 | 5.6 | 371 | 3 | US-09-643-596B-64 | Sequence 64, Appl |
| 925 | 63 | 5.6 | 318 | 4 | US-09-902-540-10266 | Sequence 10266, A | 997 | 62.5 | 5.6 | 373 | 4 | US-09-643-596B-64 | Sequence 64, Appl |
| 926 | 63 | 5.6 | 320 | 4 | US-09-248-796A-21508 | Sequence 21508, A | 998 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 927 | 63 | 5.6 | 347 | 4 | US-09-248-796A-16323 | Sequence 16323, A | 999 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 928 | 63 | 5.6 | 382 | 4 | US-09-248-796A-17276 | Sequence 17276, A | 1000 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 929 | 63 | 5.6 | 422 | 4 | US-09-949-016-8251 | Sequence 8251, Ap | 1001 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 930 | 63 | 5.6 | 424 | 1 | US-08-419-414-2 | Sequence 2, Appli | 1002 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 931 | 63 | 5.6 | 436 | 4 | US-09-252-991A-17926 | Sequence 2, Appli | 1003 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 932 | 63 | 5.6 | 442 | 4 | US-09-248-796A-26457 | Sequence 17926, A | 1004 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 933 | 63 | 5.6 | 450 | 2 | US-09-248-796A-20538 | Sequence 20538, A | 1005 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 934 | 63 | 5.6 | 456 | 2 | US-08-643-034A-4 | Sequence 4, Appli | 1006 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 935 | 63 | 5.6 | 456 | 2 | US-08-643-034A-4 | Sequence 4, Appli | 1007 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 936 | 63 | 5.6 | 456 | 2 | US-08-643-034A-4 | Sequence 4, Appli | 1008 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 937 | 63 | 5.6 | 456 | 2 | US-08-643-034A-4 | Sequence 4, Appli | 1009 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 938 | 63 | 5.6 | 462 | 2 | US-08-865-597A-2 | Sequence 2, Appli | 1010 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 939 | 63 | 5.6 | 463 | 4 | US-09-248-796A-14184 | Sequence 14184, A | 1011 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 940 | 63 | 5.6 | 519 | 4 | US-09-538-092-1292 | Sequence 1292, Ap | 1012 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 941 | 63 | 5.6 | 581 | 4 | US-09-499-522-18 | Sequence 18, Appl | 1013 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 942 | 63 | 5.6 | 581 | 4 | US-09-269-939A-12 | Sequence 12, Appl | 1014 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 943 | 63 | 5.6 | 666 | 4 | US-09-270-767-62249 | Sequence 62249, A | 1015 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 944 | 63 | 5.6 | 721 | 4 | US-09-270-767-46645 | Sequence 46645, A | 1016 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 945 | 63 | 5.6 | 756 | 1 | US-08-434-730-16 | Sequence 16, Appl | 1017 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
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| 947 | 63 | 5.6 | 817 | 4 | US-09-248-796A-20276 | Sequence 20276, A | 1019 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 948 | 63 | 5.6 | 881 | 4 | US-09-248-796A-18627 | Sequence 18627, A | 1020 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| 949 | 63 | 5.6 | 888 | 4 | US-09-134-000C-5886 | Sequence 5886, Ap | 1021 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |
| | | | | | | | 1022 | 62.5 | 5.6 | 385 | 3 | US-09-378-088A-11 | Sequence 11, Appl |

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|------|------|-----|------|---|----------------------|-------------------|------|------|-----|------|---|----------------------|-------------------|
| 1023 | 62.5 | 5.6 | 491 | 4 | US-09-270-767-44430 | Sequence 44430, A | 1096 | 62.5 | 5.6 | 2475 | 3 | US-09-413-814-48 | Sequence 48, Appl |
| 1024 | 62.5 | 5.6 | 513 | 2 | US-08-676-166A-5 | Sequence 5, Appli | 1097 | 62.5 | 5.6 | 2871 | 4 | US-09-538-082-1076 | Sequence 1076, Ap |
| 1025 | 62.5 | 5.6 | 514 | 3 | US-09-254-733-2 | Sequence 2, Appli | 1098 | 62.5 | 5.6 | 3033 | 1 | US-07-925-695-5 | Sequence 5, Appl |
| 1026 | 62.5 | 5.6 | 540 | 4 | US-09-134-000C-3745 | Sequence 3745, Ap | 1099 | 62 | 5.5 | 125 | 4 | US-09-252-991A-24005 | Sequence 24005, A |
| 1027 | 62.5 | 5.6 | 601 | 2 | US-08-606-288-7 | Sequence 7, Appli | 1100 | 62 | 5.5 | 142 | 2 | US-08-476-1761A-12 | Sequence 12, Appl |
| 1028 | 62.5 | 5.6 | 601 | 2 | US-08-606-288-10 | Sequence 10, Appl | 1101 | 62 | 5.5 | 142 | 3 | US-08-127-721A-12 | Sequence 12, Appl |
| 1029 | 62.5 | 5.6 | 601 | 3 | US-09-347-483-7 | Sequence 7, Appli | 1102 | 62 | 5.5 | 142 | 3 | US-08-485-246A-12 | Sequence 12, Appl |
| 1030 | 62.5 | 5.6 | 601 | 3 | US-09-347-483-10 | Sequence 10, Appl | 1103 | 62 | 5.5 | 154 | 1 | US-08-463-262A-9 | Sequence 9, Appli |
| 1031 | 62.5 | 5.6 | 613 | 4 | US-09-540-236-2474 | Sequence 2474, Ap | 1104 | 62 | 5.5 | 154 | 1 | US-08-463-989-9 | Sequence 9, Appli |
| 1032 | 62.5 | 5.6 | 635 | 1 | US-08-571-758-10 | Sequence 10, Appl | 1105 | 62 | 5.5 | 154 | 3 | US-09-003-570-9 | Sequence 9, Appli |
| 1033 | 62.5 | 5.6 | 635 | 1 | US-08-909-984A-10 | Sequence 10, Appl | 1106 | 62 | 5.5 | 154 | 3 | US-09-003-570-9 | Sequence 9, Appli |
| 1034 | 62.5 | 5.6 | 635 | 1 | US-08-909-983-10 | Sequence 10, Appl | 1107 | 62 | 5.5 | 154 | 4 | US-09-864-415A-9 | Sequence 9, Appli |
| 1035 | 62.5 | 5.6 | 797 | 2 | US-08-095-7288-2 | Sequence 2, Appli | 1108 | 62 | 5.5 | 165 | 4 | US-09-220-415-2 | Sequence 2, Appli |
| 1036 | 62.5 | 5.6 | 797 | 5 | PCN-US92-02320A-2 | Sequence 2, Appli | 1109 | 62 | 5.5 | 165 | 4 | US-09-675-776-2 | Sequence 2, Appli |
| 1037 | 62.5 | 5.6 | 857 | 4 | US-09-902-540-12028 | Sequence 12028, A | 1110 | 62 | 5.5 | 165 | 4 | US-09-676-739-2 | Sequence 2, Appli |
| 1038 | 62.5 | 5.6 | 875 | 1 | US-08-571-758-8 | Sequence 8, Appli | 1111 | 62 | 5.5 | 165 | 4 | US-09-675-739-2 | Sequence 2, Appli |
| 1039 | 62.5 | 5.6 | 875 | 1 | US-08-909-984A-8 | Sequence 8, Appli | 1112 | 62 | 5.5 | 165 | 4 | US-09-915-676-1 | Sequence 1, Appli |
| 1040 | 62.5 | 5.6 | 875 | 1 | US-08-909-983-8 | Sequence 8, Appli | 1113 | 62 | 5.5 | 165 | 4 | US-09-677-152-2 | Sequence 2, Appli |
| 1041 | 62.5 | 5.6 | 877 | 2 | US-08-916-917-2 | Sequence 2, Appli | 1114 | 62 | 5.5 | 166 | 4 | US-09-252-991A-17450 | Sequence 17450, A |
| 1042 | 62.5 | 5.6 | 877 | 2 | US-08-972-631-2 | Sequence 2, Appli | 1115 | 62 | 5.5 | 167 | 2 | US-08-997-080-112 | Sequence 112, App |
| 1043 | 62.5 | 5.6 | 877 | 2 | US-08-972-623-2 | Sequence 2, Appli | 1116 | 62 | 5.5 | 167 | 2 | US-08-997-362-112 | Sequence 112, App |
| 1044 | 62.5 | 5.6 | 877 | 2 | US-08-972-630-2 | Sequence 2, Appli | 1117 | 62 | 5.5 | 167 | 3 | US-09-095-855-112 | Sequence 112, App |
| 1045 | 62.5 | 5.6 | 877 | 2 | US-08-672-211-2 | Sequence 2, Appli | 1118 | 62 | 5.5 | 167 | 3 | US-09-324-542-112 | Sequence 112, App |
| 1046 | 62.5 | 5.6 | 877 | 3 | US-09-225-170-2 | Sequence 2, Appli | 1119 | 62 | 5.5 | 167 | 4 | US-09-205-426-112 | Sequence 112, App |
| 1047 | 62.5 | 5.6 | 1232 | 4 | US-09-248-796A-14563 | Sequence 14563, A | 1120 | 62 | 5.5 | 180 | 3 | US-09-133-341-12 | Sequence 12, Appl |
| 1048 | 62.5 | 5.6 | 1233 | 4 | US-09-134-000C-4971 | Sequence 4971, Ap | 1121 | 62 | 5.5 | 180 | 4 | US-09-739-852-12 | Sequence 12, Appl |
| 1049 | 62.5 | 5.6 | 1416 | 4 | US-09-071-035-404 | Sequence 404, App | 1122 | 62 | 5.5 | 192 | 4 | US-09-543-681A-8139 | Sequence 8139, Ap |
| 1050 | 62.5 | 5.6 | 1448 | 4 | US-09-071-035-402 | Sequence 402, App | 1123 | 62 | 5.5 | 194 | 4 | US-09-270-767-42380 | Sequence 42380, A |
| 1051 | 62.5 | 5.6 | 1577 | 2 | US-08-793-824-2 | Sequence 2, Appli | 1124 | 62 | 5.5 | 206 | 4 | US-09-059-625-90 | Sequence 90, Appl |
| 1052 | 62.5 | 5.6 | 1769 | 4 | US-09-949-016-8280 | Sequence 8280, Ap | 1125 | 62 | 5.5 | 209 | 4 | US-09-059-625-86 | Sequence 86, Appl |
| 1053 | 62.5 | 5.6 | 1769 | 4 | US-09-949-016-8281 | Sequence 8281, Ap | 1126 | 62 | 5.5 | 211 | 4 | US-09-252-991A-26873 | Sequence 26873, A |
| 1054 | 62.5 | 5.6 | 1769 | 4 | US-09-949-016-8282 | Sequence 8282, Ap | 1127 | 62 | 5.5 | 212 | 4 | US-09-053-625-58 | Sequence 58, Appl |
| 1055 | 62.5 | 5.6 | 1784 | 3 | US-09-040-738-2 | Sequence 2, Appli | 1128 | 62 | 5.5 | 215 | 4 | US-09-248-796A-26395 | Sequence 26395, A |
| 1056 | 62.5 | 5.6 | 1784 | 3 | US-08-652-426A-2 | Sequence 2, Appli | 1129 | 62 | 5.5 | 235 | 4 | US-09-580-235-2 | Sequence 2, Appli |
| 1057 | 62.5 | 5.6 | 1813 | 4 | US-09-949-016-8283 | Sequence 8283, Ap | 1130 | 62 | 5.5 | 235 | 4 | US-09-580-181-2 | Sequence 2, Appli |
| 1058 | 62.5 | 5.6 | 1813 | 4 | US-09-949-016-8284 | Sequence 8284, Ap | 1131 | 62 | 5.5 | 235 | 4 | US-09-102-530-2 | Sequence 2, Appli |
| 1059 | 62.5 | 5.6 | 1813 | 4 | US-09-949-016-8285 | Sequence 8285, Ap | 1132 | 62 | 5.5 | 235 | 4 | US-09-949-016-6661 | Sequence 6661, Ap |
| 1060 | 62.5 | 5.6 | 1911 | 4 | US-09-854-856-64 | Sequence 64, Appl | 1133 | 62 | 5.5 | 244 | 4 | US-09-107-532A-4536 | Sequence 4536, Ap |
| 1061 | 62.5 | 5.6 | 1935 | 4 | US-09-949-016-10403 | Sequence 10403, A | 1134 | 62 | 5.5 | 249 | 4 | US-09-252-991A-18733 | Sequence 18733, A |
| 1062 | 62.5 | 5.6 | 1939 | 4 | US-09-854-856-32 | Sequence 32, Appl | 1135 | 62 | 5.5 | 251 | 4 | US-09-252-991A-20606 | Sequence 20606, A |
| 1063 | 62.5 | 5.6 | 1971 | 4 | US-09-854-856-32 | Sequence 32, Appl | 1136 | 62 | 5.5 | 265 | 3 | US-08-918-288-3 | Sequence 3, Appli |
| 1064 | 62.5 | 5.6 | 1980 | 4 | US-09-914-272A-3 | Sequence 3, Appli | 1137 | 62 | 5.5 | 265 | 3 | US-08-918-288-39 | Sequence 39, Appl |
| 1065 | 62.5 | 5.6 | 1980 | 4 | US-10-638-333-3 | Sequence 3, Appli | 1138 | 62 | 5.5 | 265 | 3 | US-09-282-357-39 | Sequence 3, Appli |
| 1066 | 62.5 | 5.6 | 1989 | 4 | US-09-854-856-16 | Sequence 16, Appl | 1139 | 62 | 5.5 | 265 | 3 | US-09-282-357-39 | Sequence 39, Appl |
| 1067 | 62.5 | 5.6 | 2004 | 4 | US-09-854-856-58 | Sequence 58, Appl | 1140 | 62 | 5.5 | 279 | 4 | US-09-248-796A-25140 | Sequence 25140, A |
| 1068 | 62.5 | 5.6 | 2032 | 4 | US-09-854-856-42 | Sequence 42, Appl | 1141 | 62 | 5.5 | 283 | 4 | US-09-248-796A-19610 | Sequence 19610, A |
| 1069 | 62.5 | 5.6 | 2048 | 4 | US-09-854-856-62 | Sequence 62, Appl | 1142 | 62 | 5.5 | 285 | 3 | US-09-095-855-197 | Sequence 197, App |
| 1070 | 62.5 | 5.6 | 2064 | 4 | US-09-854-856-26 | Sequence 26, Appl | 1143 | 62 | 5.5 | 285 | 4 | US-09-205-426-197 | Sequence 197, App |
| 1071 | 62.5 | 5.6 | 2076 | 4 | US-09-854-856-46 | Sequence 46, Appl | 1144 | 62 | 5.5 | 321 | 4 | US-09-248-796A-16248 | Sequence 16248, A |
| 1072 | 62.5 | 5.6 | 2090 | 4 | US-09-538-092-1081 | Sequence 1081, Ap | 1145 | 62 | 5.5 | 323 | 4 | US-09-248-796A-27766 | Sequence 27766, A |
| 1073 | 62.5 | 5.6 | 2092 | 4 | US-09-854-856-10 | Sequence 10, Appl | 1146 | 62 | 5.5 | 327 | 4 | US-09-248-796A-27766 | Sequence 27766, A |
| 1074 | 62.5 | 5.6 | 2108 | 4 | US-09-854-856-30 | Sequence 30, Appl | 1147 | 62 | 5.5 | 349 | 3 | US-08-630-172-6 | Sequence 6, Appli |
| 1075 | 62.5 | 5.6 | 2120 | 4 | US-09-854-856-16 | Sequence 16, Appl | 1148 | 62 | 5.5 | 357 | 4 | US-09-375-419-6 | Sequence 6, Appli |
| 1076 | 62.5 | 5.6 | 2136 | 4 | US-09-854-856-17 | Sequence 17, Appl | 1149 | 62 | 5.5 | 357 | 4 | US-09-248-796A-15519 | Sequence 15519, A |
| 1077 | 62.5 | 5.6 | 2141 | 4 | US-09-854-856-56 | Sequence 56, Appl | 1150 | 62 | 5.5 | 380 | 4 | US-09-270-767-43987 | Sequence 43987, A |
| 1078 | 62.5 | 5.6 | 2157 | 4 | US-09-854-856-52 | Sequence 52, Appl | 1151 | 62 | 5.5 | 387 | 4 | US-09-570-778A-10 | Sequence 10, Appl |
| 1079 | 62.5 | 5.6 | 2169 | 4 | US-09-854-856-40 | Sequence 40, Appl | 1152 | 62 | 5.5 | 387 | 4 | US-09-591-138-10 | Sequence 10, Appl |
| 1080 | 62.5 | 5.6 | 2179 | 4 | US-09-949-016-8129 | Sequence 8129, Ap | 1153 | 62 | 5.5 | 388 | 4 | US-09-489-039A-13067 | Sequence 13067, A |
| 1081 | 62.5 | 5.6 | 2185 | 4 | US-09-854-856-36 | Sequence 36, Appl | 1154 | 62 | 5.5 | 394 | 4 | US-09-489-039A-9360 | Sequence 9360, Ap |
| 1082 | 62.5 | 5.6 | 2201 | 4 | US-09-854-856-24 | Sequence 24, Appl | 1155 | 62 | 5.5 | 412 | 4 | US-09-538-092-835 | Sequence 835, App |
| 1083 | 62.5 | 5.6 | 2217 | 4 | US-09-854-856-20 | Sequence 20, Appl | 1156 | 62 | 5.5 | 435 | 4 | US-09-949-016-9133 | Sequence 9133, Ap |
| 1084 | 62.5 | 5.6 | 2229 | 4 | US-09-854-856-8 | Sequence 8, Appli | 1157 | 62 | 5.5 | 454 | 4 | US-09-949-016-9823 | Sequence 9823, Ap |
| 1085 | 62.5 | 5.6 | 2245 | 4 | US-09-854-856-4 | Sequence 4, Appli | 1158 | 62 | 5.5 | 455 | 4 | US-09-489-039A-14133 | Sequence 14133, A |
| 1086 | 62.5 | 5.6 | 2294 | 4 | US-09-854-856-50 | Sequence 50, Appl | 1159 | 62 | 5.5 | 483 | 3 | US-08-477-928A-2 | Sequence 2, Appli |
| 1087 | 62.5 | 5.6 | 2322 | 4 | US-09-854-856-34 | Sequence 34, Appl | 1160 | 62 | 5.5 | 530 | 4 | US-09-614-912-174 | Sequence 174, App |
| 1088 | 62.5 | 5.6 | 2354 | 4 | US-09-854-856-18 | Sequence 18, Appl | 1161 | 62 | 5.5 | 541 | 4 | US-09-248-796A-25057 | Sequence 25057, A |
| 1089 | 62.5 | 5.6 | 2366 | 1 | US-08-480-604A-10 | Sequence 10, Appl | 1162 | 62 | 5.5 | 556 | 4 | US-09-538-092-712 | Sequence 712, App |
| 1090 | 62.5 | 5.6 | 2366 | 2 | US-08-405-496A-10 | Sequence 10, Appl | 1163 | 62 | 5.5 | 624 | 4 | US-09-270-767-42659 | Sequence 42659, A |
| 1091 | 62.5 | 5.6 | 2366 | 3 | US-08-915-136-10 | Sequence 10, Appl | 1164 | 62 | 5.5 | 646 | 4 | US-09-248-796A-16701 | Sequence 16701, A |
| 1092 | 62.5 | 5.6 | 2366 | 3 | US-08-957-310-10 | Sequence 10, Appl | 1165 | 62 | 5.5 | 654 | 1 | US-08-487-890A-12 | Sequence 12, Appl |
| 1093 | 62.5 | 5.6 | 2366 | 4 | US-10-011-366-10 | Sequence 10, Appl | 1166 | 62 | 5.5 | 654 | 2 | US-08-478-435-12 | Sequence 12, Appl |
| 1094 | 62.5 | 5.6 | 2366 | 4 | US-09-084-517-10 | Sequence 10, Appl | 1167 | 62 | 5.5 | 654 | 2 | US-08-337-483-12 | Sequence 12, Appl |
| 1095 | 62.5 | 5.6 | 2382 | 4 | US-09-854-856-2 | Sequence 2, Appli | 1168 | 62 | 5.5 | 654 | 2 | US-08-478-373-12 | Sequence 12, Appl |

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|------|------|-----|-----------|---|----------------------|--------------------|------|------|-----|------|---|----------------------|--------------------|
| 1169 | 62 | 5.5 | 654 | 3 | US-08-474-671-12 | Sequence 12, Appl | 1242 | 61.5 | 5.5 | 386 | 4 | US-09-270-767-44120 | Sequence 44120, A |
| 1170 | 62 | 5.5 | 654 | 3 | US-08-483-577A-12 | Sequence 12, Appl | 1243 | 61.5 | 5.5 | 393 | 3 | US-08-235-836C-114 | Sequence 114, App |
| 1171 | 62 | 5.5 | 654 | 3 | US-08-897-438-12 | Sequence 12, Appl | 1244 | 61.5 | 5.5 | 414 | 4 | US-09-640-211A-2247 | Sequence 2247, Ap |
| 1172 | 62 | 5.5 | 654 | 3 | US-08-637-654-12 | Sequence 12, Appl | 1245 | 61.5 | 5.5 | 440 | 4 | US-09-014-240-4 | Sequence 4, Appli |
| 1173 | 62 | 5.5 | 654 | 3 | US-08-649-518-12 | Sequence 12, Appl | 1246 | 61.5 | 5.5 | 441 | 3 | US-08-235-836C-120 | Sequence 120, App |
| 1174 | 62 | 5.5 | 681 | 3 | US-08-760-615-6 | Sequence 6, Appli | 1247 | 61.5 | 5.5 | 454 | 3 | US-08-235-836C-116 | Sequence 7, Appli |
| 1175 | 62 | 5.5 | 683 | 3 | US-09-213-2930-1 | Sequence 1, Appli | 1248 | 61.5 | 5.5 | 461 | 3 | US-09-042-785A-7 | Sequence 7, Appli |
| 1176 | 62 | 5.5 | 709 | 4 | US-09-248-796A-19045 | Sequence 19045, A | 1249 | 61.5 | 5.5 | 461 | 3 | US-09-006-353A-4 | Sequence 4, Appli |
| 1177 | 62 | 5.5 | 748 | 2 | US-08-997-080-154 | Sequence 154, App | 1250 | 61.5 | 5.5 | 461 | 4 | US-09-573-986-4 | Sequence 4, Appli |
| 1178 | 62 | 5.5 | 748 | 3 | US-08-997-362-154 | Sequence 154, App | 1251 | 61.5 | 5.5 | 461 | 4 | US-09-896-096A-17 | Sequence 17, Appli |
| 1179 | 62 | 5.5 | 748 | 3 | US-09-095-855-154 | Sequence 154, App | 1252 | 61.5 | 5.5 | 470 | 3 | US-09-118-319-8 | Sequence 8, Appli |
| 1180 | 62 | 5.5 | 748 | 3 | US-09-324-542-154 | Sequence 154, App | 1253 | 61.5 | 5.5 | 485 | 4 | US-09-248-796A-18355 | Sequence 18355, A |
| 1181 | 62 | 5.5 | 748 | 4 | US-09-205-426-154 | Sequence 154, App | 1254 | 61.5 | 5.5 | 498 | 4 | US-09-309-572-2 | Sequence 2, Appli |
| 1182 | 62 | 5.5 | 760 | 4 | US-09-720-767-43780 | Sequence 43780, A | 1255 | 61.5 | 5.5 | 498 | 4 | US-09-718-096-2 | Sequence 2, Appli |
| 1183 | 62 | 5.5 | 801 | 1 | US-08-725-012-2 | Sequence 2, Appli | 1256 | 61.5 | 5.5 | 507 | 4 | US-09-252-991A-32725 | Sequence 32725, A |
| 1184 | 62 | 5.5 | 849 | 4 | US-09-792-024-119 | Sequence 119, App | 1257 | 61.5 | 5.5 | 569 | 4 | US-09-173-053-18 | Sequence 18, Appl |
| 1185 | 62 | 5.5 | 858 | 4 | US-09-270-767-44835 | Sequence 44835, A | 1258 | 61.5 | 5.5 | 574 | 4 | US-09-248-796A-20132 | Sequence 20132, A |
| 1186 | 62 | 5.5 | 866 | 4 | US-09-527-084A-4 | Sequence 4, Appli | 1259 | 61.5 | 5.5 | 577 | 2 | US-08-435-149-3 | Sequence 3, Appli |
| 1187 | 62 | 5.5 | 1010 | 4 | US-09-248-796A-16379 | Sequence 16379, A | 1260 | 61.5 | 5.5 | 582 | 3 | US-09-034-177-1 | Sequence 1, Appli |
| 1188 | 62 | 5.5 | 1094 | 4 | US-09-377-285B-22 | Sequence 22, Appl | 1261 | 61.5 | 5.5 | 588 | 3 | US-08-235-836C-122 | Sequence 122, App |
| 1189 | 62 | 5.5 | 1262 | 4 | US-09-107-433-5067 | Sequence 5067, Ap | 1262 | 61.5 | 5.5 | 609 | 4 | US-09-443-067-30 | Sequence 30, Appl |
| 1190 | 62 | 5.5 | 1311 | 1 | US-08-340-011-5 | Sequence 5, Appli | 1263 | 61.5 | 5.5 | 611 | 3 | US-09-475-460A-32 | Sequence 32, Appl |
| 1191 | 62 | 5.5 | 1311 | 3 | US-08-901-710-5 | Sequence 5, Appli | 1264 | 61.5 | 5.5 | 611 | 4 | US-09-748-061A-32 | Sequence 32, Appl |
| 1192 | 62 | 5.5 | 1311 | 4 | US-09-169-079-5 | Sequence 5, Appli | 1265 | 61.5 | 5.5 | 642 | 4 | US-09-270-767-43064 | Sequence 43064, A |
| 1193 | 62 | 5.5 | 1385 | 4 | US-09-827-998-16 | Sequence 16, Appl | 1266 | 61.5 | 5.5 | 642 | 4 | US-09-949-016-9857 | Sequence 9857, Ap |
| 1194 | 62 | 5.5 | 1411 | 4 | US-09-538-092-413 | Sequence 413, App | 1267 | 61.5 | 5.5 | 674 | 4 | US-09-949-016-7196 | Sequence 7196, Ap |
| 1195 | 62 | 5.5 | 1770 | 4 | US-09-827-998-10 | Sequence 10, Appl | 1268 | 61.5 | 5.5 | 710 | 4 | US-09-575-081B-6 | Sequence 6, Appli |
| 1196 | 62 | 5.5 | 1791 | 4 | US-09-827-998-3 | Sequence 3, Appli | 1269 | 61.5 | 5.5 | 716 | 3 | US-08-971-188-5 | Sequence 5, Appli |
| 1197 | 62 | 5.5 | 1852 | 4 | US-10-023-649A-2 | Sequence 2, Appli | 1270 | 61.5 | 5.5 | 716 | 3 | US-08-971-188-11 | Sequence 11, Appl |
| 1198 | 61.5 | 5.5 | 88 | 4 | US-09-252-991A-22785 | Sequence 22785, A | 1271 | 61.5 | 5.5 | 737 | 3 | US-08-971-188-4 | Sequence 4, Appli |
| 1199 | 61.5 | 5.5 | 95 | 4 | US-09-270-767-46287 | Sequence 46287, A | 1272 | 61.5 | 5.5 | 847 | 4 | US-09-476-242-2 | Sequence 2, Appli |
| 1200 | 61.5 | 5.5 | 111 | 4 | US-09-248-796A-22053 | Sequence 22053, A | 1273 | 61.5 | 5.5 | 889 | 5 | PCF-US93-11725-2 | Sequence 2, Appli |
| 1201 | 61.5 | 5.5 | 156 | 4 | US-09-252-991A-26582 | Sequence 26582, A | 1274 | 61.5 | 5.5 | 970 | 4 | US-09-134-000C-5691 | Sequence 5691, Ap |
| 1202 | 61.5 | 5.5 | 156 | 4 | US-09-646-028-4 | Sequence 4, Appli | 1275 | 61.5 | 5.5 | 990 | 4 | US-09-657-931A-11 | Sequence 11, Appl |
| 1203 | 61.5 | 5.5 | 177 | 4 | US-09-252-991A-28450 | Sequence 28450, A | 1276 | 61.5 | 5.5 | 995 | 4 | US-09-657-931A-1 | Sequence 1, Appl |
| 1204 | 61.5 | 5.5 | 182 | 4 | US-09-252-991A-22314 | Sequence 22314, A | 1277 | 61.5 | 5.5 | 1060 | 4 | US-09-248-796A-14123 | Sequence 14123, A |
| 1205 | 61.5 | 5.5 | 183 | 4 | US-09-489-847-136 | Sequence 136, App | 1278 | 61.5 | 5.5 | 1198 | 4 | US-09-949-016-6989 | Sequence 6989, Ap |
| 1206 | 61.5 | 5.5 | 5168049-3 | 6 | 5168049-3 | Patent No. 5168049 | 1279 | 61.5 | 5.5 | 1203 | 4 | US-09-949-016-10916 | Sequence 10916, A |
| 1207 | 61.5 | 5.5 | 183 | 6 | 5168049-3 | Patent No. 5168049 | 1280 | 61.5 | 5.5 | 1258 | 4 | US-09-489-039A-11380 | Sequence 11380, A |
| 1208 | 61.5 | 5.5 | 199 | 4 | US-09-502-540-9868 | Sequence 9868, Ap | 1281 | 61.5 | 5.5 | 2074 | 4 | US-09-491-356C-9 | Sequence 9, Appli |
| 1209 | 61.5 | 5.5 | 200 | 4 | US-09-252-991A-28828 | Sequence 24828, A | 1282 | 61.5 | 5.5 | 2137 | 3 | US-09-134-001C-4463 | Sequence 4463, Ap |
| 1210 | 61.5 | 5.5 | 204 | 4 | US-09-252-991A-16784 | Sequence 16784, A | 1283 | 61.5 | 5.5 | 2231 | 3 | US-08-153-799-16 | Sequence 16, Appl |
| 1211 | 61.5 | 5.5 | 235 | 3 | US-09-326-394-4 | Sequence 4, Appli | 1284 | 61.5 | 5.5 | 2325 | 3 | US-08-417-089-6 | Sequence 6, Appli |
| 1212 | 61.5 | 5.5 | 263 | 1 | US-08-300-903A-2 | Sequence 2, Appli | 1285 | 61.5 | 5.5 | 2325 | 3 | US-08-695-651-6 | Sequence 6, Appli |
| 1213 | 61.5 | 5.5 | 263 | 3 | US-08-436-748-5 | Sequence 5, Appli | 1286 | 61.5 | 5.5 | 2325 | 3 | US-08-930-285-6 | Sequence 6, Appli |
| 1214 | 61.5 | 5.5 | 263 | 3 | US-08-483-857-5 | Sequence 5, Appli | 1287 | 61.5 | 5.5 | 2325 | 3 | US-08-695-421-6 | Sequence 6, Appli |
| 1215 | 61.5 | 5.5 | 263 | 4 | US-08-988-197-2 | Sequence 2, Appli | 1288 | 61.5 | 5.5 | 2325 | 4 | US-08-697-826A-10 | Sequence 10, Appl |
| 1216 | 61.5 | 5.5 | 263 | 4 | US-10-385-072-2 | Sequence 2, Appli | 1289 | 61 | 5.4 | 46 | 3 | US-08-856-074A-39 | Sequence 39, Appl |
| 1217 | 61.5 | 5.5 | 281 | 1 | US-07-941-523-23 | Sequence 23, Appl | 1290 | 61 | 5.4 | 60 | 3 | US-08-856-074A-1 | Sequence 1, Appli |
| 1218 | 61.5 | 5.5 | 291 | 4 | US-09-252-991A-17495 | Sequence 17495, A | 1291 | 61 | 5.4 | 78 | 4 | US-09-328-352-6061 | Sequence 6061, Ap |
| 1219 | 61.5 | 5.5 | 294 | 4 | US-09-248-796A-15817 | Sequence 15817, A | 1292 | 61 | 5.4 | 118 | 4 | US-09-252-991A-18728 | Sequence 18728, A |
| 1220 | 61.5 | 5.5 | 296 | 1 | US-08-320-161-11 | Sequence 11, Appl | 1293 | 61 | 5.4 | 134 | 4 | US-09-270-767-62350 | Sequence 62350, A |
| 1221 | 61.5 | 5.5 | 296 | 3 | US-08-137-175A-3 | Sequence 3, Appli | 1294 | 61 | 5.4 | 140 | 4 | US-09-252-991A-16888 | Sequence 16888, A |
| 1222 | 61.5 | 5.5 | 296 | 3 | US-08-479-017-3 | Sequence 3, Appli | 1295 | 61 | 5.4 | 164 | 4 | US-09-252-991A-25898 | Sequence 25898, A |
| 1223 | 61.5 | 5.5 | 296 | 3 | US-08-455-829-11 | Sequence 11, Appl | 1296 | 61 | 5.4 | 164 | 4 | US-09-691-270A-6 | Sequence 6, Appli |
| 1224 | 61.5 | 5.5 | 296 | 3 | US-08-235-836C-22 | Sequence 22, Appl | 1297 | 61 | 5.4 | 165 | 2 | US-08-709-924-2 | Sequence 2, Appli |
| 1225 | 61.5 | 5.5 | 296 | 3 | US-08-455-973-11 | Sequence 11, Appl | 1298 | 61 | 5.4 | 165 | 2 | US-08-709-925-2 | Sequence 2, Appli |
| 1226 | 61.5 | 5.5 | 303 | 4 | US-09-270-767-57613 | Sequence 57613, A | 1299 | 61 | 5.4 | 165 | 2 | US-08-709-948-2 | Sequence 2, Appli |
| 1227 | 61.5 | 5.5 | 322 | 4 | US-09-252-991A-31608 | Sequence 31608, A | 1300 | 61 | 5.4 | 165 | 4 | US-10-050-875-2 | Sequence 2, Appli |
| 1228 | 61.5 | 5.5 | 323 | 2 | US-08-435-149-2 | Sequence 2, Appli | 1301 | 61 | 5.4 | 186 | 4 | US-09-270-767-46733 | Sequence 46733, A |
| 1229 | 61.5 | 5.5 | 323 | 4 | US-08-311-731A-115 | Sequence 115, App | 1302 | 61 | 5.4 | 202 | 4 | US-09-248-796A-22095 | Sequence 22095, A |
| 1230 | 61.5 | 5.5 | 324 | 1 | US-08-310-416A-14 | Sequence 14, Appl | 1303 | 61 | 5.4 | 203 | 4 | US-09-253-991A-20284 | Sequence 20284, A |
| 1231 | 61.5 | 5.5 | 324 | 2 | US-08-888-171-14 | Sequence 14, Appl | 1304 | 61 | 5.4 | 212 | 4 | US-09-270-767-44947 | Sequence 44947, A |
| 1232 | 61.5 | 5.5 | 327 | 4 | US-09-270-767-42324 | Sequence 42324, A | 1305 | 61 | 5.4 | 237 | 4 | US-09-252-991A-25537 | Sequence 25537, A |
| 1233 | 61.5 | 5.5 | 340 | 2 | US-08-446-875-16 | Sequence 16, Appl | 1306 | 61 | 5.4 | 285 | 4 | US-09-230-225B-6 | Sequence 6, Appli |
| 1234 | 61.5 | 5.5 | 347 | 4 | US-09-540-236-3596 | Sequence 3596, Ap | 1307 | 61 | 5.4 | 286 | 3 | US-09-254-733-3 | Sequence 3, Appli |
| 1235 | 61.5 | 5.5 | 357 | 1 | US-08-078-683A-8 | Sequence 8, Appli | 1308 | 61 | 5.4 | 305 | 3 | US-09-230-222-1 | Sequence 1, Appli |
| 1236 | 61.5 | 5.5 | 357 | 4 | US-08-471-970A-8 | Sequence 8, Appli | 1309 | 61 | 5.4 | 317 | 4 | US-09-118-637A-2 | Sequence 2, Appli |
| 1237 | 61.5 | 5.5 | 357 | 4 | US-09-723-677B-8 | Sequence 8, Appli | 1310 | 61 | 5.4 | 330 | 4 | US-09-270-767-44544 | Sequence 44544, A |
| 1238 | 61.5 | 5.5 | 376 | 4 | US-09-844-311-2 | Sequence 2, Appli | 1311 | 61 | 5.4 | 331 | 4 | US-09-270-767-42389 | Sequence 42389, A |
| 1239 | 61.5 | 5.5 | 380 | 3 | US-08-235-836C-118 | Sequence 118, App | 1312 | 61 | 5.4 | 337 | 4 | US-09-270-767-36208 | Sequence 36208, A |
| 1240 | 61.5 | 5.5 | 381 | 4 | US-09-014-240-2 | Sequence 2, Appli | 1313 | 61 | 5.4 | 337 | 4 | US-09-270-767-51425 | Sequence 51425, A |
| 1241 | 61.5 | 5.5 | 381 | 4 | US-09-844-311-4 | Sequence 4, Appli | 1314 | 61 | 5.4 | 347 | 4 | US-09-252-991A-27730 | Sequence 27730, A |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|----------------------|--------------------|------|------|-----|-----|---|----------------------|--------------------|
| 1315 | 61 | 5.4 | 378 | 2 | US-08-986-217-6 | Sequence 6, Appli | 1388 | 60.5 | 5.4 | 178 | 4 | US-09-489-039A-12560 | Sequence 12560, A |
| 1316 | 61 | 5.4 | 380 | 2 | US-09-026-587-4 | Sequence 4, Appli | 1389 | 60.5 | 5.4 | 195 | 4 | US-09-370-838-125 | Sequence 125, App |
| 1317 | 61 | 5.4 | 380 | 2 | US-09-227-420-4 | Sequence 4, Appli | 1390 | 60.5 | 5.4 | 195 | 4 | US-09-854-133-125 | Sequence 125, App |
| 1318 | 61 | 5.4 | 380 | 4 | US-09-387-811-4 | Sequence 4, Appli | 1391 | 60.5 | 5.4 | 202 | 2 | US-08-853-261A-4 | Sequence 4, Appli |
| 1319 | 61 | 5.4 | 381 | 4 | US-09-823-240A-10 | Sequence 10, Appli | 1392 | 60.5 | 5.4 | 202 | 3 | US-08-839-711-4 | Sequence 4, Appli |
| 1320 | 61 | 5.4 | 381 | 4 | US-09-949-016-7291 | Sequence 7291, Ap | 1393 | 60.5 | 5.4 | 202 | 3 | US-09-227-224-4 | Sequence 4, Appli |
| 1321 | 61 | 5.4 | 386 | 4 | US-09-270-767-46702 | Sequence 46702, A | 1394 | 60.5 | 5.4 | 202 | 4 | US-09-855-288-10 | Sequence 10, Appli |
| 1322 | 61 | 5.4 | 387 | 3 | US-08-968-563-37 | Sequence 37, Appli | 1395 | 60.5 | 5.4 | 202 | 4 | US-09-253-991A-31172 | Sequence 31172, A |
| 1323 | 61 | 5.4 | 387 | 3 | US-08-969-683A-37 | Sequence 37, Appli | 1396 | 60.5 | 5.4 | 202 | 4 | US-09-328-352-8104 | Sequence 8104, Ap |
| 1324 | 61 | 5.4 | 394 | 4 | US-09-248-796A-17280 | Sequence 17280, A | 1397 | 60.5 | 5.4 | 230 | 4 | US-09-248-796A-15149 | Sequence 15149, A |
| 1325 | 61 | 5.4 | 410 | 4 | US-09-543-681A-5962 | Sequence 5962, Ap | 1398 | 60.5 | 5.4 | 239 | 4 | US-09-248-796A-16743 | Sequence 16743, A |
| 1326 | 61 | 5.4 | 422 | 4 | US-09-248-796A-23935 | Sequence 23935, A | 1399 | 60.5 | 5.4 | 241 | 4 | US-09-270-767-36205 | Sequence 36205, A |
| 1327 | 61 | 5.4 | 423 | 4 | US-09-248-796A-26813 | Sequence 26813, A | 1400 | 60.5 | 5.4 | 241 | 4 | US-09-270-767-36205 | Sequence 36205, A |
| 1328 | 61 | 5.4 | 441 | 4 | US-09-252-991A-27394 | Sequence 27394, A | 1401 | 60.5 | 5.4 | 251 | 4 | US-09-270-767-51422 | Sequence 51422, A |
| 1329 | 61 | 5.4 | 484 | 4 | US-09-242-913B-17 | Sequence 17, Appli | 1402 | 60.5 | 5.4 | 251 | 4 | US-09-248-796A-27961 | Sequence 27961, A |
| 1330 | 61 | 5.4 | 499 | 4 | US-09-561-763-2 | Sequence 2, Appli | 1403 | 60.5 | 5.4 | 252 | 4 | US-09-270-767-33633 | Sequence 33633, A |
| 1331 | 61 | 5.4 | 499 | 4 | US-09-431-367B-9 | Sequence 2, Appli | 1403 | 60.5 | 5.4 | 252 | 4 | US-09-270-767-48850 | Sequence 48850, A |
| 1332 | 61 | 5.4 | 523 | 3 | US-09-302-620B-95 | Sequence 2, Appli | 1404 | 60.5 | 5.4 | 271 | 4 | US-09-270-767-44644 | Sequence 44644, A |
| 1333 | 61 | 5.4 | 529 | 4 | US-09-949-016-11657 | Sequence 95, Appli | 1405 | 60.5 | 5.4 | 274 | 4 | US-09-270-767-40695 | Sequence 40695, A |
| 1334 | 61 | 5.4 | 533 | 1 | US-08-220-151-15 | Sequence 11657, A | 1406 | 60.5 | 5.4 | 274 | 4 | US-09-270-767-55911 | Sequence 55911, A |
| 1335 | 61 | 5.4 | 533 | 1 | US-08-413-118-15 | Sequence 15, Appli | 1407 | 60.5 | 5.4 | 276 | 4 | US-09-500-135C-224 | Sequence 224, App |
| 1336 | 61 | 5.4 | 533 | 3 | US-08-473-446-15 | Sequence 15, Appli | 1408 | 60.5 | 5.4 | 277 | 4 | US-09-270-767-43705 | Sequence 43705, A |
| 1337 | 61 | 5.4 | 553 | 4 | US-09-650-324A-61 | Sequence 61, Appli | 1409 | 60.5 | 5.4 | 284 | 1 | US-08-411-777-10 | Sequence 10, Appli |
| 1338 | 61 | 5.4 | 587 | 4 | US-09-857-669-6 | Sequence 6, Appli | 1410 | 60.5 | 5.4 | 284 | 3 | US-09-057-088-10 | Sequence 10, Appli |
| 1339 | 61 | 5.4 | 608 | 4 | US-09-489-039A-13204 | Sequence 13204, A | 1411 | 60.5 | 5.4 | 289 | 4 | US-09-071-035-480 | Sequence 480, App |
| 1340 | 61 | 5.4 | 630 | 4 | US-09-485-529-1 | Sequence 1, Appli | 1412 | 60.5 | 5.4 | 296 | 4 | US-09-667-135-36 | Sequence 36, Appli |
| 1341 | 61 | 5.4 | 635 | 4 | US-09-417-197-125 | Sequence 125, App | 1413 | 60.5 | 5.4 | 299 | 4 | US-09-902-540-16811 | Sequence 16811, A |
| 1342 | 61 | 5.4 | 676 | 4 | US-09-107-532A-3847 | Sequence 3847, Ap | 1414 | 60.5 | 5.4 | 305 | 1 | US-08-090-013-2 | Sequence 2, Appli |
| 1343 | 61 | 5.4 | 682 | 4 | US-09-270-767-45389 | Sequence 45389, A | 1415 | 60.5 | 5.4 | 305 | 1 | US-08-081-328-2 | Sequence 2, Appli |
| 1344 | 61 | 5.4 | 726 | 4 | US-09-583-110-2782 | Sequence 2782, Ap | 1416 | 60.5 | 5.4 | 305 | 1 | US-08-232-249-2 | Sequence 2, Appli |
| 1345 | 61 | 5.4 | 726 | 4 | US-09-107-433-3906 | Sequence 3906, Ap | 1417 | 60.5 | 5.4 | 305 | 2 | US-08-921-426-8 | Sequence 8, Appli |
| 1346 | 61 | 5.4 | 732 | 4 | US-09-134-000C-6359 | Sequence 6359, Ap | 1418 | 60.5 | 5.4 | 305 | 2 | US-08-833-642A-2 | Sequence 2, Appli |
| 1347 | 61 | 5.4 | 749 | 4 | US-08-997-685A-10 | Sequence 10, Appli | 1419 | 60.5 | 5.4 | 305 | 2 | US-08-140-008A-4 | Sequence 4, Appli |
| 1348 | 61 | 5.4 | 749 | 4 | US-09-086-436-39 | Sequence 39, Appli | 1420 | 60.5 | 5.4 | 305 | 2 | US-08-836-340-1 | Sequence 1, Appli |
| 1349 | 61 | 5.4 | 757 | 4 | US-09-823-038A-52 | Sequence 52, Appli | 1421 | 60.5 | 5.4 | 305 | 2 | US-08-389-423-2 | Sequence 2, Appli |
| 1350 | 61 | 5.4 | 784 | 3 | US-09-371-913A-7 | Sequence 7, Appli | 1422 | 60.5 | 5.4 | 305 | 2 | US-08-816-915-8 | Sequence 8, Appli |
| 1351 | 61 | 5.4 | 784 | 4 | US-09-967-805-7 | Sequence 7, Appli | 1423 | 60.5 | 5.4 | 305 | 3 | US-09-189-060B-56 | Sequence 56, Appli |
| 1352 | 61 | 5.4 | 860 | 1 | US-08-092-817-4 | Sequence 4, Appli | 1424 | 60.5 | 5.4 | 305 | 3 | US-09-230-665-2 | Sequence 2, Appli |
| 1353 | 61 | 5.4 | 860 | 1 | US-08-485-128-4 | Sequence 4, Appli | 1425 | 60.5 | 5.4 | 305 | 4 | US-09-402-664A-12 | Sequence 12, Appli |
| 1354 | 61 | 5.4 | 860 | 4 | US-09-804-778A-8 | Sequence 8, Appli | 1426 | 60.5 | 5.4 | 305 | 4 | US-09-189-028-2 | Sequence 2, Appli |
| 1355 | 61 | 5.4 | 860 | 4 | US-09-824-637-4 | Sequence 4, Appli | 1427 | 60.5 | 5.4 | 305 | 5 | PCT-US95-07743-8 | Sequence 8, Appli |
| 1356 | 61 | 5.4 | 908 | 4 | US-09-949-016-7580 | Sequence 4, Appli | 1428 | 60.5 | 5.4 | 342 | 3 | US-09-193-562D-13 | Sequence 13, Appli |
| 1357 | 61 | 5.4 | 961 | 4 | US-09-914-259-66 | Sequence 66, Appli | 1429 | 60.5 | 5.4 | 342 | 4 | US-10-055-412B-13 | Sequence 13, Appli |
| 1358 | 61 | 5.4 | 978 | 4 | US-09-198-452A-1055 | Sequence 1055, Ap | 1430 | 60.5 | 5.4 | 343 | 2 | US-08-856-444-2 | Sequence 2, Appli |
| 1359 | 61 | 5.4 | 978 | 4 | US-09-438-185A-982 | Sequence 982, App | 1431 | 60.5 | 5.4 | 343 | 4 | US-09-710-279-1626 | Sequence 1626, Ap |
| 1360 | 61 | 5.4 | 1087 | 1 | US-08-264-002-5 | Sequence 5, Appli | 1432 | 60.5 | 5.4 | 343 | 4 | US-09-710-279-1864 | Sequence 1864, Ap |
| 1361 | 61 | 5.4 | 1276 | 3 | US-08-937-236-3 | Sequence 3, Appli | 1433 | 60.5 | 5.4 | 347 | 4 | US-09-949-016-10356 | Sequence 10356, A |
| 1362 | 61 | 5.4 | 1291 | 3 | US-08-569-214-3 | Sequence 3, Appli | 1434 | 60.5 | 5.4 | 347 | 4 | US-09-949-016-10357 | Sequence 10357, A |
| 1363 | 61 | 5.4 | 1291 | 3 | US-08-937-236-2 | Sequence 2, Appli | 1435 | 60.5 | 5.4 | 348 | 4 | US-09-270-767-44163 | Sequence 44163, A |
| 1364 | 61 | 5.4 | 1295 | 3 | US-08-569-214-2 | Sequence 2, Appli | 1436 | 60.5 | 5.4 | 350 | 3 | US-09-134-001C-5150 | Sequence 5150, Ap |
| 1365 | 61 | 5.4 | 1301 | 4 | US-09-252-991A-29822 | Sequence 29822, A | 1437 | 60.5 | 5.4 | 391 | 4 | US-09-270-767-58641 | Sequence 58641, A |
| 1366 | 61 | 5.4 | 1326 | 4 | US-09-489-039A-28772 | Sequence 28772, A | 1438 | 60.5 | 5.4 | 410 | 4 | US-09-200-090-2 | Sequence 2, Appli |
| 1367 | 61 | 5.4 | 1410 | 2 | US-08-470-058-4 | Sequence 4, Appli | 1439 | 60.5 | 5.4 | 410 | 4 | US-09-252-991A-32633 | Sequence 32633, A |
| 1368 | 61 | 5.4 | 1410 | 3 | US-09-037-188-4 | Sequence 4, Appli | 1440 | 60.5 | 5.4 | 431 | 5 | PCT-US91-00909-6 | Sequence 6, Appli |
| 1369 | 61 | 5.4 | 1421 | 3 | US-09-285-310-4 | Sequence 4, Appli | 1441 | 60.5 | 5.4 | 446 | 3 | US-09-004-393B-4 | Sequence 4, Appli |
| 1370 | 61 | 5.4 | 1621 | 3 | US-09-949-016-8450 | Sequence 4, Appli | 1442 | 60.5 | 5.4 | 450 | 4 | US-09-071-035-256 | Sequence 256, App |
| 1371 | 61 | 5.4 | 2048 | 3 | US-09-268-347-48 | Sequence 8450, Ap | 1443 | 60.5 | 5.4 | 461 | 4 | US-09-248-796A-17227 | Sequence 17227, A |
| 1372 | 61 | 5.4 | 2214 | 1 | US-08-727-034-7 | Sequence 48, Appli | 1444 | 60.5 | 5.4 | 477 | 4 | US-09-248-796A-26051 | Sequence 26051, A |
| 1373 | 61 | 5.4 | 2214 | 1 | US-09-919-039-40 | Sequence 7, Appli | 1445 | 60.5 | 5.4 | 498 | 3 | US-08-889-841B-5 | Sequence 5, Appli |
| 1374 | 60.5 | 5.4 | 115 | 4 | US-09-252-991A-28404 | Sequence 40, Appli | 1446 | 60.5 | 5.4 | 498 | 4 | US-09-419-362-5 | Sequence 5, Appli |
| 1375 | 60.5 | 5.4 | 136 | 4 | US-09-252-991A-17270 | Sequence 28404, A | 1447 | 60.5 | 5.4 | 512 | 3 | US-09-270-767-43154 | Sequence 43154, A |
| 1376 | 60.5 | 5.4 | 138 | 4 | US-09-252-991A-25322 | Sequence 17270, A | 1448 | 60.5 | 5.4 | 529 | 3 | US-08-821-984-6 | Sequence 6, Appli |
| 1377 | 60.5 | 5.4 | 138 | 4 | US-09-252-991A-28372 | Sequence 25322, A | 1449 | 60.5 | 5.4 | 529 | 3 | US-08-821-984-8 | Sequence 8, Appli |
| 1378 | 60.5 | 5.4 | 152 | 4 | US-09-583-110-4216 | Sequence 4216, Ap | 1450 | 60.5 | 5.4 | 529 | 3 | US-09-329-749-6 | Sequence 6, Appli |
| 1379 | 60.5 | 5.4 | 154 | 4 | US-09-252-991A-28772 | Sequence 28772, A | 1451 | 60.5 | 5.4 | 529 | 3 | US-09-329-749-8 | Sequence 8, Appli |
| 1380 | 60.5 | 5.4 | 154 | 4 | US-09-621-976-3997 | Sequence 3997, Ap | 1452 | 60.5 | 5.4 | 529 | 4 | US-09-502-264-6 | Sequence 6, Appli |
| 1381 | 60.5 | 5.4 | 157 | 4 | US-09-270-767-36987 | Sequence 36987, A | 1453 | 60.5 | 5.4 | 529 | 4 | US-09-502-264-8 | Sequence 8, Appli |
| 1382 | 60.5 | 5.4 | 157 | 4 | US-09-270-767-52204 | Sequence 52204, A | 1454 | 60.5 | 5.4 | 538 | 4 | US-09-252-991A-16952 | Sequence 16952, A |
| 1383 | 60.5 | 5.4 | 162 | 4 | US-09-252-991A-24953 | Sequence 24953, A | 1455 | 60.5 | 5.4 | 586 | 2 | US-08-630-822A-70 | Sequence 70, Appli |
| 1384 | 60.5 | 5.4 | 172 | 4 | US-09-252-991A-26947 | Sequence 26947, A | 1456 | 60.5 | 5.4 | 586 | 2 | US-09-005-069-70 | Sequence 70, Appli |
| 1385 | 60.5 | 5.4 | 172 | 4 | US-09-270-767-42440 | Sequence 42440, A | 1457 | 60.5 | 5.4 | 586 | 3 | US-09-171-156A-30 | Sequence 30, Appli |
| 1386 | 60.5 | 5.4 | 173 | 4 | US-09-825-561A-86 | Sequence 86, Appli | 1458 | 60.5 | 5.4 | 586 | 4 | US-09-004-730A-30 | Sequence 30, Appli |
| 1387 | 60.5 | 5.4 | 174 | 4 | US-09-248-796A-25211 | Sequence 25211, A | 1459 | 60.5 | 5.4 | 608 | 4 | US-09-981-799A-30 | Sequence 30, Appli |
| | | | | | | Sequence 25211, A | 1460 | 60.5 | 5.4 | | | US-09-270-767-43297 | Sequence 43297, A |

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| 1461 | 60.5 | 5.4 | 645 | 4 | US-09-270-767-42233 | Sequence 42233, A |
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| 1463 | 60.5 | 5.4 | 661 | 2 | US-08-786-164-12 | Sequence 12, Appl |
| 1464 | 60.5 | 5.4 | 703 | 3 | US-09-367-206-5 | Sequence 5, Appl |
| 1465 | 60.5 | 5.4 | 856 | 4 | US-09-248-796A-15089 | Sequence 16089, A |
| 1466 | 60.5 | 5.4 | 859 | 4 | US-09-538-092-717 | Sequence 717, App |
| 1467 | 60.5 | 5.4 | 894 | 4 | US-09-071-035-248 | Sequence 248, App |
| 1468 | 60.5 | 5.4 | 920 | 4 | US-09-538-092-1197 | Sequence 1197, App |
| 1469 | 60.5 | 5.4 | 962 | 4 | US-09-071-035-246 | Sequence 246, App |
| 1470 | 60.5 | 5.4 | 962 | 4 | US-09-071-035-250 | Sequence 250, App |
| 1471 | 60.5 | 5.4 | 962 | 4 | US-09-071-035-254 | Sequence 254, App |
| 1472 | 60.5 | 5.4 | 962 | 4 | US-09-071-035-470 | Sequence 470, App |
| 1473 | 60.5 | 5.4 | 962 | 4 | US-09-071-035-474 | Sequence 474, App |
| 1474 | 60.5 | 5.4 | 962 | 4 | US-09-071-035-478 | Sequence 478, App |
| 1475 | 60.5 | 5.4 | 972 | 3 | US-08-335-844A-23 | Sequence 23, Appl |
| 1476 | 60.5 | 5.4 | 972 | 4 | US-09-129-366-23 | Sequence 23, Appl |
| 1477 | 60.5 | 5.4 | 1006 | 4 | US-09-949-016-7897 | Sequence 7897, App |
| 1478 | 60.5 | 5.4 | 1007 | 4 | US-10-144-198-36 | Sequence 36, Appl |
| 1479 | 60.5 | 5.4 | 1041 | 4 | US-10-144-198-14 | Sequence 14, Appl |
| 1480 | 60.5 | 5.4 | 1070 | 3 | US-08-922-635-22 | Sequence 22, Appl |
| 1481 | 60.5 | 5.4 | 1167 | 4 | US-09-661-322A-40 | Sequence 40, Appl |
| 1482 | 60.5 | 5.4 | 1234 | 2 | US-08-317-310A-15 | Sequence 15, Appl |
| 1483 | 60.5 | 5.4 | 1234 | 5 | PCT-US95-13041-15 | Sequence 15, Appl |
| 1484 | 60.5 | 5.4 | 1285 | 2 | US-08-540-406-6 | Sequence 6, Appl |
| 1485 | 60.5 | 5.4 | 1285 | 3 | US-08-656-055-6 | Sequence 6, Appl |
| 1486 | 60.5 | 5.4 | 1285 | 3 | US-08-954-668-6 | Sequence 6, Appl |
| 1487 | 60.5 | 5.4 | 1285 | 4 | US-08-918-658-6 | Sequence 6, Appl |
| 1488 | 60.5 | 5.4 | 1285 | 4 | US-09-724-631-6 | Sequence 6, Appl |
| 1489 | 60.5 | 5.4 | 1285 | 4 | US-08-954-701A-6 | Sequence 6, Appl |
| 1490 | 60.5 | 5.4 | 1285 | 5 | PCT-US95-13233-6 | Sequence 6, Appl |
| 1491 | 60.5 | 5.4 | 1286 | 3 | US-09-268-140-3 | Sequence 3, Appl |
| 1492 | 60.5 | 5.4 | 1290 | 1 | US-08-470-350B-2 | Sequence 2, Appl |
| 1493 | 60.5 | 5.4 | 1299 | 3 | US-08-460-900C-62 | Sequence 62, Appl |
| 1494 | 60.5 | 5.4 | 1299 | 3 | US-08-674-509B-48 | Sequence 48, Appl |
| 1495 | 60.5 | 5.4 | 1299 | 3 | US-08-954-698-48 | Sequence 48, Appl |
| 1496 | 60.5 | 5.4 | 1299 | 4 | US-09-639-695-62 | Sequence 62, Appl |
| 1497 | 60.5 | 5.4 | 1299 | 4 | US-09-448-188-48 | Sequence 48, Appl |
| 1498 | 60.5 | 5.4 | 1299 | 4 | US-08-954-128-48 | Sequence 48, Appl |
| 1499 | 60.5 | 5.4 | 1299 | 4 | US-08-954-740-48 | Sequence 48, Appl |
| 1500 | 60.5 | 5.4 | 1337 | 3 | US-08-854-585-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-09-232-160-21
; Sequence 21, Application US/09232160
; Patent No. 6368794
; GENERAL INFORMATION:
; APPLICANT: Steve Daniel
; APPLICANT: James Gilmore
; APPLICANT: Susan G. Stuart
; APPLICANT: Laura Stuve
; TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
; FILE REFERENCE: PA-0003 US
; CURRENT APPLICATION NUMBER: US/09/232,160
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PERL Program
; SEQ ID NO 21
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3044710
US-09-232-160-21

Query Match 100.0%; Score 1125; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 77 | ALKASFETCSYGVWGGFVVISRIISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT | 136 |
| QY | 121 | NSCIPFIITKDIPIFNTOATOTTEFIIVSDSTVSVASPYSTIPAPTTTPPAPASTSIPRR | 180 |
| Db | 137 | NSCIPFIITKDIPIFNTOATOTTEFIIVSDSTVSVASPYSTIPAPTTTPPAPASTSIPRR | 196 |
| QY | 181 | KKLICVTEVFMTSTMTSTETETEPFVENKAAFKNEAAGFG | 218 |
| Db | 197 | KKLICVTEVFMTSTMTSTETETEPFVENKAAFKNEAAGFG | 234 |

RESULT 2

; Sequence 201, Application US/09907794A
; Patent No. 6635468
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30

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; PRIOR APPLICATION NUMBER: PCT/US99/28564
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

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Best Local Similarity 100.0%; Pred. No. 7.7e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 218; Conservative 0;

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DB 17 TRLLVQGSRABELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76
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DB 137 NSCIPEIITTKDPIENTOTATOTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI 196
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAGFG 218
DB 197 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAGFG 234
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RESULT 3

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; Sequence 201, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
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; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match          100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 218; Conservative 0;

QY 1 TRLLVQGSRABELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
DB 17 TRLLVQGSRABELSIQVSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76
QY 61 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
DB 77 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
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DB 137 NSCIPEIITTKDPIENTOTATOTTEFIVSDSTYSVASPYSTIPAPTTTPPAPASTSI 196
QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAGFG 218
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RESULT 4

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; Sequence 201, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 218; Conservative 0;

QY 1 TRLLVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKQDVET 60
Db 17 TRLLVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKQDVET 76
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Db 77 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDWT 136
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Db 197 KKLICVTEVFVMTETMTSTETEPFVENKAAFNEAGFG 234

RESULT 6

; Sequence 201, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gueney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A

; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
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; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114; Mismatches 0; Indels 0; Gaps 0;
Matches 218; Conservative 0;

QY 1 TRLLVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKQDVET 60
Db 17 TRLLVQSLRAEELSIQVSCRMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKQDVET 76
QY 61 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDWT 120
Db 77 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDWT 136
QY 121 NSCIPEIITTKDPIFNTQTATQTFEIVSDSYVASPYSTIPAPTTTPAPASTSI 180
Db 137 NSCIPEIITTKDPIFNTQTATQTFEIVSDSYVASPYSTIPAPTTTPAPASTSI 196
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Db 197 KKLICVTEVFVMTETMTSTETEPFVENKAAFNEAGFG 234

RESULT 7

; Sequence 201, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

```

; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-09-08
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; PRIOR FILING DATE: 1999-09-13
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
;
Query Match 100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred No. 7,7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTEAKEACRLGLSLAGKDQVET 60
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; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein
;
Query Match 100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred No. 7,7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02

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RESULT 8

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; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02

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; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match          100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db 17 TRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76

QY 61 ALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 77 ALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136

QY 121 NSCIPEIITTKDPIFNQTOTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db 137 NSCIPEIITTKDPIFNQTOTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 196

QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFG 218
Db 197 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFG 234
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RESULT 9

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; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
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; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match          100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7.7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db 17 TRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76

QY 61 ALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db 77 ALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136

QY 121 NSCIPEIITTKDPIFNQTOTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db 137 NSCIPEIITTKDPIFNQTOTATTEFIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 196

QY 181 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFG 218
Db 197 KKLICVTEVFMTSTMTSTETEPFVENKAAFKNEAAGFG 234
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RESULT 10

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; Sequence 201, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
```

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match          100.0%; Score 1125; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 7,7e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TRLLVQGSRLAEELSIQVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db      17  TRLLVQGSRLAEELSIQVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 76
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QY      61  ALKASFETCSYGVWGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db      77  ALKASFETCSYGVWGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136
QY      121 NSCIPEIITTKDPIENTQTATQTTFEIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db      137 NSCIPEIITTKDPIENTQTATQTTFEIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 196
QY      181 KKLICVTEVFMTSTMSTETEPFVENKAAAFKNEAAGFG 218
Db      197 KKLICVTEVFMTSTMSTETEPFVENKAAAFKNEAAGFG 234

RESULT 11.
US-09-949-016-7765
; Sequence 7765: Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7765
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7765

Query Match          100.0%; Score 1125; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 8.5e-114;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TRLLVQGSRLAEELSIQVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 60
Db      39  TRLLVQGSRLAEELSIQVSCRMIGITLVSKKANQQLNFTFEAKACRLGLSLAGKQVET 98
QY      61  ALKASFETCSYGVWGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
Db      99  ALKASFETCSYGVWGDGFVVISRISPNPKGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 158
QY      121 NSCIPEIITTKDPIENTQTATQTTFEIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 180
Db      159 NSCIPEIITTKDPIENTQTATQTTFEIVSDSYVASPYSTIPAPTTTPAPASTSIPRR 218
QY      181 KKLICVTEVFMTSTMSTETEPFVENKAAAFKNEAAGFG 218
Db      219 KKLICVTEVFMTSTMSTETEPFVENKAAAFKNEAAGFG 256

RESULT 12
US-08-892-880-2
; Sequence 2, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
```

CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 322 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-892-880-2

Query Match 99.5%; Score 1119; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 3.5e-113;
Matches 217; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TRLLVQGSRLABELSIQVSCRMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVET 60
DB 17 TRLLVQGSRLABELSIQVSCRMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVET 76

QY 61 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
DB 77 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 136

QY 121 NSCIPEIITTKDPIFNTOQTATQTFEIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPIRR 180
DB 137 NSCIPEIITTKDPIFNTOQTATQTFEIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPIRR 196

QY 181 KKLICVTEVFMEITSTMSTETEPFVENKAAFKNEAAGFG 218
DB 197 KKLICVTEVFMEITSTMSTETEPFVENKAAFKNEAAGFG 234

RESULT 13
US-09-724-864-60
Sequence 60, Application US/09724864
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Murison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.1050U1
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
PRIOR FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60
LENGTH: 318
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-60

Query Match 59.5%; Score 669; DB 3; Length 318;
Best Local Similarity 61.0%; Pred. No. 2.7e-64;
Matches 133; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

QY 1 TRLLVQGSRLABELSIQVSCRMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVET 60
DB 17 TRHPVQGADLVQDLISLIS-TCRIMGVALVGRNKNPOMNFTFEACRMLGLTILASRDQVES 75

QY 61 ALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 120
DB 76 AOKSGFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWT 135

QY 121 NSCIPEIITTKDPIFNTOQTATQTFEIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPIRR 180
DB 136 NSCIPEIITTKDPIFNTOQTATQTFEIVSDSTYSVASPYSTIPAPTTTPPAPASTSIPIRR 192

QY 181 KKLICVTEVFMEITSTMSTETEPFVENKAAFKNEAAGFG 218
DB 193 TKKICITEVYTPITMATETEAFAVSGAFAFKNEAAGFG 230

RESULT 14
US-08-892-880-3
Sequence 3, Application US/08892880
Patent No. 5942417
GENERAL INFORMATION:
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK J.
TITLE OF INVENTION: CD44-LIKE PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/892,880
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 60/021,762
FILING DATE: 15-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0490001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-892-880-3

Query Match 19.0%; Score 213.5; DB 2; Length 339;
Best Local Similarity 32.1%; Pred. No. 9.6e-15;
Matches 51; Conservative 25; Mismatches 76; Indels 7; Gaps 3;

QY 4 LVQGSRLABELSIQVSCRMGITLVSKKANQQLNFTFEAKACRLGLSLAGKDOVETALK 63

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GenCore version 5.1.6
OM protein - protein search, using sw model
Run on: October 5, 2005, 17:07:32 ; Search time 93.6593 Seconds
(without alignments)
900.218 Million cell updates/sec

Title: US-10-063-510-6_COPY_17_234
Perfect score: 1125
Sequence: 1 TRLLVQSLRABELSIQVSC.....ETPEPVENKAAPKNEAGFG 218
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Database :
Listing first 1500 summaries
Maximum Match 100%
1: Geneseqp16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| No. | Score | Match | Length | DB | ID | Description |
|-----------------------|---|----------------------------|--------|-------------|----|-------------|
| RESULT 1 | | | | | | |
| ID | AAB34702 | standard; protein; 250 AA. | | | | |
| DE | Human secreted protein encoded by DNA clone vb28 1. | | | | | |
| PN | WO200055375-A1. | | | | | |
| PD | 21-SEP-2000. | | | | | |
| PA | (ALPH-) ALPHAGENE INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 3; | Length 250; | | |
| Best Local Similarity | 100.0%; | Pred. No. 4.5e-102; | | | | |
| RESULT 2 | | | | | | |
| ID | AAV13379 | standard; protein; 322 AA. | | | | |
| DE | Amino acid sequence of protein PRO263. | | | | | |
| PN | WO9914328-A2. | | | | | |
| PD | 25-MAR-1999. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 2; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 3 | | | | | | |
| ID | AAV87287 | standard; protein; 322 AA. | | | | |
| DE | Human signal peptide containing protein HSPP-64 SEQ ID NO:64. | | | | | |
| PN | WO200000610-A2. | | | | | |
| PD | 06-JAN-2000. | | | | | |
| PA | (INCY-) INCYTE PHARM INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 3; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 4 | | | | | | |
| ID | ADC78521 | standard; protein; 322 AA. | | | | |
| DE | Human PRO263 protein. | | | | | |
| PN | WO200015796-A2. | | | | | |
| PD | 23-MAR-2000. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 3; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 5 | | | | | | |
| ID | AAB80247 | standard; protein; 322 AA. | | | | |
| DE | Human PRO263 protein. | | | | | |
| PN | WO200104311-A1. | | | | | |
| PD | 18-JAN-2001. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 4; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 6 | | | | | | |
| ID | AAB87528 | standard; protein; 322 AA. | | | | |

| | | | | | | |
|-----------------------|--|----------------------------|-------|-------------|--|--|
| DE | Human PRO263. | | | | | |
| PN | WO200116318-A2. | | | | | |
| PD | 08-MAR-2001. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 4; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 7 | | | | | | |
| ID | AAB88391 | standard; protein; 322 AA. | | | | |
| DE | Human membrane or secretory protein clone PSEC0135. | | | | | |
| PN | EP1067182-A2. | | | | | |
| PD | 10-JAN-2001. | | | | | |
| PA | (HELL-) HELIX RES INST. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 4; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 8 | | | | | | |
| ID | ABG95853 | standard; protein; 322 AA. | | | | |
| DE | Human secreted/transmembrane protein PRO263. | | | | | |
| PN | US200219130-A1. | | | | | |
| PD | 29-AUG-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 5; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 9 | | | | | | |
| ID | ABB84832 | standard; protein; 322 AA. | | | | |
| DE | Human PRO263 protein sequence SEQ ID NO:32. | | | | | |
| PN | WO200200690-A2. | | | | | |
| PD | 03-JAN-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 5; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 10 | | | | | | |
| ID | ABB95438 | standard; protein; 322 AA. | | | | |
| DE | Human angiogenesis related protein PRO263 SEQ ID NO: 32. | | | | | |
| PN | WO200208284-A2. | | | | | |
| PD | 31-JAN-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| PA | (BAKE/) BAKER K P. | | | | | |
| PA | (FERR/) FERRARA N. | | | | | |
| PA | (GERB/) GERBER H. | | | | | |
| PA | (GERR/) GERRITSEN M E. | | | | | |
| PA | (GODD/) GODDARD A. | | | | | |
| PA | (GODO/) GODOWSKI P J. | | | | | |
| PA | (GURN/) GURNEY A L. | | | | | |
| PA | (HILL/) HILLAN K J. | | | | | |
| PA | (MARS/) MARSTERS S A. | | | | | |
| PA | (PANT/) PAN J. | | | | | |
| PA | (PAON/) PAONI N F. | | | | | |
| PA | (STEP/) STEPHAN J F. | | | | | |
| PA | (WATA/) WATANABE C K. | | | | | |
| PA | (WILL/) WILLIAMS P M. | | | | | |
| PA | (WOOD/) WOOD W I. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 5; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 11 | | | | | | |
| ID | ABU71625 | standard; protein; 322 AA. | | | | |
| DE | Human PRO polypeptide #36. | | | | | |
| PN | US2002146709-A1. | | | | | |
| PD | 10-OCT-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 6; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 12 | | | | | | |
| ID | ABU71480 | standard; protein; 322 AA. | | | | |
| DE | Human PRO polypeptide #36. | | | | | |
| PN | US2002192859-A1. | | | | | |
| PD | 19-DEC-2002. | | | | | |
| PA | (GETH) GENENTECH INC. | | | | | |
| Query Match | 100.0%; | Score 1125; | DB 6; | Length 322; | | |
| Best Local Similarity | 100.0%; | Pred. No. 6.3e-102; | | | | |
| RESULT 13 | | | | | | |
| ID | ABU71926 | standard; protein; 322 AA. | | | | |
| DE | Human secreted/transmembrane protein PRO263. | | | | | |
| PN | US2003003530-A1. | | | | | |

PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 14
ID ABO01809 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 15
ID ABU09078 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 16
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 17
ID ABU71954 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 18
ID ABU54382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 19
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 20
ID ABU71508 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 21
ID ABU7289 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 22
ID ABU90962 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 23
ID ABO27283 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 24
ID ABU64534 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 25
ID ABU67380 standard; protein; 322 AA.
DE Human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 26
ID ABU92478 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 27
ID ABO14900 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 28
ID ABU81148 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 29
ID ABO53263 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 30
ID ABU98265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 31
ID ABU9270 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 32
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 33
ID ABO69657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 34
ID ABO96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 35
ID ABO72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 36
ID ABO14839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 37
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 38
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 39
ID ABO44241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 40
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 41
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 42
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 43
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 44
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 45
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 46
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 47
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 48
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 49
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 50
ID ADA00337 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 51
ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 52
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 53
ID ADA41958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 54
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 55
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 56
ID AB017590 standard; protein; 322 AA.
DE Human PRO Polypeptide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 57
ID ADB85579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 58
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 59
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 60
ID ADB68258 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 61
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 62
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 63
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 64
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 65
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 66
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 67
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

RESULT 68
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

DE Human secreted/transmembrane protein, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 69
ID ADC28933 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 70
ID ADC40818 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 71
ID ADC19475 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 72
ID ADC06962 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 73
ID ADC17141 standard; protein; 322 AA.
DE Mammalian PRO polypeptide (SeqID 6).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 74
ID ADC33923 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 75
ID ADC12993 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 76
ID ADC14839 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 77
ID ADC52334 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.

PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 78
ID ADC12445 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 79
ID ADD10321 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 80
ID ADD05000 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 81
ID ADD11281 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 82
ID ADD04006 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 83
ID ADD03582 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 84
ID ADD37074 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 85
ID ADD36010 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 86
ID ADE34834 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077583-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 87
ID ADG01011 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003078387-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 88
ID ADG08564 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 89
ID ADF95185 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 90
ID ADH24038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 91
ID ADH34064 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 92
ID ADH29897 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 93
ID ADH23868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 94
ID ADG85272 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 95
ID ADH24548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 96
ID ADH37404 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 97
ID ADH01993 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 98
ID ADH37574 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 99
ID ADG85612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 100
ID ADH24208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 101
ID ADH38502 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 102
ID ADG83623 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 103
ID ADH29431 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 104
ID ADH27547 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 105
ID ADH37744 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 106
ID ADH37921 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 107
ID ADH57341 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 108
ID ADH59317 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 109
ID ADH53483 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 110
ID ADH53653 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 111
ID ADH51989 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 112
ID ADH49844 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 113
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 114
ID ADH90147 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 115
ID ADI25524 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 116
ID ADH97698 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 117
ID ADI38096 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 118
ID ADI03546 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 119
ID ADI11903 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181686-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 120
ID ADH89977 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 121
ID ADH98378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 122
ID ADI11053 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 123
ID ADI25354 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

DE Human PRO polypeptide #3.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 142
ID ADI05370 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 143
ID ADH79442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 144
ID ADI19399 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 145
ID ADI05200 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 146
ID ADH79612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 147
ID ADI01438 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 148
ID ADI01608 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 149
ID ADI01778 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 150
ID ADH7982 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 151
ID ADI04600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 152
ID ADI02736 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 153
ID ADH78055 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 154
ID ADI25694 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 155
ID ADI25864 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 156
ID ADK65376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 157
ID ADH98718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 158
ID ADH79959 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 159
ID ADJ26364 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054349-A1.

PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 160
ID ADL93690 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 161
ID ADC52144 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003130483-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 162
ID ADE79279 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 163
ID ADE79703 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 164
ID ADE73379 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 165
ID ADE41282 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 166
ID ADE71444 standard; protein; 322 AA.
DE Human PDEBC Incyte 3044710CD1.
PN US2003124543-A1.
PD 03-JUL-2003.
PA (STUA/) STUART S G.
PA (STRE/) STREETER D G.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 167
ID ADE73914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 168
ID ADE99468 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211576-A1.

PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 169
ID ADE98587 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 170
ID ADE99014 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 171
ID ADG40484 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 172
ID ADF73878 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 173
ID ADF73454 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 174
ID ADH06576 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180852-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 175
ID ADH06406 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180853-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 176
ID ADG68827 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 177
ID ADG68827 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180855-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 177
ID ADH2717 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180912-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 178
ID ADH25058 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 179
ID ADH33690 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 180
ID ADG92297 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 181
ID ADH02333 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 182
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 183
ID ADG69337 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 184
ID ADH39158 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 185
ID ADG92724 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 186
ID ADG8398 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 187
ID ADG85442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 188
ID ADH06236 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 189
ID ADH30066 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 190
ID ADH24378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 191
ID ADG69507 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 192
ID ADH07770 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 193
ID ADG85782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 194
ID ADH39328 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 195
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;

ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 196
ID ADH33860 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 197
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 198
ID ADG69677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 199
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 200
ID ADG69167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 201
ID ADG85952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 202
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 203
ID ADH39505 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 204
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 205
ID ADG68997 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 206
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 207
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 208
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 209
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 210
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 211
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 212
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 213
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.

PN US2003224984-A1.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 214
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 215
ID ADH52159 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 216
ID ADH59913 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 217
ID ADH49525 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 218
ID ADH06941 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 219
ID ADH90487 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 220
ID ADI11223 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 221
ID ADI18683 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 222
ID ADH98888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 223
ID ADI65403 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 224
ID ADI02118 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 225
ID ADH90657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 226
ID ADI37666 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 227
ID ADH97462 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 228
ID ADI65830 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 229
ID ADH60573 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.

PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 230
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 231
ID ADL08823 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 232
ID ADJ99532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 233
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 234
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 235
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 236
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 237
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 238
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 239
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 240
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 241
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 242
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 243
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 244
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 245
ID ADO06236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 246
ID ADRI1088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 247
ID ADRI1997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.

PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERE/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERE/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 248
ID ADT03673 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 249
ID ADS74636 standard; protein; 322 AA.
DE Human secreted/transmembrane protein #40.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERE/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERE/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1125; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 6.3e-102;
RESULT 250
ID ABB11979 standard; peptide; 344 AA.
DE Human PRO263 homologue, SEQ ID NO:2349.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1125; DB 4; Length 344;
Best Local Similarity 100.0%; Pred. No. 6.9e-102;
RESULT 251
ID ADR41495 standard; protein; 344 AA.
DE Human CD-like molecule HEMFC27, SEQ ID NO:294.
PN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 1125; DB 5; Length 344;
Best Local Similarity 100.0%; Pred. No. 6.9e-102;
RESULT 252
ID AAW56249 standard; protein; 322 AA.
DE Amino acid sequence of a CD44-like protein.
PN WO9806839-A1.
PD 19-FEB-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.5%; Score 1119; DB 2; Length 322;
Best Local Similarity 99.5%; Pred. No. 2.5e-101;
RESULT 253
ID ABB90289 standard; protein; 322 AA.
DE Human polypeptide SEQ ID NO 2665.
PN WO200130304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 99.5%; Score 1119; DB 5; Length 322;
Best Local Similarity 99.5%; Pred. No. 2.5e-101;
RESULT 254
ID ADN05866 standard; protein; 322 AA.
DE Antipsoriatic protein sequence #1096.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 98.3%; Score 1106; DB 8; Length 322;
Best Local Similarity 98.6%; Pred. No. 4.7e-100;
RESULT 255
ID ADQ21089 standard; protein; 322 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 3909.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 98.3%; Score 1106; DB 8; Length 322;
Best Local Similarity 98.6%; Pred. No. 4.7e-100;
RESULT 256
ID ABU69126 standard; protein; 297 AA.
DE Human NOVX polypeptide #1.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 87.1%; Score 979.5; DB 6; Length 297;
Best Local Similarity 88.5%; Pred. No. 1.2e-87;
RESULT 257
ID ADO08255 standard; protein; 297 AA.
DE Human NOVX polypeptide #1.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.

PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 87.1%; Score 979.5; DB 8; Length 297;
Best Local Similarity 88.5%; Pred. No. 1.2e-87;
RESULT 258
ID ABB72376 standard; protein; 255 AA.
DE Murine protein isolated from skin cells SEQ ID NO: 700.
PN WO200190357-A1.
PD 29-NOV-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 59.5%; Score 669; DB 5; Length 255;
Best Local Similarity 61.0%; Pred. No. 3.4e-57;
RESULT 259
ID AAE05364 standard; protein; 318 AA.
DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
PN WO200148192-A1.
PD 05-JUL-2001.
PA (GENE-) GENESIS RES & DEV CORP LTD.
Query Match 59.5%; Score 669; DB 4; Length 318;
Best Local Similarity 61.0%; Pred. No. 4.6e-57;
RESULT 260
ID AAY12323 standard; protein; 116 AA.
DE Human 5' EST secreted protein SEQ ID NO:354.
PN WO9906548-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 45.3%; Score 510; DB 2; Length 116;
Best Local Similarity 100.0%; Pred. No. 5.3e-42;
RESULT 261
ID ABB81033 standard; protein; 364 AA.
DE Rat glycoprotein CD44 polypeptide.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 19.0%; Score 213.5; DB 5; Length 364;
Best Local Similarity 32.1%; Pred. No. 3.6e-12;
RESULT 262
ID AAR14768 standard; protein; 503 AA.
DE Metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Query Match 19.0%; Score 213.5; DB 2; Length 503;
Best Local Similarity 32.1%; Pred. No. 5.6e-12;
RESULT 263
ID ADE57911 standard; protein; 503 AA.
DE Rat Protein P26051, SEQ ID NO 3777.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 19.0%; Score 213.5; DB 7; Length 503;
Best Local Similarity 32.1%; Pred. No. 5.6e-12;
RESULT 264
ID ABU04619 standard; protein; 668 AA.
DE Human expressed protein tag (EPT) #1285.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.5%; Score 208.5; DB 6; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.5e-11;
RESULT 265
ID ADQ39384 standard; protein; 668 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.5%; Score 208.5; DB 8; Length 668;
Best Local Similarity 29.3%; Pred. No. 2.5e-11;
RESULT 266
ID AAR07355 standard; protein; 362 AA.
DE B7 adhesion receptor.
PN WO9011365-A.
PD 04-OCT-1990.
PA (HUTC-) HUTCHINSON F CANCER.
Query Match 18.1%; Score 203.5; DB 2; Length 362;
Best Local Similarity 27.3%; Pred. No. 3.5e-11;
RESULT 267
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 268
ID ABU04616 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1282.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 269
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 18.0%; Score 203; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 270
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 18.0%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 271
ID ADQ39391 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.0%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 272
ID ADR67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 18.0%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-10;
RESULT 273
ID ABU04618 standard; protein; 675 AA.
DE Human expressed protein tag (EPT) #1284.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.

Query Match 18.0%; Score 202; DB 6; Length 675;
Best Local Similarity 26.0%; Pred. No. 1.1e-10;
RESULT 274
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 202; DB 6; Length 691;
Best Local Similarity 26.0%; Pred. No. 1.2e-10;
RESULT 275
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.0%; Score 202; DB 8; Length 691;
Best Local Similarity 26.0%; Pred. No. 1.2e-10;
RESULT 276
ID ABU04620 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 277
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 18.0%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 278
ID ADN95511 standard; protein; 742 AA.
DE Human BEC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN-) LICENTIA LTD.
Query Match 18.0%; Score 202; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 279
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 280
ID ADQ55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 281
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 282
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.

Query Match 18.0%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1.3e-10;
RESULT 283
ID ABP72424 standard; protein; 608 AA.
DE Human CD44 variant CD44VRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.8%; Score 200.5; DB 6; Length 608;
Best Local Similarity 25.2%; Pred. No. 1.4e-10;
RESULT 284
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.8%; Score 200.5; DB 7; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 285
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 17.8%; Score 200.5; DB 4; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 286
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.8%; Score 200.5; DB 6; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 287
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.8%; Score 200.5; DB 7; Length 700;
Best Local Similarity 25.2%; Pred. No. 1.7e-10;
RESULT 288
ID AAR20817 standard; protein; 493 AA.
DE Epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GHO) GEN HOSPITAL CORP.
Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.3e-10;
RESULT 289
ID AAR91445 standard; protein; 493 AA.
DE Human epithelial CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GHO) GEN HOSPITAL CORP.
Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.3e-10;
RESULT 290
ID AAW80454 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GHO) GEN HOSPITAL CORP.
Query Match 17.7%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 1.3e-10;
RESULT 291
ID AAW89151 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5849898-A.
PD 15-DEC-1998.

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| PA (GEHO) GEN HOSPITAL CORP. Query Match 17.7%; Score 199.5; DB 2; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 292 ID AAY96140 standard; protein; 493 AA. DE Human epithelial CD44. PN US6111093-A. PD 29-AUG-2000. PA (GEHO) GEN HOSPITAL CORP. Query Match 17.7%; Score 199.5; DB 3; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 293 ID AAU02449 standard; protein; 493 AA. DE Human epithelial antigen CD44 polypeptide. PN US6218525-B1. PD 17-APR-2001. PA (GEHO) GEN HOSPITAL CORP. Query Match 17.7%; Score 199.5; DB 4; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 294 ID ABU04637 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1303. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 295 ID ABU04627 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1293. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 296 ID ABU04639 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1305. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 297 ID ABU04631 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1297. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 298 ID ABU04633 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1299. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 299 ID ABU04635 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1301. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 300 ID ABU04613 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1279. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. | Query Match 17.7%; Score 199.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 301 ID ADO49375 standard; protein; 493 AA. DE Human CD44 #2. PN US2004072283-A1. PD 15-APR-2004. PA (SEED/) SEED B. PA (ALIE/) ALLEN J. PA (ARUF/) ARUFFO A. PA (CAME/) CAMERINI D. PA (LAUF/) LAUFFER L. PA (OQUE/) OQUENDO C. PA (SINK/) SIMMONS D. PA (STAM/) STAMENKOVIC I. PA (STEN/) STENGELIN S. PA (AMIO/) AMIOT M. Query Match 17.7%; Score 199.5; DB 8; Length 493; Best Local Similarity 23.6%; Pred. No. 1.3e-10; RESULT 302 ID ABU79109 standard; protein; 365 AA. DE CD44 protein. PN US2002177551-A1. PD 28-NOV-2002. PA (TERM/) TERMAN D S. Query Match 17.6%; Score 198.5; DB 6; Length 365; Best Local Similarity 31.8%; Pred. No. 1.1e-10; RESULT 303 ID ADF43353 standard; protein; 365 AA. DE CD44 receptor polypeptide seq id 73. PN US2003157113-A1. PD 21-AUG-2003. PA (TERM/) TERMAN D S. Query Match 17.6%; Score 198.5; DB 7; Length 365; Best Local Similarity 31.8%; Pred. No. 1.1e-10; RESULT 304 ID AAU99123 standard; protein; 493 AA. DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein. PN WO200244342-A2. PD 06-JUN-2002. PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC. Query Match 17.6%; Score 198.5; DB 5; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 305 ID ABU04623 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1289. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.6%; Score 198.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 306 ID ABU04612 standard; protein; 493 AA. DE Human expressed protein tag (EPT) #1278. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. Query Match 17.6%; Score 198.5; DB 6; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 307 ID ADL93507 standard; protein; 493 AA. DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2. PN WO2004024750-A2. PD 25-MAR-2004. PA (DYAX-) DYAX CORP. Query Match 17.6%; Score 198.5; DB 8; Length 493; Best Local Similarity 23.6%; Pred. No. 1.6e-10; RESULT 308 ID ABU04617 standard; protein; 425 AA. DE Human expressed protein tag (EPT) #1283. PN WO200278524-A2. PD 10-OCT-2002. PA (ZYCO-) ZYCOS INC. |
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Query Match 17.6%; Score 198; DB 6; Length 425;
Best Local Similarity 24.4%; Pred. No. 1.5e-10;
RESULT 309
ID AAR20816 standard; protein; 361 AA.
DE Haematopoietic CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 310
ID AAR91444 standard; protein; 361 AA.
DE Human haematopoietic CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 311
ID AAW80453 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US830731-A.
PD 03-NOV-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 312
ID AAW86200 standard; protein; 361 AA.
DE Human CD44 antigen (membrane form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 2; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 313
ID AAY9851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 17.5%; Score 197; DB 3; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 314
ID AAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US6111091-A.
PD 29-AUG-2000.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 3; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 315
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 17.5%; Score 197; DB 4; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 316
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 317
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 318
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 319
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 320
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 321
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1294.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 322
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 323
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 324
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 325
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 326
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALIE/) ALLEN J.
PA (ARUF/) ARUFFO A.

PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAN/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 17.5%; Score 197; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.5e-10;
RESULT 327
ID AAY97650 standard; protein; 431 AA.
DE CD44HextraFASm/cyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 17.5%; Score 197; DB 4; Length 431;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 328
ID ABU04641 standard; protein; 431 AA.
DE Human expressed protein tag (EPT) #1307.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 431;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 329
ID AAY97651 standard; protein; 436 AA.
DE CD44Hextra/cmfAScyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 17.5%; Score 197; DB 4; Length 436;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 330
ID ABU04642 standard; protein; 436 AA.
DE Human expressed protein tag (EPT) #1308.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 436;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 331
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 3.8e-10;
RESULT 332
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 3.8e-10;
RESULT 333
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 17.5%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.9e-10;
RESULT 334
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.5%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.9e-10;
RESULT 335
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 336
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 337
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 338
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.5%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 4.1e-10;
RESULT 339
ID ADI60182 standard; protein; 261 AA.
DE Secreted polypeptide #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HVSE-) HVSEQ INC.
Query Match 17.4%; Score 196; DB 7; Length 261;
Best Local Similarity 30.9%; Pred. No. 1.2e-10;
RESULT 340
ID ABU04611 standard; protein; 293 AA.
DE Human expressed protein tag (EPT) #1277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 293;
Best Local Similarity 30.9%; Pred. No. 1.4e-10;
RESULT 341
ID ABU04624 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1290.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.4e-10;
RESULT 342
ID ABU04646 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1312.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1.4e-10;
RESULT 343
ID ADH18898 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CAECW-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 17.4%; Score 196; DB 8; Length 330;
Best Local Similarity 30.9%; Pred. No. 1.7e-10;
RESULT 344

ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1288.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 345
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 17.4%; Score 196; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 346
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 17.4%; Score 196; DB 7; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 347
ID ADL93508 standard; protein; 361 AA.
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 17.4%; Score 196; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 348
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 361;
Best Local Similarity 30.9%; Pred. No. 1.9e-10;
RESULT 349
ID ABU04615 standard; protein; 395 AA.
DE Human expressed protein tag (EPT) #1281.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.4%; Score 196; DB 6; Length 395;
Best Local Similarity 30.9%; Pred. No. 2.1e-10;
RESULT 350
ID ADQ39389 standard; protein; 395 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 395;
Best Local Similarity 30.9%; Pred. No. 2.1e-10;
RESULT 351
ID ADQ39382 standard; protein; 425 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 425;
Best Local Similarity 30.9%; Pred. No. 2.4e-10;
RESULT 352
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 17.4%; Score 196; DB 8; Length 493;
Best Local Similarity 30.9%; Pred. No. 2.9e-10;
RESULT 353

ID AAY12853 standard; protein; 58 AA.
DE Human 5' EST secreted protein SEQ ID NO:443.
PN WO9906549-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 17.3%; Score 195; DB 2; Length 58;
Best Local Similarity 97.6%; Pred. No. 2.1e-11;
RESULT 354
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.3%; Score 194.5; DB 4; Length 742;
Best Local Similarity 25.4%; Pred. No. 7e-10;
RESULT 355
ID AAM48306 standard; protein; 194 AA.
DE Protein R2 SEQ ID 29.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.2%; Score 194; DB 5; Length 194;
Best Local Similarity 30.8%; Pred. No. 1.3e-10;
RESULT 356
ID AAM48307 standard; protein; 200 AA.
DE Protein R3 SEQ ID 30.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.2%; Score 194; DB 5; Length 200;
Best Local Similarity 30.8%; Pred. No. 1.4e-10;
RESULT 357
ID AAM48308 standard; protein; 273 AA.
DE Protein R4 SEQ ID 31.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 17.2%; Score 194; DB 5; Length 273;
Best Local Similarity 30.8%; Pred. No. 2.1e-10;
RESULT 358
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.2%; Score 194; DB 6; Length 361;
Best Local Similarity 30.9%; Pred. No. 3e-10;
RESULT 359
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 1.2e-09;
RESULT 360
ID ABU04652 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1318.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 1.2e-09;
RESULT 361
ID ABU04648 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1314.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 4e-10;
RESULT 362
ID ABU04606 standard; protein; 271 AA.

DE Human expressed protein tag (EPT) #1272.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 4e-10;
RESULT 363
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 338;
Best Local Similarity 31.5%; Pred. No. 5.4e-10;
RESULT 364
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 338;
Best Local Similarity 31.5%; Pred. No. 5.4e-10;
RESULT 365
ID ABU04651 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1317.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 8.4e-10;
RESULT 366
ID ABU04603 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1269.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 17.0%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 8.4e-10;
RESULT 367
ID AAM48305 standard; protein; 170 AA.
DE Protein R1 SEQ ID 28.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 16.7%; Score 188; DB 5; Length 170;
Best Local Similarity 35.7%; Pred. No. 4.3e-10;
RESULT 368
ID ABP73148 standard; protein; 112 AA.
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.6%; Score 187; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 3.1e-10;
RESULT 369
ID ABP73150 standard; protein; 113 AA.
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.6%; Score 186.5; DB 6; Length 113;
Best Local Similarity 36.3%; Pred. No. 3.5e-10;
RESULT 370
ID ABP73151 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
Query Match 15.1%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-09;
PA (PAEL/) PAELL T.
Query Match 16.4%; Score 185; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 4.8e-10;
RESULT 371
ID ABP73152 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.3%; Score 183; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 7.6e-10;
RESULT 372
ID ABP73149 standard; protein; 112 AA.
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.2%; Score 182; DB 6; Length 112;
Best Local Similarity 34.2%; Pred. No. 9.5e-10;
RESULT 373
ID ABP73153 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 16.1%; Score 181; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 1.2e-09;
RESULT 374
ID AAY12170 standard; protein; 69 AA.
DE Human 5' EST secreted protein SEQ ID NO: 483.
PN WO9906554-A2.
PD 11-FEB-1999.
PA (GEST) GENSET.
Query Match 15.9%; Score 179; DB 2; Length 69;
Best Local Similarity 95.0%; Pred. No. 9.9e-10;
RESULT 375
ID ABG17067 standard; protein; 920 AA.
DE Novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 15.6%; Score 175.5; DB 4; Length 920;
Best Local Similarity 25.9%; Pred. No. 6.9e-08;
RESULT 376
ID ADI60410 standard; protein; 920 AA.
DE Secreted polypeptide encoded by gene splice variant #46.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 15.6%; Score 175.5; DB 7; Length 920;
Best Local Similarity 25.9%; Pred. No. 6.9e-08;
RESULT 377
ID AAM28056 standard; protein; 34 AA.
DE Peptide #2093 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 15.1%; Score 170; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-09;
RESULT 378
ID ABG37308 standard; peptide; 34 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 15.1%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e-09;

RESULT 379
ID ADB64426 standard; protein; 510 AA.
DE Human protein encoded by clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 13.3%; Score 150; DB 7; Length 510;
Best Local Similarity 23.6%; Pred. No. 1e-05;
RESULT 380
ID ABP73154 standard; protein; 80 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 13.2%; Score 148.5; DB 6; Length 80;
Best Local Similarity 37.0%; Pred. No. 1.2e-06;
RESULT 381
ID ADP07712 standard; protein; 162 AA.
DE Human secreted protein; seq id 195.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 12.9%; Score 145; DB 8; Length 162;
Best Local Similarity 33.0%; Pred. No. 6.8e-06;
RESULT 382
ID ADM80807 standard; protein; 237 AA.
DE Human CADECM-36 protein SEQ ID NO:36.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 12.9%; Score 145; DB 8; Length 237;
Best Local Similarity 33.0%; Pred. No. 1.1e-05;
RESULT 383
ID AAR36044 standard; protein; 277 AA.
DE Tumour necrosis factor-induced glycoprotein TSG-6.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 384
ID AAW13654 standard; protein; 277 AA.
DE Tumour necrosis factor-stimulated gene-6 protein.
PN WO9704075-A1.
PD 06-FEB-1997.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 385
ID AAW84087 standard; protein; 277 AA.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
PN US5846763-A.
PD 08-DEC-1998.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 386
ID AAE02361 standard; protein; 277 AA.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.
PN US6210905-B1.
PD 03-APR-2001.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 4; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 387
ID ABG70870 standard; protein; 277 AA.
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UINY-) UNIV NEW YORK STATE.
Query Match 12.9%; Score 145; DB 5; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
ID ABR58556 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:213.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 389
ID ABU56653 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 390
ID ADE25781 standard; protein; 277 AA.
DE Human protein differentially expressed in foam cells #58.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 12.9%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 391
ID ADN39919 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 392
ID ADN38974 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 12.9%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 393
ID ADQ21506 standard; protein; 277 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4326.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 12.9%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 394
ID ADR51534 standard; protein; 277 AA.
DE Human lipopolysaccharide-sensitive polypeptide #14.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 12.9%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 1.4e-05;
RESULT 395
ID ADK67822 standard; protein; 2626 AA.
DE Human BRCC300 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 12.9%; Score 145; DB 8; Length 2626;
Best Local Similarity 33.0%; Pred. No. 0.00028;
RESULT 396
ID ADS85081 standard; protein; 275 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID83.
PN WO2004031386-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.

Query Match 12.8%; Score 144; DB 8; Length 275;
Best Local Similarity 33.0%; Pred. No. 1.7e-05;
RESULT 397
ID ABM84174 standard; protein; 2285 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.8%; Score 132.5; DB 8; Length 2285;
Best Local Similarity 27.4%; Pred. No. 0.0039;
RESULT 398
ID ABM84173 standard; protein; 2384 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.8%; Score 132.5; DB 8; Length 2384;
Best Local Similarity 27.4%; Pred. No. 0.0042;
RESULT 399
ID ABP72603 standard; protein; 883 AA.
DE Rat mutant brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (WATT/) MATTHEWS R T.
Query Match 11.7%; Score 131.5; DB 6; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0014;
RESULT 400
ID ADK67779 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match 11.7%; Score 131.5; DB 8; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0014;
RESULT 401
ID AAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 402
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.6%; Score 130.5; DB 6; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 403
ID ADB90787 standard; protein; 883 AA.
DE Mouse brevicin protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 404
ID ADF71522 standard; protein; 883 AA.
DE Murine brevidin protein.

PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 405
ID ADQ10338 standard; protein; 883 AA.
DE Human polypeptide #172.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.6%; Score 130.5; DB 8; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0017;
RESULT 406
ID AAM47675 standard; protein; 1431 AA.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 11.5%; Score 129; DB 5; Length 1431;
Best Local Similarity 32.3%; Pred. No. 0.0047;
RESULT 407
ID ABG72498 standard; protein; 1431 AA.
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 11.5%; Score 129; DB 6; Length 1431;
Best Local Similarity 32.3%; Pred. No. 0.0047;
RESULT 408
ID AAB08023 standard; protein; 95 AA.
DE The domain of hyaluronic acid which interacts with CD44.
PN WO200047163-A2.
PD 17-AUG-2000.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 11.4%; Score 128.5; DB 3; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00014;
RESULT 409
ID ABU04625 standard; protein; 95 AA.
DE Human expressed protein tag (EPT) #1291.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.4%; Score 128.5; DB 6; Length 95;
Best Local Similarity 28.7%; Pred. No. 0.00014;
RESULT 410
ID AAB61236 standard; protein; 649 AA.
DE Mature human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 4; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 411
ID ABO32673 standard; protein; 649 AA.
DE Secreted polypeptide-related protein #74.
PN US200302279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.3%; Score 127.5; DB 6; Length 649;

Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 412
ID ADB90778 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 413
ID ADF71511 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 414
ID ADQ10331 standard; protein; 649 AA.
DE Human polypeptide #167.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 8; Length 649;
Best Local Similarity 24.7%; Pred. No. 0.0023;
RESULT 415
ID AAB61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 4; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 416
ID ABO32671 standard; protein; 671 AA.
DE Secreted polypeptide-related protein #73.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 11.3%; Score 127.5; DB 6; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 417
ID ADB90776 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 418
ID ADF71511 standard; protein; 671 AA.
DE Human TANGO 332.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 11.3%; Score 127.5; DB 7; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 419
ID ADQ10329 standard; protein; 671 AA.
DE Human polypeptide #165.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.

Query Match 11.3%; Score 127.5; DB 8; Length 671;
Best Local Similarity 24.7%; Pred. No. 0.0024;
RESULT 420
ID ABM83434 standard; protein; 761 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 761;
Best Local Similarity 24.7%; Pred. No. 0.0028;
RESULT 421
ID ADH1892 standard; protein; 806 AA.
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 806;
Best Local Similarity 24.7%; Pred. No. 0.003;
RESULT 422
ID ABM83431 standard; protein; 825 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 825;
Best Local Similarity 24.7%; Pred. No. 0.0031;
RESULT 423
ID ABM83430 standard; protein; 863 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.3%; Score 127.5; DB 8; Length 863;
Best Local Similarity 24.7%; Pred. No. 0.0033;
RESULT 424
ID ABP72604 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV VALE
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match 11.3%; Score 127.5; DB 6; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0034;
RESULT 425
ID ADE62581 standard; protein; 883 AA.
DE Rat Protein P55068, SEQ ID NO 8512.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 11.3%; Score 127.5; DB 7; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0034;
RESULT 426
ID ADK67782 standard; protein; 883 AA.
DE Rat glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV VALE.
Query Match 11.3%; Score 127.5; DB 8; Length 883;
Best Local Similarity 23.0%; Pred. No. 0.0034;
RESULT 427
ID AAY97583 standard; protein; 911 AA.
DE Human secreted protein PRO6018.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 4; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 428
ID ABG34055 standard; protein; 911 AA.
DE Human Pro peptide #26.
PN WO200224888-A2.

PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 5; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 429
ID ADI28032 standard; protein; 911 AA.
DE ECMCAD protein 6755002CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 11.3%; Score 127.5; DB 5; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 430
ID AAE30340 standard; protein; 911 AA.
DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 431
ID ADA01320 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 432
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 433
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 434
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 6; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 435
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 436
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 437
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 438
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 439
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 440
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 441
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 442
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 443
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 444
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 445
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 446
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

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Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 447
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 448
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 449
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 450
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 451
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 452
ID ADE06378 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 453
ID ADE38153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 454
ID ADD88269 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 455
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.

Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 456
ID ADF99405 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 457
ID ADG06498 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 458
ID ADG05449 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077741-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 459
ID ADG82450 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077744-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 460
ID ADN38942 standard; protein; 911 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match      11.3%; Score 127.5; DB 7; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 461
ID ADE51703 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 462
ID ADE51819 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 463
ID ADE37677 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 464
ID ADE37561 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match      11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 465
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 465
ID ADE95332 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 466
ID ADE38032 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 467
ID ADE76121 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 468
ID ADE39444 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 469
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 470
ID ADE39845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 471
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 472
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 473
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 474
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 475
ID ADE37916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 476
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 477
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096363-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 478
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 479
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 480
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 481
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 482
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 483
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
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ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 484
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 485
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 486
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 487
ID ADD88932 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 488
ID ADE19826 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 489
ID ADE77404 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 490
ID ADE65280 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 491
ID ADE39328 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 492
ID ADE38513 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 493
ID ADG11066 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 494
ID ADG10950 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 495
ID ADH31478 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 496
ID ADH38726 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 497
ID ADH29361 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 498
ID ADH23664 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 499
ID ADH26994 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 500
ID ADH38262 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 501
ID ADH26878 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.

PD US2003119134-A1.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 502
ID ADH38146 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 503
ID ADH38842 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 504
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 505
ID ADH40156 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 506
ID ADH40040 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 507
ID ADH31362 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 508
ID ADH29240 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 509
ID ADH49455 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 510
ID ADH51919 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119125-A1.

PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 511
ID ADH49774 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 512
ID ADH52375 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 513
ID ADH52491 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 514
ID ADH58488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 515
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 516
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 517
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 518
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 519
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 520
ID ADK67784 standard; protein; 911 AA.
DE Human glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYA) UNIV YALE.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 521
ID ABM80156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127.5; DB 8; Length 911;
Best Local Similarity 24.7%; Pred. No. 0.0036;
RESULT 522
ID ABR59557 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:214.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.3%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 523
ID ABUS6654 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #247.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.3%; Score 127; DB 6; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 524
ID ADN38976 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.3%; Score 127; DB 7; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 525
ID ADO24439 standard; protein; 277 AA.
DE Human PRO87335 protein SEQ ID NO:78.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 11.3%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 526
ID ADRI4117 standard; protein; 277 AA.
DE Human NF-kappaB pathway-associated protein SeqID118.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 11.3%; Score 127; DB 8; Length 277;
Best Local Similarity 30.7%; Pred. No. 0.00082;
RESULT 527
ID ADO24485 standard; protein; 277 AA.
DE Human PRO87343 protein SEQ ID NO:124.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 11.2%; Score 126; DB 8; Length 277;
Best Local Similarity 34.1%; Pred. No. 0.001;
RESULT 528
ID ADB65640 standard; protein; 482 AA.
DE Human protein encoded by clone THYWU20143230.
PN EP108459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 11.0%; Score 124; DB 7; Length 482;
Best Local Similarity 34.5%; Pred. No. 0.0034;
RESULT 529
ID ABR82200 standard; protein; 2570 AA.
DE Human CLEVER-1 protein SEQ ID NO:1.
PN WO2003057130-A2.
PD 17-JUL-2003.
PA (JALK/) JALKANEN S.
PA (IRJA/) IRJALA H.
PA (SALM/) SALMI M.
Query Match 11.0%; Score 124; DB 6; Length 2570;
Best Local Similarity 34.5%; Pred. No. 0.032;
RESULT 530
ID AAY93911 standard; protein; 457 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO2003039166-A1.
PD 06-JUL-2000.
PA (HUNA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 10.9%; Score 123; DB 3; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.004;
RESULT 531
ID ABR90349 standard; protein; 1082 AA.
DE Human polypeptide SEQ ID NO 2725.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 10.9%; Score 123; DB 5; Length 1082;
Best Local Similarity 33.3%; Pred. No. 0.012;
RESULT 532
ID AAY93910 standard; protein; 2157 AA.
DE A human hyaluronan-binding protein, designated WF-HABP.
PN WO2003039166-A1.
PD 06-JUL-2000.
PA (HUNA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match 10.9%; Score 123; DB 3; Length 2157;
Best Local Similarity 33.3%; Pred. No. 0.031;
RESULT 533
ID ABM80463 standard; protein; 2570 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 10.9%; Score 123; DB 8; Length 2570;
Best Local Similarity 33.3%; Pred. No. 0.04;
RESULT 534
ID ADM80804 standard; protein; 259 AA.
DE Human CADEC-33 protein SEQ ID NO:33.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 10.8%; Score 121.5; DB 8; Length 259;
Best Local Similarity 34.9%; Pred. No. 0.0026;
RESULT 535
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 2; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 536
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 3; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 537
ID AAB80249 standard; protein; 360 AA.

DE Human PRO271 protein.
PN WO200104311-A1.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 538
ID AAU29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 539
ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.8%; Score 121.5; DB 4; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 540
ID ABUS8413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US200302722-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 541
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 542
ID ABU87961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 543
ID ABU84276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 544
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 545
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 546
ID ABU99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 547
ID ABUS2719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 548
ID ABUS9840 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 549
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 550
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027264-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 551
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 552
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 553
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 554
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040052-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 555
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 556
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 557
ID ABUS591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.

PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 558
ID ABU98751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US200303153-A1.
PD 16-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 559
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 560
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 561
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 562
ID ABU89365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 563
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 564
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 565
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 566
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 567
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 568
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 569
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 570
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 571
ID ABO18819 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 572
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 573
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 574
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 575
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 576
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 577
ID ABU54384 standard; protein; 360 AA.

DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 578
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 579
ID ABU89666 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 580
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 581
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 582
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 583
ID ABO19124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 584
ID ABO11142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 585
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 586
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 587
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036143-A1.

PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 588
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 589
ID ABU65582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 590
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 591
ID ABO03617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 592
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 593
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 594
ID ABU55949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 595
ID ABU65277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 596
ID ABU95222 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 597
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.

PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 598
ID ABO07735 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 599
ID ABR69976 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 10.8%; Score 121.5; DB 6; Length 360;
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 600
ID ABR69309 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 601
ID ABO01450 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Best Local Similarity 10.8%; Score 121.5; DB 6; Length 360;
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 602
ID ABU81252 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 603
ID ABR60049 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 604
ID ABR67784 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 605
ID ABR65172 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 606
ID ABR68394 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 607
ID ABR71806 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032135-A1.
PD 13-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 608
ID ABUS286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 609
ID ABUS8976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 610
ID ABUS3056 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 611
ID ABUS4912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 612
ID ABUS0460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 613
ID ABUS3971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 614
ID ABUS3622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 615
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 616
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 617
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;

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Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 618
ID ABR99060 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040088-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 619
ID ABUS6944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 620
ID ABUS6436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 621
ID ABUS8586 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 622
ID ABUS7382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 623
ID ABUS2183 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 624
ID ABUS7194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 625
ID ABUS3666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 626
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040086-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 627
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 628
ID ABUS1751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 629
ID ABUS5915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 630
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 631
ID ABUS93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 632
ID ABUS99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 633
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 634
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 635
ID ABUS94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 636
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 637
ID ABUS86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 638
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ID ABU86916 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 639
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 640
ID ABO04532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 641
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 642
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 643
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 644
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 645
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 646
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 647
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 648
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.

PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 649
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 650
ID ABO09565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 651
ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 652
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040089-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 653
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 654
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 655
ID ABU84581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 656
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 657
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 658
ID ABU9659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 659
ID ABU93317 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 660
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 661
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 662
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 663
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 664
ID ABU96741 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 665
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 666
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 667
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 668
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 669
ID ABO05552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 670
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 671
ID ABR95533 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 672
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 673
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 674
ID ABM00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 675
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 676
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 677
ID ABM77254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 678
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;

RESULT 678
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 679
ID ABO07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 680
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 681
ID ABO35805 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 682
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 683
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 684
ID ABM24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 685
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 686
ID ABO3007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 687
ID ABR30263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 688
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 689
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 690
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 691
ID ABO21466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 692
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 693
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 694
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 695
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 696
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;

Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 697
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 698
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 699
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 700
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 701
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 702
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 703
ID ABM11560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 704
ID ABM2661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 705
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 706
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 707
ID ABM29009 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 708
ID ABM06985 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 709
ID ABM21079 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 710
ID ABM09425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 711
ID ABO41295 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 712
ID ABO36110 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 713
ID ABO43639 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 714
ID ABM76339 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 715
ID ABM76035 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104548-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 716
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 717
ID ABM25959 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 718
ID ABO03312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 719
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 720
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 721
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 722
ID ABO16888 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 723
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 724
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 725
ID ADA18274 standard; protein; 360 AA.

DE Human secreted/transmembrane protein, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 726
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 727
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 728
ID ABR93093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 729
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 730
ID ABR87823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 731
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 732
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 733
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 734
ID ABM04855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 735
ID ABM08815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 736
ID ABO36415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 737
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 738
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 739
ID ABM10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 740
ID ABM11865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 741
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 742
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 743
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.

PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 744
ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 745
ID ABR86908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 746
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 747
ID ABM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 748
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 749
ID ABM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 750
ID ABM06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 751
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 752
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 753
ID ABM07595 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 754
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 755
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 756
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 757
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 758
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 759
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 760
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 761
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 762
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.

PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 763
ID ABM18397 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 764
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 765
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 766
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 767
ID ABM01136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 768
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 769
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 770
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 771
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 772
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 773
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 774
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 775
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 776
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 777
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US200309353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 778
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 779
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 780
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 781
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 782
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 783
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 784
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 785
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 786
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 787
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 788
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 789
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6;
Best Local Similarity 34.9%; Pred. No. 0.0041;
Length 360;
RESULT 790
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

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PN US2003082715-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 791
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 792
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 793
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 794
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 795
ID ABM4315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 796
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 797
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 798
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 799
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 800
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 801
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 802
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 803
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 804
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 805
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 806
ID ABM29314 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 807
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 808
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 809
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
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PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 810
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 811
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 812
ID ABO16583 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 813
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 814
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027285-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 815
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 816
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 817
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 818
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #39.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 819
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 820
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 821
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032121-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 822
ID ABM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 823
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 824
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 825
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 826
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 827
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 828
ID ABO41600 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 829
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 830
ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 831
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 832
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 833
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 834
ID ABO51401 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 835
ID ABO51706 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 836
ID ABO50486 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 837
ID ABR79610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040059-A1.

PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 838
ID ABM16872 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 839
ID ABO17904 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044918-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 840
ID ABO20856 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032132-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 841
ID ABR96815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 842
ID ABM12170 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 843
ID ABM16262 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 844
ID ABM24129 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064441-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 845
ID ABM14610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 846
ID ABM04491 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 847

PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 867
ID ABO25599 standard; protein; 360 AA.
DE Human secreted polypeptide #14.
PN US200305446-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 868
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 869
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 870
ID ABM11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064489-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 871
ID ABO2862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 872
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 873
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 874
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 875
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 876
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 877
ID ABM15525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 878
ID ABM08510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 879
ID ABO42210 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 880
ID ABO37940 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 881
ID ABO45850 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 882
ID ABM66653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 883
ID ADB20140 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 884
ID ABM19554 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 885

ID ABO49266 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 886
ID ABO49571 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 887
ID ADA78392 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 888
ID ABR88128 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 889
ID ABM26874 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 890
ID ABM3271 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 891
ID ABO39770 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003058689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 892
ID ABO49876 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 893
ID ABO50791 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 894
ID ABO5247 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 895
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 896
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 897
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 898
ID ABM17787 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 899
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 900
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 901
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 902
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 903
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 904

ID ABR5993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 905
ID ABM10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 906
ID ABM76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 907
ID ABR89348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 908
ID ABM12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 909
ID ABM05765 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 910
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 911
ID ABM02966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003058764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 912
ID ABM18944 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 913
ID ABM19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 914
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 915
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 916
ID ADA1970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 917
ID ABR69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 918
ID ABR89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 919
ID ABR72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 920
ID ABR74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 921
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 922
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;

RESULT 923
ID ABR80220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 924
ID ABM01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 925
ID ABM02051 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 926
ID ABR87213 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 927
ID ABM12780 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 928
ID ABM30534 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 929
ID ABM24434 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 930
ID ABO29348 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 931
ID ABO31178 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 932
ID ABR77635 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 933
ID ABO3855 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 934
ID ABO38855 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 935
ID ABM34620 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 936
ID ABO51096 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 937
ID ADA42820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 938
ID ABO03922 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 939
ID ABO10392 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 940
ID ABR77635 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 941
ID ABR78845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 942
ID ABO23939 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 943
ID ABR93703 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 944
ID ABM01746 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 945
ID ABM78169 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 946
ID ABR89958 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 947
ID ABM27484 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 948
ID ABM13085 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 949
ID ABO31788 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 950
ID ABM14000 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 951
ID ABO08205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068754-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 952
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 953
ID ABM74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 954
ID ABM33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 955
ID ABM20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 956
ID ABO48656 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 957
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 958
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 959
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 960
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US200304919-A1.
PD 06-MAR-2003.

Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 961
ID ABO17193 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 962
ID ABM17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 963
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 964
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 965
ID ABM76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 966
ID ABO28128 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 967
ID ABM22909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 968
ID ABM30229 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 969
ID ABM21689 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 970
ID ABM31754 standard; protein; 360 AA.

ID ABM21384 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 971
ID ABM14915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 972
ID ABO40990 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 973
ID ABO36720 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 974
ID ABO37330 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 975
ID ABM75120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 976
ID ABM33400 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 977
ID ABO46155 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 978
ID ADA82463 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 979
ID ABM31754 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 980
ID ABM31144 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 981
ID ADB77739 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 982
ID ADB74875 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 983
ID ADB85771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 984
ID ABM32059 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 985
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 986
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 987
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 988
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.

PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 989
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 990
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 991
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 992
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 993
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 994
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 995
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 996
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 997
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 998
ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 999
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1000
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1001
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1002
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1003
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1004
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1005
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1006
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1007
ID ADF95378 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1008
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1009
ID ADH08853 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1010
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1011
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1012
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1013
ID ADL32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1014
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1015
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
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RESULT 1016
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1017
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1018
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1019
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1020
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1021
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1022
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1023
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1024
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1025
ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1026
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1027
ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1028
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1029
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1030
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1031
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1032
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1033
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;

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| PD | 22-MAY-2003. |
| PA | (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1042 ID ADH97474 standard; protein; 360 AA. DE Human secreted/transmembrane protein, #42. PN US2003190610-A1. PD 09-OCT-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1043 ID ADI65842 standard; protein; 360 AA. DE Human secreted/transmembrane protein, #42. PN US2003148371-A1. PD 07-AUG-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1044 ID ADH60585 standard; protein; 360 AA. DE Human secreted/transmembrane protein, #42. PN US2004023331-A1. PD 05-FEB-2004. PA (DESN/) DESNOYERS L. PA (GODD/) GODDARD A. PA (GODO/) GODOWSKI P J. PA (GURN/) GURNEY A L. PA (MATH/) MATHER J P. PA (WILL/) WILLIAMS P M. PA (WOOD/) WOOD W I. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1045 ID ADJ99642 standard; protein; 360 AA. DE Human secreted/transmembrane protein, #42. PN US2003187238-A1. PD 02-OCT-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1046 ID ADL08835 standard; protein; 360 AA. DE Human secreted/transmembrane protein, #42. PN US2003186358-A1. PD 02-OCT-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1047 ID ADJ54666 standard; protein; 360 AA. DE Human PRO polypeptide #14. PN US2004023321-A1. PD 05-FEB-2004. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1048 ID ADM25176 standard; protein; 360 AA. DE Human secreted/transmembrane protein, #42. PN US2003096233-A1. PD 22-MAY-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; RESULT 1049 ID ADM29526 standard; protein; 360 AA. DE Human secreted/transmembrane protein, #42. PN US2003190611-A1. PD 09-OCT-2003. PA (GETH) GENENTECH INC. Query Match Best Local Similarity 10.8%; Score 121.5; DB 8; Length 360; |

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Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1050
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1051
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1052
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1053
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1054
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1055
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1056
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1057
ID ADRI1100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1058
ID ADRI8009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1059
ID ADT03685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH ) GENENTECH INC.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1060
ID ADS74648 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #42.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 10.8%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.0041;
RESULT 1061
ID AAM59882 standard; protein; 528 AA.
DE Amino acid sequence of the cDNA clone BEF (HSXCK41).
PN WO9831800-A2.
PD 23-JUL-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
Query Match 10.8%; Score 121; DB 2; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1062
ID AAB61241 standard; protein; 528 AA.
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DE Human BEF protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 4; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1063
ID ABO32677 standard; protein; 528 AA.
DE Secreted polypeptide-related protein #75.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (WACK/) WACKAY C R.
PA (GOOD/) GOODERL A D J.
Query Match 10.8%; Score 121; DB 6; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1064
ID ADB90786 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1065
ID ADF71521 standard; protein; 528 AA.
DE Human BEF protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 7; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1066
ID ADQ10337 standard; protein; 528 AA.
DE Human polypeptide #171.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 10.8%; Score 121; DB 8; Length 528;
Best Local Similarity 24.1%; Pred. No. 0.0076;
RESULT 1067
ID AAR85442 standard; protein; 912 AA.
DE Bovine brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 10.7%; Score 120.5; DB 2; Length 912;
Best Local Similarity 24.6%; Pred. No. 0.018;
RESULT 1068
ID ADB47827 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NICU/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Query Match 10.6%; Score 119; DB 7; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.0098;
RESULT 1069
ID ADJ55382 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 10.6%; Score 119; DB 8; Length 457;
Best Local Similarity 33.3%; Pred. No. 0.0098;
RESULT 1070
ID ADQ39513 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.5%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.06;
RESULT 1071
ID ADQ39515 standard; protein; 1642 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 10.5%; Score 118.5; DB 8; Length 1642;
Best Local Similarity 25.5%; Pred. No. 0.06;
RESULT 1072
ID ADN04531 standard; protein; 2000 AA.
DE Antipsoriatic protein sequence #458.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 10.5%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.079;
RESULT 1073
ID ADP23738 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:916.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 10.5%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.079;
RESULT 1074
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 10.5%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.16;
RESULT 1075
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN-) LICENTIA LTD.
Query Match 10.5%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.16;
RESULT 1076
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 10.5%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.16;
RESULT 1077
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
PN WO2004058052-A2.

PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 10.5%; Score 118.5; DB 8; Length 3396;
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 5; Length 287;
RESULT 1078
ID AQ039510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 10.5%; Score 118.5; DB 8; Length 3396;
RESULT 1079
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match
Best Local Similarity 10.5%; Score 118.5; DB 8; Length 3396;
RESULT 1080
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 10.3%; Score 116; DB 8; Length 2397;
RESULT 1081
ID AAR46627 standard; protein; 1257 AA.
DE Neurocan core protein.
PN WO9403601-A2.
PD 17-FEB-1994.
PA (UVNY) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 10.3%; Score 115.5; DB 2; Length 1257;
RESULT 1082
ID AAR85443 standard; protein; 908 AA.
DE Rat brevicain core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match
Best Local Similarity 10.2%; Score 115; DB 2; Length 908;
RESULT 1083
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO200306475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 10.1%; Score 114; DB 7; Length 656;
RESULT 1084
ID ADP71273 standard; protein; 191 AA.
DE Human LP2 protein B-B' domain SeqID8.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 8; Length 191;
RESULT 1085
ID ABB10268 standard; protein; 287 AA.
DE Human cDNA SEQ ID NO: 576.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 4; Length 287;
RESULT 1086
ID ASP68655 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 576.
PN US2002090672-A1.

PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 5; Length 287;
RESULT 1087
ID ADM87304 standard; protein; 340 AA.
DE Human protein SEQ ID NO:397.
PN WO2004009834-A2.
PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 8; Length 340;
RESULT 1088
ID ABU11635 standard; protein; 143 AA.
DE Human MDDT polypeptide SEQ ID 582.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 10.0%; Score 112.5; DB 6; Length 343;
RESULT 1089
ID ABU10588 standard; protein; 897 AA.
DE Human novel protein NOV1C SEQ ID NO: 211.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 112; DB 5; Length 897;
RESULT 1090
ID ADH71312 standard; protein; 897 AA.
DE Human protein of the invention NOV9a SEQ ID NO:208.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 10.0%; Score 112; DB 8; Length 897;
RESULT 1091
ID AD009968 standard; protein; 897 AA.
DE Human NOV1C cDNA.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match
Best Local Similarity 10.0%; Score 112; DB 8; Length 897;
RESULT 1092
ID AAM47684 standard; protein; 1394 AA.
DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.

PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match 10.0%; Score 112; DB 5; Length 1394;
Best Local Similarity 29.0%; Pred. No. 0.21;
RESULT 1093
ID ABG72499 standard; protein; 1416 AA.
DE Human 150kDa Hyaluronan receptor for endocytosis (HARE) #1.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 10.0%; Score 112; DB 6; Length 1416;
Best Local Similarity 29.0%; Pred. No. 0.22;
RESULT 1094
ID ADH71356 standard; protein; 1502 AA.
DE Human protein of the invention NOV9w SEQ ID NO:252.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 112; DB 8; Length 1502;
Best Local Similarity 29.0%; Pred. No. 0.23;
RESULT 1095
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 112; DB 8; Length 1510;
Best Local Similarity 29.0%; Pred. No. 0.24;
RESULT 1096
ID ABG72514 standard; protein; 1633 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 10.0%; Score 112; DB 6; Length 1653;
Best Local Similarity 29.0%; Pred. No. 0.27;
RESULT 1097
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match 10.0%; Score 112; DB 8; Length 1895;
Best Local Similarity 29.0%; Pred. No. 0.32;
RESULT 1098
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 10.0%; Score 112; DB 8; Length 2551;
Best Local Similarity 29.0%; Pred. No. 0.47;
RESULT 1099
ID ADP71271 standard; protein; 200 AA.
DE Human aggrecan protein B-B' domain SeqID6.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG-) SEIKAGAKU KOGYO CO LTD.
Query Match 9.9%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.02;
RESULT 1100
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 SEQ ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (MERR/) MERRILEES M.
Query Match 9.9%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.097;
RESULT 1101
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.9%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.097;
RESULT 1102
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 9.9%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1103
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence SEQ ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 9.9%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1104
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1177.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.9%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1105
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.9%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 0.55;
RESULT 1106
ID ABJ10586 standard; protein; 2675 AA.
DE Human novel protein NOV1a SEQ ID NO: 2.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.8%; Score 110; DB 5; Length 2675;
Best Local Similarity 28.0%; Pred. No. 0.79;
RESULT 1107
ID ADO09971 standard; protein; 2675 AA.
DE Human NOV1a variant.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM-) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SPYT/) SHENOY S G.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOGF L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.

PA (TCHE/) TCHERNEV V T.
PA (SIJU/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match
Best Local Similarity 9.8%; Score 110; DB 8; Length 2675;
Best Local Similarity 28.0%; Pred. No. 0.79;
RESULT 1108
ID ADO09836 standard; protein; 2675 AA.
DE Human NOV1a.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALX/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERH/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCHE/) TCHERNEV V T.
PA (SIJU/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match
Best Local Similarity 9.8%; Score 110; DB 8; Length 2675;
Best Local Similarity 28.0%; Pred. No. 0.79;
RESULT 1109
ID ADO31200 standard; protein; 1257 AA.
DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match
Best Local Similarity 9.7%; Score 109.5; DB 8; Length 1257;
Best Local Similarity 23.6%; Pred. No. 0.33;
RESULT 1110
ID AAY93913 standard; protein; 353 AA.
DE A human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match
Best Local Similarity 9.7%; Score 109; DB 3; Length 353;
Best Local Similarity 24.3%; Pred. No. 0.067;
RESULT 1111
ID ABP97200 standard; protein; 1321 AA.
DE Tumour-associated antigenic target protein TAT185 SEQ ID NO:82.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH-) GENENTECH INC.
Query Match
Best Local Similarity 9.7%; Score 109; DB 6; Length 1321;
Best Local Similarity 21.4%; Pred. No. 0.39;
RESULT 1112
ID ADJ69615 standard; protein; 1321 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 9.7%; Score 109; DB 7; Length 1321;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1113
ID ADN38944 standard; protein; 1321 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:262.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 9.7%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 0.39;
RESULT 1114
ID ADO31196 standard; protein; 1321 AA.
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match
Best Local Similarity 9.7%; Score 109; DB 8; Length 1321;
Best Local Similarity 21.4%; Pred. No. 0.39;
RESULT 1115
ID ABJ56909 standard; protein; 322 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.074;
RESULT 1116
ID ABJ56908 standard; protein; 322 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.074;
RESULT 1117
ID ABJ56918 standard; protein; 353 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 353;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1118
ID AAY57081 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (RECG-) UNIV CALIFORNIA.
Query Match
Best Local Similarity 9.6%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1119
ID AAY57084 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor #2.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (RECG-) UNIV CALIFORNIA.
Query Match
Best Local Similarity 9.6%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1120
ID ABJ56902 standard; protein; 354 AA.
DE 151P3D4 v-1 354aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1121
ID ABJ56906 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;

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RESULT 1122
ID ABJ56914 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1123
ID ABJ56898 standard; protein; 354 AA.
DE 151P3D4 v-8 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1124
ID ABJ56895 standard; protein; 354 AA.
DE 151P3D4 v-5 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1125
ID ABJ56897 standard; protein; 354 AA.
DE 151P3D4 v-7 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1126
ID ABJ56901 standard; protein; 354 AA.
DE 151P3D4 v-11 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1127
ID ABJ56894 standard; protein; 354 AA.
DE 151P3D4 v-4 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1128
ID ABJ56905 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1129
ID ABJ56899 standard; protein; 354 AA.
DE 151P3D4 v-9 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1130
ID ABJ56912 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1131
ID ABJ56890 standard; protein; 721 AA.
DE 151P3D4 v-3 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1132
ID ABJ56891 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1133
ID ABJ56896 standard; protein; 354 AA.
DE 151P3D4 v-6 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1134
ID ABJ56900 standard; protein; 354 AA.
DE 151P3D4 v-10 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1135
ID ABJ56889 standard; protein; 354 AA.
DE Transcript variant I21P1F1 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1136
ID ABJ56904 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match          9.6%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1137
ID ADP07795 standard; protein; 354 AA.
DE Human secreted protein, seq id 278.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match          9.6%; Score 108; DB 8; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.084;
RESULT 1138
ID AAR77034 standard; protein; 355 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV YALE.
Query Match          9.6%; Score 108; DB 2; Length 355;
Best Local Similarity 28.9%; Pred. No. 0.085;
RESULT 1139
ID ADH71348 standard; protein; 552 AA.
DE Human protein of the invention NOV9s SEQ ID NO:244.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match          9.6%; Score 108; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.15;
RESULT 1140
ID ABJ56890 standard; protein; 721 AA.
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DE Transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.6%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.22;
RESULT 1141
ID ABJ56892 standard; protein; 721 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.6%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.22;
RESULT 1142
ID ABJ56903 standard; protein; 721 AA.
DE 151P3D4 v-1 721aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.6%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.22;
RESULT 1143
ID ABG72500 standard; protein; 93 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 9.5%; Score 107; DB 6; Length 93;
Best Local Similarity 29.2%; Pred. No. 0.018;
RESULT 1144
ID AAB83358 standard; protein; 315 AA.
DE NOV2 protein sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 4; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.091;
RESULT 1145
ID ADH71316 standard; protein; 315 AA.
DE Human protein of the invention NOV9c SEQ ID NO:212.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.091;
RESULT 1146
ID AAY57083 standard; protein; 339 AA.
DE Rat proteoglycan link protein precursor.
PN WO956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.5%; Score 107; DB 3; Length 339;
Best Local Similarity 28.6%; Pred. No. 0.1;
RESULT 1147
ID ABJ56915 standard; protein; 354 AA.
DE Rat cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 107; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.11;
RESULT 1148
ID AAY57082 standard; protein; 355 AA.
DE Chicken proteoglycan link protein precursor.
PN WO956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.5%; Score 107; DB 3; Length 355;
Best Local Similarity 34.9%; Pred. No. 0.11;
RESULT 1149
ID ABJ56907 standard; protein; 355 AA.

DE Mouse cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.5%; Score 107; DB 6; Length 355;
Best Local Similarity 28.6%; Pred. No. 0.11;
RESULT 1150
ID ADH71336 standard; protein; 533 AA.
DE Human protein of the invention NOV9m SEQ ID NO:232.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.18;
RESULT 1151
ID ADH71334 standard; protein; 533 AA.
DE Human protein of the invention NOV9l SEQ ID NO:230.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.18;
RESULT 1152
ID ADH71340 standard; protein; 552 AA.
DE Human protein of the invention NOV9o SEQ ID NO:236.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1153
ID ADH71346 standard; protein; 552 AA.
DE Human protein of the invention NOV9r SEQ ID NO:242.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1154
ID ADH71354 standard; protein; 552 AA.
DE Human protein of the invention NOV9v SEQ ID NO:250.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1155
ID ADH71344 standard; protein; 552 AA.
DE Human protein of the invention NOV9q SEQ ID NO:240.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1156
ID ADH71342 standard; protein; 552 AA.
DE Human protein of the invention NOV9p SEQ ID NO:238.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1157
ID ADH71350 standard; protein; 552 AA.
DE Human protein of the invention NOV9t SEQ ID NO:246.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1158
ID ADH71314 standard; protein; 556 AA.
DE Human protein of the invention NOV9b SEQ ID NO:210.

PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 556;
Best Local Similarity 29.2%; Pred. No. 0.19;
RESULT 1159
ID ABM83433 standard; protein; 774 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3682.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.5%; Score 107; DB 8; Length 774;
Best Local Similarity 21.5%; Pred. No. 0.3;
RESULT 1160
ID ABM83432 standard; protein; 822 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3681.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 9.5%; Score 107; DB 8; Length 822;
Best Local Similarity 21.5%; Pred. No. 0.33;
RESULT 1161
ID ADO31202 standard; protein; 1268 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 9.5%; Score 107; DB 8; Length 1268;
Best Local Similarity 26.2%; Pred. No. 0.58;
RESULT 1162
ID ADH71332 standard; protein; 2417 AA.
DE Human protein of the invention NOV9k SEQ ID NO:228.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 8; Length 2417;
Best Local Similarity 29.2%; Pred. No. 1.4;
RESULT 1163
ID ABJ10587 standard; protein; 2420 AA.
DE Human novel protein NOV1b SEQ ID NO: 4.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 107; DB 5; Length 2420;
Best Local Similarity 29.2%; Pred. No. 1.4;
RESULT 1164
ID ADO09838 standard; protein; 2420 AA.
DE Human NOV1b.
PN US2004018970-A1.
PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PAT/) PATURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTER K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KERU/) KERUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCH/) TCHERNEV V T.
PA (SIJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.

PA (ROTH/) ROTHENBERG M E.
Query Match 9.5%; Score 107; DB 8; Length 2420;
Best Local Similarity 29.2%; Pred. No. 1.4;
RESULT 1165
ID ADH71338 standard; protein; 552 AA.
DE Human protein of the invention NOV9n SEQ ID NO:234.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 9.4%; Score 106; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.24;
RESULT 1166
ID AAB12304 standard; protein; 341 AA.
DE Human secreted protein encoded by gene 4 clone HFXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 9.4%; Score 105.5; DB 3; Length 341;
Best Local Similarity 28.9%; Pred. No. 0.14;
RESULT 1167
ID AAY57080 standard; protein; 354 AA.
DE Human link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 9.3%; Score 105; DB 3; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.17;
RESULT 1168
ID ABJ56913 standard; protein; 354 AA.
DE Bovine cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 9.3%; Score 105; DB 6; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.17;
RESULT 1169
ID ABU07339 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2040.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.2%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.06;
RESULT 1170
ID ABU07336 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2037.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 9.2%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.06;
RESULT 1171
ID ADQ39387 standard; protein; 139 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 9.2%; Score 104; DB 8; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.06;
RESULT 1172
ID ADP71269 standard; protein; 195 AA.
DE Human LP1 protein B-B' domain SeqID4.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 9.2%; Score 104; DB 8; Length 195;
Best Local Similarity 33.7%; Pred. No. 0.094;
RESULT 1173
ID ADP71267 standard; protein; 200 AA.
DE Human versican protein B-B' domain SeqID2.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.

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Query Match
Best Local Similarity 9.2%; Score 104; DB 8; Length 200;
RESULT 1174
ID ADH71352 standard; protein; 552 AA.
DE Human protein of the invention NOV9u SEQ ID NO:248.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 9.2%; Score 104; DB 8; Length 552;
RESULT 1175
ID ADN23553 standard; protein; 380 AA.
DE Bacterial polypeptide #6206.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 9.0%; Score 101.5; DB 8; Length 380;
RESULT 1176
ID AAU76528 standard; protein; 402 AA.
DE Human LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match
Best Local Similarity 8.9%; Score 100.5; DB 5; Length 402;
RESULT 1177
ID AAU09883 standard; protein; 402 AA.
DE Novel human secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 8.9%; Score 100.5; DB 5; Length 402;
RESULT 1178
ID ADF59259 standard; protein; 402 AA.
DE Human polypeptide sequence SEQ ID NO:1667.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 8.9%; Score 100.5; DB 7; Length 402;
RESULT 1179
ID ADF74155 standard; protein; 412 AA.
DE Human novel brain/hippocampus protein #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match
Best Local Similarity 8.9%; Score 100.5; DB 7; Length 412;
RESULT 1180
ID AAR77035 standard; protein; 378 AA.
DE Cat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA ) UNIV VALE.
Query Match
Best Local Similarity 8.9%; Score 100; DB 2; Length 378;
RESULT 1181
ID ABP57346 standard; protein; 402 AA.
DE Human secreted protein SECP-17 SEQ ID NO:17.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUYU/) LU Y.
Query Match
Best Local Similarity 8.8%; Score 99.5; DB 6; Length 402;
RESULT 1182
ID ABJ56917 standard; protein; 201 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 8.8%; Score 99; DB 6; Length 201;
RESULT 1183
ID ABJ56916 standard; protein; 201 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 8.8%; Score 99; DB 6; Length 201;
RESULT 1184
ID ABJ56919 standard; protein; 600 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 8.8%; Score 99; DB 6; Length 600;
RESULT 1185
ID ABB70377 standard; protein; 1428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 8.8%; Score 99; DB 4; Length 1428;
RESULT 1186
ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match
Best Local Similarity 8.7%; Score 98; DB 4; Length 2112;
RESULT 1187
ID AAY95559 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 8.5%; Score 96; DB 3; Length 2870;
RESULT 1188
ID ADN07634 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV -1 deletion mutant protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 8.5%; Score 96; DB 8; Length 2870;
RESULT 1189
ID AAY95556 standard; protein; 3178 AA.
DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 8.5%; Score 96; DB 3; Length 3178;
RESULT 1190
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 8.5%; Score 96; DB 8; Length 3178;
RESULT 1191
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match
Best Local Similarity 8.5%; Score 96; DB 8; Length 3178;
RESULT 1191
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ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.
PN WO2004048529-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.5%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 0.81;
RESULT 1192
ID ABB5987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 8.4%; Score 94.5; DB 4; Length 183;
Best Local Similarity 34.5%; Pred. No. 0.75;
RESULT 1193
ID ABB5986 standard; protein; 1795 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match 8.4%; Score 94.5; DB 4; Length 1795;
Best Local Similarity 33.0%; Pred. No. 16;
RESULT 1194
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID No 205.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1195
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1196
ID ABB67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.3%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1197
ID ADB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1198
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID No 144.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1199
ID ABB10361 standard; protein; 261 AA.
DE Human cDNA SEQ ID NO: 669.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;

RESULT 1200
ID ABP66948 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 669.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.3%; Score 93.5; DB 5; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1201
ID ADB31623 standard; protein; 261 AA.
DE Human novel protein SEQ ID NO 144.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.3%; Score 93.5; DB 7; Length 261;
Best Local Similarity 24.6%; Pred. No. 1.5;
RESULT 1202
ID ABP73157 standard; protein; 40 AA.
DE Deletion mutant of a CD44-Hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PARELL T.
Query Match 8.2%; Score 92.5; DB 6; Length 40;
Best Local Similarity 54.1%; Pred. No. 0.15;
RESULT 1203
ID ADP04445 standard; protein; 1381 AA.
DE Sea squirt protein with tissue specific expression in development Seq40.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 8.2%; Score 92.5; DB 8; Length 1381;
Best Local Similarity 22.6%; Pred. No. 17;
RESULT 1204
ID AAU18036 standard; protein; 166 AA.
DE Human immunoglobulin polypeptide SEQ ID No 181.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1205
ID ABB10469 standard; protein; 166 AA.
DE Human cDNA SEQ ID NO: 777.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1206
ID ABP67056 standard; protein; 166 AA.
DE Human polypeptide SEQ ID NO 777.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 8.1%; Score 91.5; DB 5; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1207
ID ADB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.1%; Score 91.5; DB 7; Length 166;
Best Local Similarity 31.9%; Pred. No. 1.3;
RESULT 1208
ID ABB69720 standard; protein; 1126 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.

PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.1%; Score 91.5; DB 4; Length 1126;
Best Local Similarity 32.3%; Pred. No. 17;
RESULT 1209
ID ADG73740 standard; protein; 505 AA.
DE Aspergillus niger Brea-109.
PN US2003215950-A1.
PD 20-NOV-2003.
PA (LASU/) LASURE L L.
PA (DAIZ/) DAI Z.
Query Match 8.0%; Score 90.5; DB 8; Length 505;
Best Local Similarity 27.0%; Pred. No. 7.1;
RESULT 1210
ID ABB69419 standard; protein; 1976 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 8.0%; Score 90.5; DB 4; Length 1976;
Best Local Similarity 38.5%; Pred. No. 44;
RESULT 1211
ID ABU36285 standard; protein; 402 AA.
DE Protein encoded by Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 8.0%; Score 90; DB 6; Length 402;
Best Local Similarity 22.4%; Pred. No. 5.9;
RESULT 1212
ID ADN20575 standard; protein; 1103 AA.
DE Bacterial polypeptide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 8.0%; Score 90; DB 8; Length 1103;
Best Local Similarity 23.5%; Pred. No. 23;
RESULT 1213
ID ABB65879 standard; protein; 307 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.9%; Score 89; DB 4; Length 307;
Best Local Similarity 31.6%; Pred. No. 5.2;
RESULT 1214
ID AAR69554 standard; protein; 416 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-1.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 7.9%; Score 89; DB 2; Length 416;
Best Local Similarity 23.6%; Pred. No. 7.8;
RESULT 1215
ID AAY52550 standard; protein; 416 AA.
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).
PN WO9958658-A2.
PD 18-NOV-1999.
PA (EPTM-) EPIMUNE INC.
Query Match 7.9%; Score 89; DB 3; Length 416;
Best Local Similarity 23.6%; Pred. No. 7.8;
RESULT 1216
ID ADP65283 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.

Query Match 7.9%; Score 89; DB 7; Length 416;
Best Local Similarity 23.6%; Pred. No. 7.8;
RESULT 1217
ID ADN03755 standard; protein; 416 AA.
DE Antipsoriatic protein sequence #74.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 7.8;
RESULT 1218
ID ADP49321 standard; protein; 416 AA.
DE Human lysosomal associated membrane protein LAMP #1.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 7.9%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 7.8;
RESULT 1219
ID ADP23231 standard; protein; 416 AA.
DE PRO polypeptide SEQ ID NO:325.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 7.8;
RESULT 1220
ID ABO68455 standard; protein; 451 AA.
DE Pseudomonas aeruginosa polypeptide #630.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.9%; Score 88.5; DB 7; Length 451;
Best Local Similarity 20.7%; Pred. No. 9.7;
RESULT 1221
ID AAY52525 standard; protein; 536 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 7.8%; Score 87.5; DB 3; Length 536;
Best Local Similarity 23.9%; Pred. No. 15;
RESULT 1222
ID AAU96329 standard; protein; 536 AA.
DE Der HMW-map polypeptide #16.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 7.8%; Score 87.5; DB 5; Length 536;
Best Local Similarity 23.9%; Pred. No. 15;
RESULT 1223
ID AAY52523 standard; protein; 555 AA.
DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
PN WO9954349-A2.
PD 28-OCT-1999.
PA (HESK-) HESKA CORP.
Query Match 7.8%; Score 87.5; DB 3; Length 555;
Best Local Similarity 23.9%; Pred. No. 16;
RESULT 1224
ID AAU96327 standard; protein; 555 AA.
DE Der HMW-map polypeptide #14.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 7.8%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 16;
RESULT 1225
ID AAU96328 standard; protein; 555 AA.
DE Der HMW-map polypeptide #15.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 7.8%; Score 87.5; DB 5; Length 555;
Best Local Similarity 23.9%; Pred. No. 16;
RESULT 1226
ID AAU96328 standard; protein; 555 AA.
DE Der HMW-map polypeptide #15.
PN WO200222807-A2.
PD 21-MAR-2002.
PA (HESK-) HESKA CORP.
Query Match 7.8%; Score 87.5; DB 5; Length 555;

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Best Local Similarity 23.9%; Pred. No. 16;
RESULT 1226
ID AAW54844 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein 5kb fragment.
PN US5763569-A.
PD 09-JUN-1998.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1227
ID AAY41778 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor 1 protein sequence.
PN US5962314-A.
PD 05-OCT-1999.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1228
ID AAW89563 standard; protein; 1085 AA.
DE Bovine parathyroid calcium receptor BopCar 1.
PN US5858684-A.
PD 12-JAN-1999.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 2; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1229
ID AAY51825 standard; protein; 1085 AA.
DE Bovine calcium receptor BopCar1 protein.
PN US6031003-A.
PD 29-FEB-2000.
PA (NPSF-) NPS PHARM INC.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL.
Query Match 7.8%; Score 87.5; DB 3; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1230
ID AAB47820 standard; protein; 1085 AA.
DE BopCar1.
PN US6313146-B1.
PD 06-NOV-2001.
PA (NPSF-) NPS PHARM INC.
Query Match 7.8%; Score 87.5; DB 5; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1231
ID ADJ93194 standard; protein; 1085 AA.
DE Bovine extracellular Ca-sensing receptor.
PN WO200296946-A1.
PD 05-DEC-2002.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 7.8%; Score 87.5; DB 7; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1232
ID ADI40961 standard; protein; 1085 AA.
DE Bovine GPCR CASR.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAWA/) RAMANATHAN C S.
Query Match 7.8%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1233
ID ADI41015 standard; protein; 1085 AA.
DE Bovine GPCR CASR #2.
PN US2004018976-A1.
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAWA/) RAMANATHAN C S.
Query Match 7.8%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 39;
RESULT 1234
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.7%; Score 87; DB 7; Length 235;
Best Local Similarity 27.8%; Pred. No. 5.7;
RESULT 1235
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1236
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 7.7%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1237
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTG1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1238
ID AAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein PTG288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1239
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1240
ID ADG17394 standard; protein; 288 AA.
DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J.
Query Match 7.7%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 7.5;
RESULT 1241
ID AAR01940 standard; protein; 417 AA.
DE Tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC ) GREEN CROSS CORP.
Query Match 7.7%; Score 87; DB 2; Length 417;
Best Local Similarity 23.6%; Pred. No. 12;
RESULT 1242
ID AAP91941 standard; peptide; 400 AA.
DE Sequence of preprospasmodysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 7.7%; Score 86.5; DB 1; Length 400;
Best Local Similarity 30.8%; Pred. No. 13;
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RESULT 1243
ID AAR69555 standard; protein; 410 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-2.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 7.7%; Score 86.5; DB 2; Length 410;
Best Local Similarity 20.7%; Pred. No. 13;
RESULT 1244
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 7.7%; Score 86.5; DB 2; Length 708;
Best Local Similarity 23.4%; Pred. No. 28;
RESULT 1245
ID ABM82857 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3106.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.6%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 18;
RESULT 1246
ID ABM83144 standard; protein; 476 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:3393.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 7.6%; Score 86; DB 8; Length 476;
Best Local Similarity 32.1%; Pred. No. 18;
RESULT 1247
ID ABP69313 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 1360.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.6%; Score 85.5; DB 5; Length 343;
Best Local Similarity 30.2%; Pred. No. 13;
RESULT 1248
ID AAR57350 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO9415627-A1.
PD 21-JUL-1994.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 2; Length 354;
Best Local Similarity 26.2%; Pred. No. 14;
RESULT 1249
ID ABB78250 standard; protein; 652 AA.
DE Amino acid sequence of a human heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 5; Length 652;
Best Local Similarity 22.4%; Pred. No. 31;
RESULT 1250
ID ABB78248 standard; protein; 841 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 5; Length 841;
Best Local Similarity 22.4%; Pred. No. 44;
RESULT 1251
ID ADQ37103 standard; protein; 951 AA.
DE Cell proliferation-related polypeptide #118.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 7.6%; Score 85.5; DB 8; Length 951;
Best Local Similarity 26.0%; Pred. No. 52;
RESULT 1252
ID ABB78249 standard; protein; 977 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEO) GEN HOSPITAL CORP.
Query Match 7.6%; Score 85.5; DB 5; Length 977;
Best Local Similarity 22.4%; Pred. No. 53;
RESULT 1253
ID ABUS4710 standard; protein; 1784 AA.
DE Human CAL25 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 1784;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1254
ID ABUS4858 standard; protein; 1794 AA.
DE Human CAL25 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 1794;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1255
ID ABUS4707 standard; protein; 1821 AA.
DE Human CAL25 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 1821;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1256
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 7.6%; Score 85.5; DB 6; Length 5877;
Best Local Similarity 27.2%; Pred. No. 5.8e+02;
RESULT 1257
ID ABUS4721 standard; protein; 11721 AA.
DE Human CAL25 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 6; Length 11721;
Best Local Similarity 27.2%; Pred. No. 1.5e+03;
RESULT 1258
ID ADP84155 standard; protein; 22157 AA.
DE Human CAL25 protein sequence SeqID 5.
PN WO2004045553-A2.
PD 03-JUN-2004.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.6%; Score 85.5; DB 8; Length 22157;
Best Local Similarity 27.2%; Pred. No. 3.4e+03;
RESULT 1259
ID ABB50001 standard; protein; 569 AA.
DE Listeria monocytogenes protein #2705.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 7.6%; Score 85; DB 5; Length 569;
Best Local Similarity 22.9%; Pred. No. 29;
RESULT 1260
ID ABU32518 standard; protein; 569 AA.
DE Protein encoded by Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.6%; Score 85; DB 6; Length 569;
Best Local Similarity 22.9%; Pred. No. 29;
RESULT 1261
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ID ABB5236 standard; protein; 627 AA.
DE Lactococcus lactis protein ytfC.
PD FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 7.6%; Score 85; DB 5; Length 627;
Best Local Similarity 21.5%; Pred. No. 33;
RESULT 1262
ID ADS29466 standard; protein; 627 AA.
DE Bacterial polypeptide #18499.
PD US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.6%; Score 85; DB 8; Length 627;
Best Local Similarity 21.5%; Pred. No. 33;
RESULT 1263
ID AAG93274 standard; protein; 631 AA.
DE Chlamydia trachomatis PmpH(N-term) fusion protein.
PD WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.6%; Score 85; DB 4; Length 631;
Best Local Similarity 27.7%; Pred. No. 33;
RESULT 1264
ID ABB94245 standard; protein; 631 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.
PD WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.6%; Score 85; DB 5; Length 631;
Best Local Similarity 27.7%; Pred. No. 33;
RESULT 1265
ID ADD42755 standard; protein; 664 AA.
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.
PD WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.6%; Score 85; DB 7; Length 664;
Best Local Similarity 27.7%; Pred. No. 36;
RESULT 1266
ID AAU38901 standard; protein; 1016 AA.
DE C. trachomatis CT872 protein.
PD WO200181379-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.6%; Score 85; DB 4; Length 1016;
Best Local Similarity 27.7%; Pred. No. 63;
RESULT 1267
ID ABG91037 standard; protein; 1016 AA.
DE Chlamydia trachomatis outer membrane protein H protein.
PD WO200262380-A2.
PD 15-AUG-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 7.6%; Score 85; DB 5; Length 1016;
Best Local Similarity 27.7%; Pred. No. 63;
RESULT 1268
ID ADD42682 standard; protein; 1016 AA.
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.
PD WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.6%; Score 85; DB 7; Length 1016;
Best Local Similarity 27.7%; Pred. No. 63;
RESULT 1269
ID ADD43800 standard; protein; 1016 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 95.
PD WO2003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 7.5%; Score 84; DB 8; Length 335;
Best Local Similarity 30.6%; Pred. No. 18;
RESULT 1270
ID ABB60387 standard; protein; 1049 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7953.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.6%; Score 85; DB 4; Length 1049;
Best Local Similarity 22.1%; Pred. No. 66;
RESULT 1271
ID ADJ66747 standard; protein; 2234 AA.
DE Human Muc16 GST fusion protein amino acid sequence SeqID20.
PD WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Query Match 7.5%; Score 84.5; DB 8; Length 2234;
Best Local Similarity 27.2%; Pred. No. 2e+02;
RESULT 1272
ID ADR72871 standard; protein; 22152 AA.
DE Human ovarian cancer-related tumour marker CA125 protein.
PD WO2004075713-A2.
PD 10-SEP-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 7.5%; Score 84.5; DB 8; Length 22152;
Best Local Similarity 27.2%; Pred. No. 4.3e+03;
RESULT 1273
ID AAB11729 standard; protein; 216 AA.
DE Cryptosporidium parvum Iowa isolate GP900, domain 2.
PD US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 3; Length 216;
Best Local Similarity 26.7%; Pred. No. 10;
RESULT 1274
ID AAB11734 standard; protein; 216 AA.
DE Cryptosporidium parvum NINC isolate GP900, domain 2.
PD US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 3; Length 216;
Best Local Similarity 26.7%; Pred. No. 10;
RESULT 1275
ID ABJ04047 standard; protein; 216 AA.
DE C. parvum GP900 protein fragment SEQ ID NO: 8.
PD WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 5; Length 216;
Best Local Similarity 26.7%; Pred. No. 10;
RESULT 1276
ID AAB42164 standard; protein; 330 AA.
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
PD WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 7.5%; Score 84; DB 3; Length 330;
Best Local Similarity 27.5%; Pred. No. 18;
RESULT 1277
ID ABB59598 standard; protein; 330 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5586.
PD WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.5%; Score 84; DB 4; Length 330;
Best Local Similarity 30.6%; Pred. No. 18;
RESULT 1278
ID ADO61979 standard; protein; 335 AA.
DE Transcription factor G2571, SEQ ID 446.
PD WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 7.5%; Score 84; DB 8; Length 335;
Best Local Similarity 30.6%; Pred. No. 18;
RESULT 1279
ID ADO61979 standard; protein; 335 AA.
DE Transcription factor G2571, SEQ ID 446.
PD WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 7.5%; Score 84; DB 8; Length 335;
Best Local Similarity 30.6%; Pred. No. 18;
RESULT 1279

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Best Local Similarity 26.4%; Pred. No. 18;
RESULT 1279
ID AAB96091 standard; protein; 1362 AA.
DE Putative P. abyssi amylpullulanase.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS ) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 7.5%; Score 84; DB 4; Length 1362;
Best Local Similarity 26.5%; Pred. No. 1.2e+02;
RESULT 1280
ID AAW48299 standard; protein; 1721 AA.
DE Cryptosporidium parvum GP900 antigen.
PN WO9806430-A1.
PD 19-FEB-1998.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 2; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.6e+02;
RESULT 1281
ID AAB11727 standard; protein; 1721 AA.
DE Portion of Cryptosporidium parvum NINC isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 3; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.6e+02;
RESULT 1282
ID ABJ04045 standard; protein; 1721 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 6.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 5; Length 1721;
Best Local Similarity 26.7%; Pred. No. 1.6e+02;
RESULT 1283
ID AAB11726 standard; protein; 1837 AA.
DE Cryptosporidium parvum Iowa isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 3; Length 1837;
Best Local Similarity 26.7%; Pred. No. 1.7e+02;
RESULT 1284
ID ABJ04044 standard; protein; 1837 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 5.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.5%; Score 84; DB 5; Length 1837;
Best Local Similarity 26.7%; Pred. No. 1.7e+02;
RESULT 1285
ID ABUS3165 standard; protein; 143 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #25.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 143;
Best Local Similarity 30.7%; Pred. No. 6.5;
RESULT 1286
ID ABUS3163 standard; protein; 247 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #23.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 247;
Best Local Similarity 30.7%; Pred. No. 13;
RESULT 1287
ID ABUS3158 standard; protein; 260 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #18.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 260;
Best Local Similarity 30.7%; Pred. No. 13;
RESULT 1288
ID ABUS3157 standard; protein; 368 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #17.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 368;
Best Local Similarity 30.7%; Pred. No. 23;
RESULT 1289
ID ABUS3156 standard; protein; 385 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #16.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 385;
Best Local Similarity 30.7%; Pred. No. 24;
RESULT 1290
ID ABUS3159 standard; protein; 387 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #21.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 387;
Best Local Similarity 30.7%; Pred. No. 24;
RESULT 1291
ID ABUS3161 standard; protein; 387 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #21.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 387;
Best Local Similarity 30.7%; Pred. No. 24;
RESULT 1292
ID AAM50241 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase.
PN US6297055-B1.
PD 02-OCT-2001.
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
Query Match 7.4%; Score 83.5; DB 4; Length 393;
Best Local Similarity 26.5%; Pred. No. 25;
RESULT 1293
ID AAU76423 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase clone wr1.pk0059.g9.
PN US2002009801-A1.
PD 24-JAN-2002.
PA (FALC/) FALCO S C.
PA (FAMO/) FAMODU O O.
PA (OROZ/) OROZCO E R.
Query Match 7.4%; Score 83.5; DB 5; Length 393;
Best Local Similarity 26.5%; Pred. No. 25;
RESULT 1294
ID ABUS3160 standard; protein; 395 AA.
DE Human testes-derived DKFZphtes3_2a11 homologue #20.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 395;
Best Local Similarity 30.7%; Pred. No. 25;
RESULT 1295
ID ABB10349 standard; protein; 553 AA.
DE Human cDNA SEQ ID NO: 657.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 7.4%; Score 83.5; DB 4; Length 553;
Best Local Similarity 22.9%; Pred. No. 39;
RESULT 1296
ID ABP66936 standard; protein; 553 AA.
DE Human polypeptide SEQ ID NO 657.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
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PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 7.4%; Score 83.5; DB 5; Length 553;
Best Local Similarity 22.9%; Pred. No. 39;
RESULT 1297
ID ABUS3144 standard; protein; 717 AA.
DE Human testes-derived DKF2phes3_2a11 homologue #4.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GERU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.4%; Score 83.5; DB 4; Length 717;
Best Local Similarity 30.7%; Pred. No. 56;
RESULT 1298
ID AAY54466 standard; protein; 788 AA.
DE Amino acid sequence of intestinal insect mucin isoform IIM14.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 7.4%; Score 83.5; DB 3; Length 788;
Best Local Similarity 26.5%; Pred. No. 63;
RESULT 1299
ID AAY54467 standard; protein; 807 AA.
DE Amini acid sequence of intestinal insect mucin isoform IIM22.
PN WO9967373-A2.
PD 29-DEC-1999.
PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
Query Match 7.4%; Score 83.5; DB 3; Length 807;
Best Local Similarity 26.5%; Pred. No. 65;
RESULT 1300
ID ABU62079 standard; protein; 4123 AA.
DE Human jelly belly (jeb) protein.
PN US2003054485-A1.
PD 20-MAR-2003.
PA (SCOT/) SCOTT M P.
PA (WEIS/) WEISS J B.
Query Match 7.4%; Score 83.5; DB 7; Length 4123;
Best Local Similarity 22.7%; Pred. No. 5.7e+02;
RESULT 1301
ID ADH48718 standard; protein; 4219 AA.
DE NOV1 protein sequence, SEQ ID 2.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 7.4%; Score 83.5; DB 5; Length 4219;
Best Local Similarity 22.7%; Pred. No. 5.9e+02;
RESULT 1302
ID AAM24516 standard; protein; 5179 AA.
DE C899P predicted amino acid sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.4%; Score 83.5; DB 4; Length 5179;
Best Local Similarity 30.7%; Pred. No. 7.8e+02;
RESULT 1303
ID ABP55365 standard; protein; 5179 AA.
DE Human colon tumour protein for clone C899P SEQ ID NO:1068.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP.
Query Match 7.4%; Score 83.5; DB 6; Length 5179;
Best Local Similarity 30.7%; Pred. No. 7.8e+02;
RESULT 1304
ID ABO07258 standard; protein; 5179 AA.
DE Human p53 modifying protein, SEQ ID 218.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 7.4%; Score 83.5; DB 6; Length 5179;
Best Local Similarity 30.7%; Pred. No. 7.8e+02;
RESULT 1305
ID ADD48091 standard; protein; 5179 AA.
DE Human Protein NP_002448, SEQ ID NO 13789.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 7.4%; Score 83.5; DB 7; Length 5179;
Best Local Similarity 30.7%; Pred. No. 7.8e+02;
RESULT 1306
ID AD044998 standard; protein; 5179 AA.
DE Human Protein Q02817, SEQ ID NO 10430.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
Query Match 7.4%; Score 83.5; DB 7; Length 5179;
Best Local Similarity 30.7%; Pred. No. 7.8e+02;
RESULT 1307
ID ADQ29695 standard; protein; 5179 AA.
DE Human colorectal cancer-associated protein #50.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB ) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
Query Match 7.4%; Score 83.5; DB 8; Length 5179;
Best Local Similarity 30.7%; Pred. No. 7.8e+02;
RESULT 1308
ID ADQ80379 standard; protein; 5179 AA.
DE Intestinal/tracheal mucin 2 protein.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
Query Match 7.4%; Score 83.5; DB 8; Length 5179;
Best Local Similarity 30.7%; Pred. No. 7.8e+02;
RESULT 1309
ID ADM95228 standard; protein; 5737 AA.
DE Human BEC/LEC-related protein sequence SeqID150.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN ) LICENTIA LTD.
Query Match 7.4%; Score 83.5; DB 7; Length 5737;
Best Local Similarity 22.7%; Pred. No. 8.9e+02;
RESULT 1310
ID AAR07670 standard; protein; 166 AA.
DE Intestinal mucin deduced from clone SMUC 40.
PN WO9012892-A.
PD 01-NOV-1990.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.4%; Score 83; DB 2; Length 166;
Best Local Similarity 29.9%; Pred. No. 8.9;
RESULT 1311
ID AAW75700 standard; peptide; 409 AA.
DE Vpr protein binding HHR23B amino acid sequence.
PN WO9835234-A1.
PD 13-AUG-1998.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.4%; Score 83; DB 2; Length 409;
Best Local Similarity 28.6%; Pred. No. 30;
RESULT 1312
ID AAW68186 standard; protein; 409 AA.
DE Vpr binding protein HHR23B amino acid sequence.
PN WO9835032-A2.
PD 13-AUG-1998.
PA (REGC ) UNIV CALIFORNIA.
Query Match 7.4%; Score 83; DB 2; Length 409;
Best Local Similarity 28.6%; Pred. No. 30;
RESULT 1313
ID ABU07460 standard; protein; 409 AA.
DE Protein differentially regulated in prostate cancer #63.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 7.4%; Score 83; DB 6; Length 409;
Best Local Similarity 28.6%; Pred. No. 30;
RESULT 1314

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ID ADN03716 standard; protein; 409 AA.
DE Antiplatelet protein sequence #55.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.4%; Score 83; DB 8; Length 409;
Best Local Similarity 28.8%; Pred. No. 30;
RESULT 1315
ID ADQ65876 standard; protein; 409 AA.
DE Novel human protein sequence #849.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (KEAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.4%; Score 83; DB 8; Length 409;
Best Local Similarity 28.6%; Pred. No. 30;
RESULT 1316
ID ABB61785 standard; protein; 471 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12147.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.4%; Score 83; DB 4; Length 471;
Best Local Similarity 35.0%; Pred. No. 36;
RESULT 1317
ID ADS43586 standard; protein; 605 AA.
DE Bacterial polypeptide #22016.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.4%; Score 83; DB 8; Length 605;
Best Local Similarity 31.8%; Pred. No. 50;
RESULT 1318
ID AAG34201 standard; protein; 280 AA.
DE Zea mays protein fragment SEQ ID NO: 41576.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 82.5; DB 3; Length 280;
Best Local Similarity 28.7%; Pred. No. 20;
RESULT 1319
ID AAG40817 standard; protein; 346 AA.
DE Zea mays protein fragment SEQ ID NO: 50697.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 82.5; DB 3; Length 346;
Best Local Similarity 28.7%; Pred. No. 26;
RESULT 1320
ID ADS44071 standard; protein; 825 AA.
DE Bacterial polypeptide #22501.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.3%; Score 82.5; DB 8; Length 825;
Best Local Similarity 24.8%; Pred. No. 84;
RESULT 1321
ID ABB71012 standard; protein; 843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 82.5; DB 4; Length 843;
Best Local Similarity 24.0%; Pred. No. 87;
RESULT 1322
ID AAW38272 standard; protein; 1085 AA.
DE Bovine parathyroid cell calcium receptor 1 (BoPCar 1).
PN US5688938-A.

PD 18-NOV-1997.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
PA (NPSP-) NPS PHARM INC.
Query Match 7.3%; Score 82.5; DB 2; Length 1085;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1323
ID ABB69011 standard; protein; 1371 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33825.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.3%; Score 82.5; DB 4; Length 1371;
Best Local Similarity 33.0%; Pred. No. 1.7e+02;
RESULT 1324
ID AAM21657 standard; protein; 89 AA.
DE Peptide #8091 encoded by probe for measuring cervical gene expression.
PN WO200157278-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1325
ID ABB44016 standard; peptide; 89 AA.
DE Peptide #11522 encoded by human foetal liver single exon probe.
PN WO200157277-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1326
ID AAM37960 standard; protein; 89 AA.
DE Peptide #11997 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1327
ID ABB26922 standard; protein; 89 AA.
DE Protein #8921 encoded by probe for measuring heart cell gene expression.
PN WO200157274-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1328
ID AAM77746 standard; protein; 89 AA.
DE Human bone marrow expressed probe encoded protein SEQ ID NO: 38052.
PN WO200157276-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1329
ID AAM65031 standard; protein; 89 AA.
DE Human brain expressed single exon probe encoded protein SEQ ID NO: 37136.
PN WO200157275-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1330
ID ABB59403 standard; peptide; 89 AA.
DE Human liver peptide, SEQ ID NO 38051.
PN WO200157273-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 4; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1331
ID ABB46774 standard; peptide; 89 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 36439.
PN WO200186003-A2.

PD 15-NOV-2001.
PA (MOLB-) MOLECULAR DYNAMICS INC.
Query Match 7.3%; Score 82; DB 5; Length 89;
Best Local Similarity 28.9%; Pred. No. 4.9;
RESULT 1332
ID ABB67754 standard; protein; 339 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30054.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE-) PE CORP NY.
Query Match 7.3%; Score 82; DB 4; Length 339;
Best Local Similarity 25.4%; Pred. No. 29;
RESULT 1333
ID ADQ18080 standard; protein; 477 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 897.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.3%; Score 82; DB 8; Length 477;
Best Local Similarity 32.1%; Pred. No. 45;
RESULT 1334
ID ABG70759 standard; protein; 553 AA.
DE T. maritima endoglucanase protein.
PN US2002120118-A1.
PD 29-AUG-2002.
PA (SHOR/) SHORT J M.
PA (LAMD/) LAM D E.
PA (MATH/) MATHUR E J.
Query Match 7.3%; Score 82; DB 5; Length 553;
Best Local Similarity 28.2%; Pred. No. 55;
RESULT 1335
ID AAW34999 standard; protein; 628 AA.
DE Archaeobacterium ABP11a endoglucanase.
PN WO9744361-A1.
PD 27-NOV-1997.
PA (RECO-) RECOMBINANT BIOTECNOLOGY INC.
Query Match 7.3%; Score 82; DB 2; Length 628;
Best Local Similarity 28.2%; Pred. No. 66;
RESULT 1336
ID ADA55053 standard; protein; 637 AA.
DE Human protein, SEQ ID 2621.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.3%; Score 82; DB 6; Length 637;
Best Local Similarity 24.2%; Pred. No. 67;
RESULT 1337
ID AAB29654 standard; protein; 667 AA.
DE Human membrane-associated protein HUMAP-11.
PN WO200065054-A2.
PD 02-NOV-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.3%; Score 82; DB 3; Length 667;
Best Local Similarity 24.2%; Pred. No. 71;
RESULT 1338
ID AAW34985 standard; protein; 841 AA.
DE Archaeobacterial thermostable endoglucanase.
PN WO9744361-A1.
PD 27-NOV-1997.
PA (RECO-) RECOMBINANT BIOTECNOLOGY INC.
Query Match 7.3%; Score 82; DB 2; Length 841;
Best Local Similarity 28.2%; Pred. No. 97;
RESULT 1339
ID AAR22234 standard; protein; 995 AA.
DE Sequence encoded by ILTV gp60 gene.
PN WO9203554-A.
PD 05-MAR-1992.
PA (WEBS-) WEBSTER A PTY LTD.
Query Match 7.3%; Score 82; DB 2; Length 995;
Best Local Similarity 31.7%; Pred. No. 1.2e+02;
RESULT 1340
ID ADM47185 standard; protein; 1671 AA.

DE Neurexin III-alpha membrane-bound type I precursor like NOVX 3a protein.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.3%; Score 82; DB 7; Length 1671;
Best Local Similarity 24.2%; Pred. No. 2.4e+02;
RESULT 1341
ID AAB09826 standard; protein; 346 AA.
DE Endoglucanase protein sequence 6.
PN WO200024879-A1.
PD 04-MAY-2000.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 3; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1342
ID AAO15057 standard; protein; 346 AA.
DE Phycomyces nitens endoglucanase-related protein.
PN WO200242474-A1.
PD 30-MAY-2002.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 5; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1343
ID ABB08065 standard; protein; 346 AA.
DE P. nitens CP99002 PCEI protein.
PN WO200238754-A1.
PD 16-MAY-2002.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 5; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1344
ID ADA37114 standard; protein; 346 AA.
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO:6.
PN WO2003052105-A1.
PD 26-JUN-2003.
PA (MEIJ-) MEIJI SEIKA KAISHA LTD.
Query Match 7.2%; Score 81.5; DB 6; Length 346;
Best Local Similarity 23.3%; Pred. No. 33;
RESULT 1345
ID ABU23564 standard; protein; 386 AA.
DE Protein encoded by Prokaryotic essential gene #9091.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 81.5; DB 6; Length 386;
Best Local Similarity 22.0%; Pred. No. 38;
RESULT 1346
ID AB058564 standard; protein; 800 AA.
DE Human genome derived single exon protein #4798.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN/) PENN S G.
PA (RANK/) RANK D R.
PA (HANZ/) HANZEL D K.
Query Match 7.2%; Score 81.5; DB 8; Length 800;
Best Local Similarity 35.8%; Pred. No. 1e+02;
RESULT 1347
ID AAY59288 standard; protein; 957 AA.
DE Human MUC11 polypeptide.
PN WO200004142-A1.
PD 27-JAN-2000.
PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
Query Match 7.2%; Score 81.5; DB 3; Length 957;
Best Local Similarity 29.0%; Pred. No. 1.3e+02;
RESULT 1348
ID AAM24513 standard; protein; 957 AA.
DE C900P predicted amino acid sequence.
PN WO200149716-A2.
PD 12-JUL-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 81.5; DB 4; Length 957;
Best Local Similarity 29.0%; Pred. No. 1.3e+02;

RESULT 1349
ID ABP5362 standard; protein; 957 AA.
DE Human colon tumour protein for clone C900P SEQ ID NO:1065.
PN WO200283070-A2.
PD 24-OCT-2002.
PA (CORI-) CORIXA CORP. 7.2%; Score 81.5; DB 6; Length 957;
Query Match Best Local Similarity 29.0%; Pred. No. 1.3e+02;
RESULT 1350
ID ADC31682 standard; protein; 1205 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1764.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYS-) HYSQ INC. 7.2%; Score 81.5; DB 7; Length 1205;
Query Match Best Local Similarity 29.0%; Pred. No. 1.7e+02;
RESULT 1351
ID ABB69973 standard; protein; 1354 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36711.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 7.2%; Score 81.5; DB 4; Length 1354;
Query Match Best Local Similarity 21.9%; Pred. No. 2e+02;
RESULT 1352
ID AAY93912 standard; protein; 289 AA.
DE A human hyaluronan-binding protein, designated OE-RABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match Best Local Similarity 7.2%; Score 81; DB 3; Length 289;
Query Match Best Local Similarity 24.4%; Pred. No. 29;
RESULT 1353
ID ABB64749 standard; protein; 294 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21039.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY. 7.2%; Score 81; DB 4; Length 294;
Query Match Best Local Similarity 22.0%; Pred. No. 30;
RESULT 1354
ID AAR60563 standard; protein; 862 AA.
DE Yeast 2.6 kB agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGERILABORATORIUM.
Query Match Best Local Similarity 7.2%; Score 81; DB 2; Length 862;
Query Match Best Local Similarity 21.8%; Pred. No. 1.3e+02;
RESULT 1355
ID AAR58754 standard; protein; 894 AA.
DE S. cerevisiae FLO1.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV. 7.2%; Score 81; DB 2; Length 894;
Query Match Best Local Similarity 21.8%; Pred. No. 1.3e+02;
RESULT 1356
ID AAR47578 standard; protein; 894 AA.
DE Flocculation protein of Saccharomyces cerevisiae.
PN WO9401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV. 7.2%; Score 81; DB 2; Length 894;
Query Match Best Local Similarity 21.8%; Pred. No. 1.3e+02;
RESULT 1357
ID ADS44054 standard; protein; 1128 AA.
DE Bacterial polypeptide #22484.
PN WO2003233675-A1.
PD 18-DEC-2003.

PA (CAOY/) CAO Y. 7.2%; Score 81; DB 8; Length 1128;
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match Best Local Similarity 22.8%; Pred. No. 1.8e+02;
RESULT 1358
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 kB agglutination gene FLO1L.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGERILABORATORIUM.
Query Match Best Local Similarity 7.2%; Score 81; DB 2; Length 1537;
Query Match Best Local Similarity 21.8%; Pred. No. 2.7e+02;
RESULT 1359
ID ADP87475 standard; protein; 1537 AA.
DE S cerevisiae glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN WO2004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match Best Local Similarity 7.2%; Score 81; DB 8; Length 1537;
Query Match Best Local Similarity 21.8%; Pred. No. 2.7e+02;
RESULT 1360
ID ADNI8745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match Best Local Similarity 7.2%; Score 81; DB 8; Length 1537;
Query Match Best Local Similarity 21.8%; Pred. No. 2.7e+02;
RESULT 1361
ID ADRI8921 standard; protein; 1569 AA.
DE Human mucin glycoprotein, MUC6.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match Best Local Similarity 7.2%; Score 81; DB 8; Length 1569;
Query Match Best Local Similarity 25.5%; Pred. No. 2.8e+02;
RESULT 1362
ID ADNI8882 standard; protein; 1609 AA.
DE Bacterial polypeptide #1535.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match Best Local Similarity 7.2%; Score 81; DB 8; Length 1609;
Query Match Best Local Similarity 22.4%; Pred. No. 2.9e+02;
RESULT 1363
ID ADRI8914 standard; protein; 2240 AA.
DE Mature Human mucin-like protein, SCS0004, variant SEQ ID 4.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match Best Local Similarity 7.2%; Score 81; DB 8; Length 2240;
Query Match Best Local Similarity 25.5%; Pred. No. 4.5e+02;
RESULT 1364
ID ADRI8913 standard; protein; 2258 AA.
DE Human mucin-like protein, SCS0004, variant SEQ ID 3.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match Best Local Similarity 7.2%; Score 81; DB 8; Length 2258;
Query Match Best Local Similarity 25.5%; Pred. No. 4.5e+02;
RESULT 1365

ID ADR18915 standard; protein; 2264 AA.
DE His-tagged Human mucin-like protein, SCS0004, variant SEQ ID 5.
PN WO2004069136-A2.
PD 19-AUG-2004.
PA (ISTF) ARS APPLIED RES SYSTEMS HOLDING NV.
Query Match 7.2%; Score 81; DB 8; Length 2264;
Best Local Similarity 25.5%; Pred. No. 4.5e+02;
RESULT 1366
ID ABB69480 standard; protein; 2977 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35232.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.2%; Score 81; DB 4; Length 2977;
Best Local Similarity 18.8%; Pred. No. 6.5e+02;
RESULT 1367
ID ABP07042 standard; protein; 128 AA.
DE Human ORFX protein sequence SEQ ID NO:14066.
PN WO200192523-A2.
PD 06-DEC-2001.
PA (CURA-) CURAGEN CORP.
Query Match 7.2%; Score 80.5; DB 5; Length 128;
Best Local Similarity 33.8%; Pred. No. 11;
RESULT 1368
ID ADD46369 standard; protein; 148 AA.
DE Rat Protein CAA34501, SEQ ID NO 12049.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 80.5; DB 7; Length 148;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 1369
ID AAU50934 standard; protein; 176 AA.
DE Propionibacterium acnes immunogenic protein #11830.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 80.5; DB 4; Length 176;
Best Local Similarity 27.8%; Pred. No. 17;
RESULT 1370
ID ABM47453 standard; protein; 176 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #12129.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 7.2%; Score 80.5; DB 6; Length 176;
Best Local Similarity 27.8%; Pred. No. 17;
RESULT 1371
ID ABU26248 standard; protein; 323 AA.
DE Protein encoded by Prokaryotic essential gene #11775.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 80.5; DB 6; Length 323;
Best Local Similarity 27.1%; Pred. No. 38;
RESULT 1372
ID ABP28528 standard; protein; 540 AA.
DE Streptococcus polypeptide SEQ ID NO 6232.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.2%; Score 80.5; DB 5; Length 540;
Best Local Similarity 22.5%; Pred. No. 75;
RESULT 1373
ID ABB57757 standard; protein; 1167 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 63.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.2%; Score 80.5; DB 4; Length 1167;
Best Local Similarity 28.2%; Pred. No. 2.1e+02;

RESULT 1374
ID AAR77036 standard; protein; 52 AA.
DE Human brain-enriched hyaluronan binding protein PTR1 domain.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV YALE.
Query Match 7.1%; Score 80; DB 2; Length 52;
Best Local Similarity 35.0%; Pred. No. 3.7;
RESULT 1375
ID ABP63646 standard; protein; 89 AA.
DE Human ORF16.
PN US2002082206-A1.
PD 27-JUN-2002.
PA (LEAC/) LEACH M D.
PA (MEHR/) MEHRABAN F.
PA (CONL/) CONLEY P B.
PA (TOPP/) TOPPER J N.
PA (LAWD/) LAW D.
Query Match 7.1%; Score 80; DB 5; Length 89;
Best Local Similarity 32.6%; Pred. No. 7.6;
RESULT 1376
ID ABO79758 standard; protein; 95 AA.
DE Pseudomonas aeruginosa polypeptide #11933.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.1%; Score 80; DB 7; Length 95;
Best Local Similarity 28.3%; Pred. No. 8.3;
RESULT 1377
ID ADR09088 standard; protein; 272 AA.
DE Human protein useful for treating neurological disease Seq 2594.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.1%; Score 80; DB 8; Length 272;
Best Local Similarity 23.4%; Pred. No. 34;
RESULT 1378
ID ADF58702 standard; protein; 351 AA.
DE Human polypeptide sequence SEQ ID NO:1110.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 80; DB 7; Length 351;
Best Local Similarity 23.4%; Pred. No. 47;
RESULT 1379
ID ABB66171 standard; protein; 449 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 25305.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.1%; Score 80; DB 4; Length 449;
Best Local Similarity 23.9%; Pred. No. 66;
RESULT 1380
ID AAY01077 standard; protein; 473 AA.
DE H. insolens Cel16A fungal cellulase protien sequence.
PN WO9501544-A1.
PD 14-JAN-1999.
PA (NOVO) NOVO-NORDISK AS.
Query Match 7.1%; Score 80; DB 2; Length 473;
Best Local Similarity 28.1%; Pred. No. 71;
RESULT 1381
ID ADN19351 standard; protein; 725 AA.
DE Bacterial polypeptide #2004.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 7.1%; Score 80; DB 8; Length 725;
Best Local Similarity 27.2%; Pred. No. 1.2e+02;
RESULT 1382

ID ABU09610 standard; protein; 729 AA.
DE Mouse retinoic acid-regulated nuclear matrix-associated protein.
PN US2003003485-A1.
PD 02-JAN-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
Query Match 7.1%; Score 80; DB 6; Length 729;
Best Local Similarity 20.8%; Pred. No. 1.3e+02;
RESULT 1383
ID ABG23210 standard; protein; 791 AA.
DE Novel human diagnostic protein #23201.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 80; DB 4; Length 791;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1384
ID ADS12299 standard; protein; 791 AA.
DE Human therapeutic contig protein - SEQ ID 2536.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.1%; Score 80; DB 8; Length 791;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1385
ID AAG70752 standard; protein; 881 AA.
DE S cerevisiae apoptosis associated protein YJL070C.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC-) JANSSEN PHARM NV.
Query Match 7.1%; Score 80; DB 4; Length 881;
Best Local Similarity 23.6%; Pred. No. 1.6e+02;
RESULT 1386
ID ABUS4861 standard; protein; 10431 AA.
DE Human CA125 amino terminal extension.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 7.1%; Score 80; DB 6; Length 10431;
Best Local Similarity 22.3%; Pred. No. 4.4e+03;
RESULT 1387
ID ABUS3162 standard; protein; 277 AA.
DE Human testes-derived DKFphtes3_2a11 homologue #22.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.1%; Score 79.5; DB 4; Length 277;
Best Local Similarity 29.4%; Pred. No. 39;
RESULT 1388
ID ABG01510 standard; protein; 320 AA.
DE Novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 4; Length 320;
Best Local Similarity 25.7%; Pred. No. 47;
RESULT 1389
ID ABG62076 standard; protein; 324 AA.
DE Klebsiella pneumoniae polypeptide seqid 8593.
PN US610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 7.1%; Score 79.5; DB 7; Length 324;
Best Local Similarity 21.3%; Pred. No. 48;
RESULT 1390
ID ADJ76313 standard; protein; 363 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1565.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.1%; Score 79.5; DB 8; Length 363;
Best Local Similarity 25.2%; Pred. No. 56;
RESULT 1391
ID ABG07923 standard; protein; 366 AA.

DE Novel human diagnostic protein #7914.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 4; Length 366;
Best Local Similarity 25.7%; Pred. No. 56;
RESULT 1392
ID ABUS3155 standard; protein; 692 AA.
DE Human testes-derived DKFphtes3_2a11 homologue #15.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 7.1%; Score 79.5; DB 4; Length 692;
Best Local Similarity 29.4%; Pred. No. 1.3e+02;
RESULT 1393
ID ABB63128 standard; protein; 796 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16176.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 7.1%; Score 79.5; DB 4; Length 796;
Best Local Similarity 26.3%; Pred. No. 1.6e+02;
RESULT 1394
ID ABB49326 standard; protein; 860 AA.
DE Listeria monocytogenes protein #2030.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTEUR.
Query Match 7.1%; Score 79.5; DB 5; Length 860;
Best Local Similarity 20.3%; Pred. No. 1.8e+02;
RESULT 1395
ID ABUS32996 standard; protein; 860 AA.
DE Protein encoded by Prokaryotic essential gene #18523.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 79.5; DB 6; Length 860;
Best Local Similarity 20.3%; Pred. No. 1.8e+02;
RESULT 1396
ID ABB71072 standard; protein; 875 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40008.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 7.1%; Score 79.5; DB 4; Length 875;
Best Local Similarity 29.5%; Pred. No. 1.8e+02;
RESULT 1397
ID AAW00634 standard; protein; 985 AA.
DE ILTV glycoprotein g60.
PN WO9508622-A1.
PD 30-MAR-1995.
PA (SYTR-) SYNTRO CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 985;
Best Local Similarity 30.9%; Pred. No. 2.1e+02;
RESULT 1398
ID AAW06786 standard; protein; 985 AA.
DE ILTV glycoprotein g60.
PN WO9629396-A1.
PD 26-SEP-1996.
PA (SYTR-) SYNTRO CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 985;
Best Local Similarity 30.9%; Pred. No. 2.1e+02;
RESULT 1399
ID AAY41092 standard; protein; 1114 AA.
DE Peptide Seq ID No: 34 of WO9945111.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1114;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1400
ID AAB15730 standard; protein; 1114 AA.
DE Protein encoded by cDNA generated from RACE3.3 and clone 3.3 sequences.

PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1114;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1401
ID AAY41086 standard; protein; 1123 AA.
DE Human lectomedin-beta polypeptide.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1123;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1402
ID AAB15724 standard; protein; 1123 AA.
DE Human lectomedin-beta.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1123;
Best Local Similarity 20.8%; Pred. No. 2.5e+02;
RESULT 1403
ID AAY41085 standard; protein; 1177 AA.
DE Human lectomedin-lalpa.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1177;
Best Local Similarity 20.8%; Pred. No. 2.7e+02;
RESULT 1404
ID AAB15723 standard; protein; 1177 AA.
DE Human lectomedin-lalpa.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1177;
Best Local Similarity 20.8%; Pred. No. 2.7e+02;
RESULT 1405
ID ADD46682 standard; protein; 1318 AA.
DE Human Protein CAC19796, SEQ ID NO 12367.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 79.5; DB 7; Length 1318;
Best Local Similarity 20.8%; Pred. No. 3.1e+02;
RESULT 1406
ID ADE55337 standard; protein; 1318 AA.
DE Human Protein CAC19796, SEQ ID NO 1151.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.1%; Score 79.5; DB 7; Length 1318;
Best Local Similarity 20.8%; Pred. No. 3.1e+02;
RESULT 1407
ID AAY41087 standard; protein; 1403 AA.
DE Human lectomedin-igamma polypeptide.
PN WO9945111-A1.
PD 10-SEP-1999.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 2; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1408
ID AAB15725 standard; protein; 1403 AA.
DE Human lectomedin-Igama cDNA.
PN WO200052039-A2.
PD 08-SEP-2000.
PA (ICOS-) ICOS CORP.
Query Match 7.1%; Score 79.5; DB 3; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1409
ID ABP81675 standard; protein; 1403 AA.

DE Human latrophilin-2 protein SEQ ID NO:526.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 7.1%; Score 79.5; DB 6; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1410
ID ADD89067 standard; protein; 1403 AA.
DE TAT254.
PN WO2003057160-A2.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.1%; Score 79.5; DB 7; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1411
ID ADN95548 standard; protein; 1403 AA.
DE Human BEC/LEC-related protein sequence SeqID471.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.1%; Score 79.5; DB 7; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1412
ID ADO29115 standard; protein; 1403 AA.
DE Human novel GPCR LEC1, SEQ ID NO:214.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 7.1%; Score 79.5; DB 8; Length 1403;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1413
ID AAU30676 standard; protein; 1425 AA.
DE Novel human secreted protein #1167.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 4; Length 1425;
Best Local Similarity 20.8%; Pred. No. 3.4e+02;
RESULT 1414
ID ADC26275 standard; protein; 1459 AA.
DE Human NOV22 protein.
PN WO2003004687-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 7.1%; Score 79.5; DB 7; Length 1459;
Best Local Similarity 20.8%; Pred. No. 3.5e+02;
RESULT 1415
ID ABB59325 standard; protein; 1486 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 4767.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.1%; Score 79.5; DB 4; Length 1486;
Best Local Similarity 24.2%; Pred. No. 3.6e+02;
RESULT 1416
ID ADM97582 standard; protein; 1488 AA.
DE Human calcium-independent alpha-latrotoxin receptor.
PN WO2004031235-A1.
PD 15-APR-2004.
PA (FARB) BAYER HEALTHCARE AG.
Query Match 7.1%; Score 79.5; DB 8; Length 1488;
Best Local Similarity 20.8%; Pred. No. 3.6e+02;
RESULT 1417
ID ABP43908 standard; protein; 4315 AA.
DE MUC5B partial gene protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 7.1%; Score 79.5; DB 5; Length 4315;
Best Local Similarity 33.0%; Pred. No. 1.5e+03;
RESULT 1418
ID ADL23265 standard; protein; 5703 AA.

DE Human MUC5B.
PN WO2004019041-A1.
PD 04-MAR-2004.
PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.
PA (PACK/) PACKER N H.
PA (KARL/) KARLSSON N.
PA (SCHU/) SCHULZ B L.
Query Match 7.1%; Score 79.5; DB 8; Length 5703;
Best Local Similarity 33.0%; Pred. No. 2.2e+03;
RESULT 1419
ID AAB11743 standard; protein; 175 AA.
DE C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:17.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.0%; Score 79; DB 3; Length 175;
Best Local Similarity 24.2%; Pred. No. 24;
RESULT 1420
ID ABJ04056 standard; protein; 175 AA.
DE C. parvum GP900 protein fragment SEQ ID NO: 17.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 7.0%; Score 79; DB 5; Length 175;
Best Local Similarity 24.2%; Pred. No. 24;
RESULT 1421
ID ABB69342 standard; protein; 195 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 34818.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 79; DB 4; Length 195;
Best Local Similarity 29.1%; Pred. No. 27;
RESULT 1422
ID ADO66739 standard; protein; 213 AA.
DE Novel human protein sequence #1712.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 7.0%; Score 79; DB 8; Length 213;
Best Local Similarity 25.9%; Pred. No. 31;
RESULT 1423
ID AAU93021 standard; protein; 352 AA.
DE Arabidopsis transcription factor #59.
PN WO200215675-A1.
PD 28-FEB-2002.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (PILG/) PILGRIM M.
PA (CREE/) CREELMAN R.
PA (DUBE/) DUBELL A J.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (KEDD/) KEDDIE J.
PA (ADAM/) ADAM L.
PA (RATC/) RATCLIFF O.
PA (REUB/) REUBER J L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (PINE/) PINEDA O.
Query Match 7.0%; Score 79; DB 5; Length 352;
Best Local Similarity 27.1%; Pred. No. 60;
RESULT 1424
ID ADA15555 standard; protein; 352 AA.
DE A. thaliana protein, SEQ ID NO:110.
PN US2003061637-A1.
PD 27-MAR-2003.
PA (JIAN/) JIANG C.
PA (BROU/) BROUN P.
PA (RIEC/) RIECHMANN J L.
PA (PINE/) PINEDA O.
PA (ZHAN/) ZHANG J.
PA (YUGG/) YU G.
PA (PILG/) PILGRIM M.
PA (KEDD/) KEDDIE J.
PA (HEAR/) HEARD J.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 7.0%; Score 79; DB 8; Length 352;
Best Local Similarity 27.1%; Pred. No. 60;
RESULT 1425
ID ADD30080 standard; protein; 352 AA.
DE Plant yield-related protein from clone G671.
PN WO2003013227-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 7.0%; Score 79; DB 7; Length 352;
Best Local Similarity 27.1%; Pred. No. 60;
RESULT 1426
ID ADE31453 standard; protein; 352 AA.
DE Plant yield related protein from clone G671.
PN WO2003013228-A2.
PD 20-FEB-2003.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 7.0%; Score 79; DB 7; Length 352;
Best Local Similarity 27.1%; Pred. No. 60;
RESULT 1427
ID ADI43589 standard; protein; 352 AA.
DE Plant transcription factor #667.
PN US2004019927-A1.
PD 29-JAN-2004.
PA (SHER/) SHERMAN B K.
PA (RIEC/) RIECHMANN J L.
PA (JIAN/) JIANG C.
PA (HEAR/) HEARD J E.
PA (HAAR/) HAAKE V.
PA (CREE/) CREELMAN R A.
PA (RATC/) RATCLIFFE O.
PA (ADAM/) ADAM L J.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J.
PA (BROU/) BROUN P E.
PA (PILG/) PILGRIM M L.
PA (DUBE/) DUBELL A N.
PA (PINE/) PINEDA O.
PA (YUGG/) YU G.
Query Match 7.0%; Score 79; DB 8; Length 352;
Best Local Similarity 27.1%; Pred. No. 60;
RESULT 1428
ID ADO02037 standard; protein; 352 AA.
DE Thalecress transcription factor protein #225.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PILG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 7.0%; Score 79; DB 8; Length 352;
Best Local Similarity 27.1%; Pred. No. 60;
RESULT 1429
ID ABU07483 standard; protein; 410 AA.

DE Protein differentially regulated in prostate cancer #86.
PN WO200281638-A2.
PD 17-OCT-2002.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 7.0%; Score 79; DB 6; Length 410;
Best Local Similarity 20.5%; Pred. No. 73;
RESULT 1430
ID ADE58847 standard; protein; 410 AA.
DE Human Protein P13473, SEQ ID NO 4735.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 79; DB 7; Length 410;
Best Local Similarity 20.5%; Pred. No. 73;
RESULT 1431
ID ADL14997 standard; protein; 410 AA.
DE Human lysosome associated protein 2 protein for cancer treatment.
PN WO2003068268-A2.
PD 21-AUG-2003.
PA (BIOI-) BIOINVENT INT AB.
Query Match 7.0%; Score 79; DB 7; Length 410;
Best Local Similarity 20.5%; Pred. No. 73;
RESULT 1432
ID ADN95768 standard; protein; 410 AA.
DE Human BSC/LEC-related protein sequence SeqID692.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.0%; Score 79; DB 7; Length 410;
Best Local Similarity 20.5%; Pred. No. 73;
RESULT 1433
ID ADP49322 standard; protein; 410 AA.
DE Human lysosomal associated membrane protein LAMP #2.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 7.0%; Score 79; DB 8; Length 410;
Best Local Similarity 20.5%; Pred. No. 73;
RESULT 1434
ID ADP23470 standard; protein; 410 AA.
DE PRO polypeptide SEQ ID NO:648.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.0%; Score 79; DB 8; Length 410;
Best Local Similarity 20.5%; Pred. No. 73;
RESULT 1435
ID AAO29892 standard; protein; 411 AA.
DE Human organelle-associated protein (ORGA)-5.
PN WO2003044171-A2.
PD 30-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.0%; Score 79; DB 6; Length 411;
Best Local Similarity 20.5%; Pred. No. 74;
RESULT 1436
ID ADK68630 standard; protein; 599 AA.
DE HSP65-MUC1 antigen CTL epitope related protein.
PN CN1368384-A.
PD 11-SEP-2002.
PA (DIWE-) DIWEIHUAYU BIO TECHNOLOGY CO LTD BEIJING.
Query Match 7.0%; Score 79; DB 7; Length 599;
Best Local Similarity 19.0%; Pred. No. 1.2e+02;
RESULT 1437
ID AAR88466 standard; protein; 629 AA.
DE Drosophila scavenger receptor class CI.
PN WO9600288-A2.
PD 04-JAN-1996.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 7.0%; Score 79; DB 2; Length 629;
Best Local Similarity 22.2%; Pred. No. 1.3e+02;
RESULT 1438

ID ABB59507 standard; protein; 629 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5313.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 79; DB 4; Length 629;
Best Local Similarity 22.2%; Pred. No. 1.3e+02;
RESULT 1439
ID ABB67438 standard; protein; 629 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29106.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 7.0%; Score 79; DB 4; Length 629;
Best Local Similarity 29.2%; Pred. No. 1.3e+02;
RESULT 1440
ID ABG33057 standard; protein; 629 AA.
DE Fruit fly scavenger receptor type CI (dsr-CI).
PN US6429289-B1.
PD 06-AUG-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 7.0%; Score 79; DB 5; Length 629;
Best Local Similarity 22.2%; Pred. No. 1.3e+02;
RESULT 1441
ID AAE21524 standard; protein; 629 AA.
DE Drosophila melanogaster scavenger receptor class CI (dsr-CI).
PN US6350859-B1.
PD 26-FEB-2002.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
Query Match 7.0%; Score 79; DB 5; Length 629;
Best Local Similarity 22.2%; Pred. No. 1.3e+02;
RESULT 1442
ID ADQ97694 standard; protein; 786 AA.
DE Mouse cancer associated sequence MP10-029, SEQ ID 671.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 7.0%; Score 79; DB 8; Length 786;
Best Local Similarity 20.6%; Pred. No. 1.7e+02;
RESULT 1443
ID ABB91667 standard; protein; 980 AA.
DE Herbicidially active polypeptide SEQ ID NO 878.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 79; DB 5; Length 980;
Best Local Similarity 21.0%; Pred. No. 2.3e+02;
RESULT 1444
ID ADE58456 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4331.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 79; DB 7; Length 1031;
Best Local Similarity 22.0%; Pred. No. 2.5e+02;
RESULT 1445
ID ADE58468 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4343.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 79; DB 7; Length 1031;
Best Local Similarity 22.0%; Pred. No. 2.5e+02;
RESULT 1446
ID ADE58460 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4335.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.0%; Score 79; DB 7; Length 1031;
Best Local Similarity 22.0%; Pred. No. 2.5e+02;
RESULT 1447

Best Local Similarity 22.0%; Pred. No. 2.5e+02;
RESULT 1447
ID ADE58464 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4339.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 7.0%; Score 79; DB 7; Length 1031;
Pred. No. 2.5e+02;
RESULT 1448
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 7.0%; Score 79; DB 7; Length 1031;
Pred. No. 2.5e+02;
RESULT 1449
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 7.0%; Score 79; DB 7; Length 1031;
Pred. No. 2.5e+02;
RESULT 1450
ID ABB64889 standard; protein; 2616 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 21459.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NV.
Query Match
Best Local Similarity 7.0%; Score 79; DB 4; Length 2616;
Pred. No. 8.7e+02;
RESULT 1451
ID AAB11740 standard; protein; 130 AA.
DE C. parvum Iowa isolate GP900 variant domain 2, SEQ ID NO:14.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 130;
Pred. No. 18;
RESULT 1452
ID ABJ04053 standard; protein; 130 AA.
DE C. parvum GP900 protein fragment SEQ ID NO: 14.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 5; Length 130;
Pred. No. 18;
RESULT 1453
ID ADQ30914 standard; protein; 252 AA.
DE Avian pneumovirus (Colorado) protein SeqID36.
PN WO2004050843-A2.
PD 17-JUN-2004.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 8; Length 252;
Pred. No. 43;
RESULT 1454
ID AAY75301 standard; protein; 286 AA.
DE Neisseria gonorrhoeae ORF 645 protein sequence SEQ ID NO:2076.
PN WO9957280-A2.
PD 11-NOV-1999.
PA (CHIR) CHIRON CORP.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 286;
Pred. No. 51;
RESULT 1455
ID ADO29463 standard; protein; 410 AA.
DE Mouse GPCR GPRC5B, SEQ ID NO:565.
PN WO2004040000-A2.

PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 8; Length 410;
Pred. No. 82;
RESULT 1456
ID AAW25156 standard; protein; 562 AA.
DE HIV-1 Rev/HTLV-1 Rex activation domain binding protein.
PN WO9706257-A1.
PD 20-FEB-1997.
PA (UYDU-) UNIV DUKE.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 2; Length 562;
Pred. No. 1.2e+02;
RESULT 1457
ID AAW83285 standard; protein; 562 AA.
DE Human h-RAB.
PN WO9846744-A1.
PD 22-OCT-1998.
PA (EUON-) IST EURO DI ONCOLOGIA SRL.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 2; Length 562;
Pred. No. 1.2e+02;
RESULT 1458
ID ADM05676 standard; protein; 569 AA.
DE Human protein of the invention SEQ ID NO:4361.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 7; Length 569;
Pred. No. 1.3e+02;
RESULT 1459
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 590;
Pred. No. 1.3e+02;
RESULT 1460
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 6; Length 590;
Pred. No. 1.3e+02;
RESULT 1461
ID ADA23287 standard; protein; 653 AA.
DE Human SECX polypeptide, SEC5 #1.
PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (LARO/) LAROCHELLE W J.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 6; Length 653;
Pred. No. 1.5e+02;
RESULT 1462
ID AAB23033 standard; protein; 694 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-1.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 3; Length 694;
Pred. No. 1.7e+02;
RESULT 1463
ID AAB94736 standard; protein; 858 AA.
DE Human protein sequence SEQ ID NO:15772.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 7.0%; Score 78.5; DB 4; Length 858;
Pred. No. 2.2e+02;
RESULT 1464
ID AAU10540 standard; protein; 1478 AA.
DE Rat CIRL-2 variant BC (YSG2) polypeptide.

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PN WO200175440-A2.
PD 11-OCT-2001.
PA (WELF-) WELFIDE CORP.
Query Match 7.0%; Score 78.5; DB 5; Length 1478;
Best Local Similarity 19.6%; Pred. No. 4.5e+02;
RESULT 1465
ID ADD46680 standard; protein; 1478 AA.
DE Rat Protein AAC62654, SEQ ID NO 12365.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1478;
Best Local Similarity 19.6%; Pred. No. 4.5e+02;
RESULT 1466
ID ADE55162 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 967.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1467
ID ADE55174 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 979.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1468
ID ADE55170 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 975.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1469
ID ADE55166 standard; protein; 1488 AA.
DE Rat Protein AF063102, SEQ ID NO 971.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 7.0%; Score 78.5; DB 7; Length 1488;
Best Local Similarity 19.6%; Pred. No. 4.6e+02;
RESULT 1470
ID ABB63883 standard; protein; 2040 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 18441.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 7.0%; Score 78.5; DB 4; Length 2040;
Best Local Similarity 22.0%; Pred. No. 7e+02;
RESULT 1471
ID ABR63235 standard; protein; 2055 AA.
DE Glucanase sequence from strain KG15.
PN WO2003008618-A2.
PD 30-JAN-2003.
PA (NEDE ) NEDERLANDSE ORG TOEGEPAST.
Query Match 7.0%; Score 78.5; DB 6; Length 2055;
Best Local Similarity 26.2%; Pred. No. 7e+02;
RESULT 1472
ID ABM70225 standard; protein; 2466 AA.
DE Photorhabdus luminescens protein sequence #3322.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP ) INST PASTEUR.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match 7.0%; Score 78.5; DB 6; Length 2466;
Best Local Similarity 24.3%; Pred. No. 9e+02;
RESULT 1473
ID AAW74522 standard; protein; 116 AA.
DE Amino acid sequence of the human aggrecan GI-B domain.
PN EP861903-A1.
PD 02-SEP-1998.
PA (LANS/) LANSING M.
PA (UHLE/) UHLENKUEKEN J.
PA (SCHM/) SCHMIDT G.
Query Match 6.9%; Score 78; DB 2; Length 116;
Best Local Similarity 23.3%; Pred. No. 17;
RESULT 1474
ID AAW74523 standard; protein; 252 AA.
DE Cloned duplicate of human aggrecan GI-B domain.
PN EP861903-A1.
PD 02-SEP-1998.
PA (LANS/) LANSING M.
PA (UHLE/) UHLENKUEKEN J.
PA (SCHM/) SCHMIDT G.
Query Match 6.9%; Score 78; DB 2; Length 252;
Best Local Similarity 22.3%; Pred. No. 48;
RESULT 1475
ID AAY00274 standard; protein; 268 AA.
DE Human secreted protein encoded by gene 17.
PN WO9506423-A1.
PD 11-FEB-1999.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 78; DB 2; Length 268;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1476
ID ADD50303 standard; protein; 268 AA.
DE Novel human secreted protein seq id 118.
PN US2003199683-A1.
PD 23-OCT-2003.
PA (RUBE/) RUBEN S M.
PA (FENG/) FENG P.
PA (LAFU/) LAFLEUR D W.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (KIYAW/) KYAW H.
PA (LIYV/) LI Y.
PA (ZENG/) ZENG Z.
PA (CART/) CARTER K C.
PA (ENDR/) ENDRESS G A.
PA (WEIY/) WEI Y.
PA (FANP/) FAN P.
PA (ROSE/) ROSEN C A.
Query Match 6.9%; Score 78; DB 7; Length 268;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1477
ID ADG90122 standard; protein; 268 AA.
DE Human protein from secreted protein gene 17.
PN US2003166541-A1.
PD 04-SEP-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.9%; Score 78; DB 7; Length 268;
Best Local Similarity 23.1%; Pred. No. 52;
RESULT 1478
ID ADP07513 standard; protein; 287 AA.
DE Partial cell-recognition and cell-damage protein seqid 4.
PN JP2004129608-A.
PD 30-APR-2004.
PA (UYKY-) UNIV KYUSHU.
PA (FUKU-) FUKUOKA KEN.
Query Match 6.9%; Score 78; DB 8; Length 287;
Best Local Similarity 24.2%; Pred. No. 57;
RESULT 1479
ID ABU05689 standard; protein; 293 AA.
DE M. tuberculosis and M. leprae marker protein #340.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP ) INST PASTEUR.
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Query Match 6.9%; Score 78; DB 5; Length 293;
Best Local Similarity 31.3%; Pred. No. 59;
RESULT 1480
ID ADP07511 standard; protein; 338 AA.
DE B. thuringiensis cell-recognition and cell-damage protein seqid 2.
PN JP2004129608-A.
PD 30-APR-2004.
PA (UYKY-) UNIV KYUSHU.
PA (FUKU-) FUKUOKA KEN.
Query Match 6.9%; Score 78; DB 8; Length 338;
Best Local Similarity 24.2%; Pred. No. 71;
RESULT 1481
ID ADC29743 standard; protein; 400 AA.
DE B. juncea chitinase (BjCHI1).
PN US2003097682-A1.
PD 22-MAY-2003.
PA (CHYE/) CHYE M L.
PA (ZHAO/) ZHAO K.
Query Match 6.9%; Score 78; DB 7; Length 400;
Best Local Similarity 25.3%; Pred. No. 89;
RESULT 1482
ID ADN46313 standard; protein; 510 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID191.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 6.9%; Score 78; DB 8; Length 510;
Best Local Similarity 25.5%; Pred. No. 1.2e+02;
RESULT 1483
ID ABG66756 standard; protein; 1296 AA.
DE Human novel polypeptide #91.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 78; DB 5; Length 1296;
Best Local Similarity 28.8%; Pred. No. 4.3e+02;
RESULT 1484
ID ABG66702 standard; protein; 1296 AA.
DE Human novel polypeptide #37.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 78; DB 5; Length 1296;
Best Local Similarity 28.8%; Pred. No. 4.3e+02;
RESULT 1485
ID ADI17257 standard; protein; 1955 AA.
DE NOVX protein homologue SeqID 733.
PN WO200268649-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 78; DB 5; Length 1955;
Best Local Similarity 22.9%; Pred. No. 7.4e+02;
RESULT 1486
ID ABB60750 standard; protein; 2162 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9042.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.9%; Score 78; DB 4; Length 2162;
Best Local Similarity 21.3%; Pred. No. 8.4e+02;
RESULT 1487
ID ADO28932 standard; protein; 2590 AA.
DE Mouse novel GPCR PGRI7, SEQ ID NO:31.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.9%; Score 78; DB 8; Length 2590;
Best Local Similarity 21.4%; Pred. No. 1.1e+03;
RESULT 1488
ID ABP76679 standard; protein; 1938 AA.
DE Streptomyces viridochromogenes Avi gene cluster polypeptide frame 3.
PN WO200268436-A1.
PD 06-SEP-2002.

PA (COMB-) COMBINATURE BIOPHARM AG.
Query Match 6.9%; Score 78; DB 6; Length 19938;
Best Local Similarity 27.2%; Pred. No. 1.6e+04;
RESULT 1489
ID AAM50239 standard; protein; 497 AA.
DE Rice tyrosine decarboxylase.
PN US6297055-B1.
PD 02-OCT-2001.
PA (DUPO-) DU PONT DE NEMOURS & CO E I.
Query Match 6.9%; Score 77.5; DB 4; Length 497;
Best Local Similarity 23.6%; Pred. No. 1.3e+02;
RESULT 1490
ID AAU76421 standard; protein; 497 AA.
DE Rice tyrosine decarboxylase clone r186.pk0031.bs.
PN US2002009801-A1.
PD 24-JAN-2002.
PA (FALC/) FALCO S C.
PA (FAMC/) FAMODU O O.
PA (OROZ/) OROZCO E R.
Query Match 6.9%; Score 77.5; DB 5; Length 497;
Best Local Similarity 23.6%; Pred. No. 1.3e+02;
RESULT 1491
ID AAW12713 standard; protein; 562 AA.
DE hRIP, a protein critical for HIV replication.
PN WO9701648-A1.
PD 16-JAN-1997.
PA (UYNA-) UNIV MASSACHUSETTS MEDICAL CENT.
Query Match 6.9%; Score 77.5; DB 2; Length 562;
Best Local Similarity 25.0%; Pred. No. 1.6e+02;
RESULT 1492
ID ADO00991 standard; protein; 562 AA.
DE Human homologue of Fruit fly AD-related protein CG3365.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIPE-) LIFE SCI DEV CORP.
Query Match 6.9%; Score 77.5; DB 8; Length 562;
Best Local Similarity 25.0%; Pred. No. 1.6e+02;
RESULT 1493
ID ADP55222 standard; protein; 562 AA.
DE Human PRO protein sequence SEQ ID NO:1198.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.9%; Score 77.5; DB 8; Length 562;
Best Local Similarity 25.0%; Pred. No. 1.6e+02;
RESULT 1494
ID ABB63033 standard; protein; 583 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15891.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.9%; Score 77.5; DB 4; Length 583;
Best Local Similarity 23.3%; Pred. No. 1.6e+02;
RESULT 1495
ID AAU38948 standard; protein; 583 AA.
DE Drosophila G-protein coupled receptor, GCPR #26.
PN WO200170980-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.9%; Score 77.5; DB 4; Length 583;
Best Local Similarity 23.3%; Pred. No. 1.6e+02;
RESULT 1496
ID ADC35826 standard; protein; 583 AA.
DE Drosophila G-protein coupled receptor seq id 28.
PN US2003092124-A1.
PD 15-MAY-2003.
PA (APPL-) APPLERA CORP.
Query Match 6.9%; Score 77.5; DB 7; Length 583;
Best Local Similarity 23.3%; Pred. No. 1.6e+02;
RESULT 1497
ID ADM47277 standard; protein; 620 AA.
DE Protocadherin like NOVX 26a protein.
PN WO2003083039-A2.

PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.9%; Score 77.5; DB 7; Length 620;
Best Local Similarity 22.1%; Pred. No. 1.8e+02;
RESULT 1498
ID AAU33234 standard; protein; 644 AA.
DE Novel human secreted protein #3725.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.9%; Score 77.5; DB 4; Length 644;
Best Local Similarity 25.0%; Pred. No. 1.9e+02;
RESULT 1499
ID ABB60849 standard; protein; 826 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9339.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.9%; Score 77.5; DB 4; Length 826;
Best Local Similarity 21.1%; Pred. No. 2.6e+02;
RESULT 1500
ID ADD01209 standard; protein; 874 AA.
DE Human nucleic acid-associated protein NAAP-47 SEQ ID NO:47.
PN WO2003054219-A2.
PD 03-JUL-2003.
PA (INCY-) INCVTE GENOMICS INC.
Query Match 6.9%; Score 77.5; DB 7; Length 874;
Best Local Similarity 26.4%; Pred. No. 2.8e+02;

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OM protein - protein search, using sw model

Run on: October 5, 2005, 17:19:28 ; Search time 137.744 Seconds
(without alignments)
1197.068 Million cell updates/sec

Title: US-10-063-510-6

Perfect score: 1657

Sequence: 1 MARCSLVLLTSTWTRLL.....NPEESKSPSTVRCLEAEV 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Uniprot_03.*

1: uniprot_spport.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1657 | 100.0 | 322 | 2 | Q9unf4 homo sapien |
| 2 | 1643 | 99.2 | 322 | 2 | Q8TC18 |
| 3 | 1638 | 98.9 | 322 | 2 | Q9Y5Y7 homo sapien |
| 4 | 1174 | 70.9 | 322 | 2 | Q6UC88 |
| 5 | 1103 | 66.6 | 318 | 2 | Q8BHC0 |
| 6 | 1095 | 66.1 | 318 | 2 | Q99NE4 |
| 7 | 726.5 | 43.8 | 201 | 2 | Q7YS22 |
| 8 | 241 | 14.5 | 441 | 2 | Q6QM56 |
| 9 | 233.5 | 14.1 | 362 | 1 | CD44_CRIGR |
| 10 | 229.5 | 13.9 | 437 | 2 | Q6P8A2 |
| 11 | 227 | 13.7 | 364 | 2 | Q70509 |
| 12 | 222.5 | 13.4 | 362 | 1 | CD44_PAPHA |
| 13 | 222 | 13.4 | 503 | 1 | CD44_RAT |
| 14 | 219.5 | 13.2 | 780 | 2 | Q08779 |
| 15 | 219 | 13.2 | 265 | 2 | Q98SR5 |
| 16 | 217.5 | 13.1 | 398 | 2 | Q90ZL8 |
| 17 | 212.5 | 12.8 | 431 | 1 | CD44_WESAU |
| 18 | 210 | 12.7 | 778 | 1 | CD44_MOUSE |
| 19 | 208.5 | 12.6 | 366 | 1 | CD44_BOVIN |
| 20 | 206.5 | 12.5 | 168 | 2 | Q90ZL6 |
| 21 | 204 | 12.3 | 361 | 2 | Q8ET72 |
| 22 | 203.5 | 12.3 | 364 | 2 | Q97569 |
| 23 | 203.5 | 12.3 | 396 | 2 | Q9W6S4 |
| 24 | 203 | 12.3 | 742 | 2 | Q9UU36 |
| 25 | 202.5 | 12.2 | 351 | 1 | CD44_CANFA |
| 26 | 202 | 12.2 | 361 | 2 | Q8N694 |
| 27 | 202 | 12.2 | 742 | 1 | CD44_HUMAN |
| 28 | 201 | 12.1 | 580 | 2 | Q8OX37 |
| 29 | 199.5 | 12.0 | 493 | 2 | Q86Z27 |
| 30 | 199 | 12.0 | 338 | 2 | Q9H5A4 |
| 31 | 197 | 11.9 | 719 | 2 | Q9H5A5 |

| | | | | | | |
|-----|-------|------|------|---|------------|---------------------|
| 32 | 196 | 11.8 | 294 | 2 | Q92493 | Q92493 homo sapien |
| 33 | 191.5 | 11.6 | 676 | 2 | Q9H5A7 | Q9H5A7 homo sapien |
| 34 | 191 | 11.5 | 271 | 2 | Q9H5A3 | Q9H5A3 homo sapien |
| 35 | 191 | 11.5 | 470 | 2 | Q9H5A6 | Q9H5A6 homo sapien |
| 36 | 186 | 11.2 | 359 | 1 | CD44_HORSE | Q05078 equus caball |
| 37 | 150 | 9.1 | 537 | 1 | PGCA_FIG | Q29011 sus scrofa |
| 38 | 149.5 | 9.0 | 2109 | 2 | P79787 | P79787 gallus gall |
| 39 | 148.5 | 9.0 | 2109 | 1 | PGCA_CHICK | P07898 gallus gall |
| 40 | 145.5 | 8.8 | 494 | 2 | Q9BGH3 | Q9BGH3 sus scrofa |
| 41 | 145.5 | 8.8 | 3562 | 1 | PGCV_CHICK | Q90553 gallus gall |
| 42 | 145 | 8.8 | 277 | 1 | TS66_HUMAN | P98066 homo sapien |
| 43 | 144 | 8.7 | 275 | 1 | TS66_MOUSE | O08859 mus musculus |
| 44 | 143 | 8.6 | 2149 | 2 | Q6XL68 | O08168 bos taurus |
| 45 | 143 | 8.6 | 2364 | 1 | PGCA_BOVIN | P13608 bos taurus |
| 46 | 143 | 8.6 | 2365 | 2 | Q6XL67 | Q6XL67 bos taurus |
| 47 | 140.5 | 8.5 | 2571 | 1 | SBN1_MOUSE | Q84544 mus musculus |
| 48 | 139.5 | 8.4 | 2333 | 1 | PGCA_CANFA | Q28343 canis famil |
| 49 | 137 | 8.3 | 276 | 1 | TS66_RABIT | P98065 oryctolagus |
| 50 | 136 | 8.2 | 2559 | 1 | SBN2_MOUSE | Q62913 rattus norv |
| 51 | 133 | 8.0 | 514 | 2 | Q62913 | Q62913 rattus norv |
| 52 | 133 | 8.0 | 1431 | 1 | SBN2_RAT | Q8CFM6 rattus norv |
| 53 | 133 | 8.0 | 2551 | 1 | SBN2_HUMAN | O8WQ8 h stabilin |
| 54 | 132.5 | 8.0 | 721 | 2 | Q8PID9 | Q6PID9 homo sapien |
| 55 | 131.5 | 7.9 | 2124 | 1 | PGCA_RAT | P07897 rattus norv |
| 56 | 131 | 7.9 | 911 | 1 | PGCB_HUMAN | Q969W7 homo sapien |
| 57 | 131 | 7.9 | 2132 | 1 | PGCA_MOUSE | Q61282 mus musculus |
| 58 | 130.5 | 7.9 | 883 | 1 | PGCB_MOUSE | Q61361 mus musculus |
| 59 | 130.5 | 7.9 | 883 | 1 | PGCB_RAT | P55068 rattus norv |
| 60 | 130.5 | 7.9 | 883 | 2 | Q8OWT7 | Q8OWT7 mus musculus |
| 61 | 130.5 | 7.9 | 1152 | 2 | Q90WM2 | Q90WM2 xenopus lae |
| 62 | 130.5 | 7.9 | 2415 | 1 | PGCA_HUMAN | P16112 homo sapien |
| 63 | 130.5 | 7.9 | 2570 | 1 | SBN1_HUMAN | Q9N915 homo sapien |
| 64 | 128.5 | 7.8 | 912 | 1 | PGCB_BOVIN | Q28062 bos taurus |
| 65 | 126 | 7.6 | 3358 | 1 | PGCB_MOUSE | Q62059 mus musculus |
| 66 | 122 | 7.4 | 394 | 1 | PGCA_RABIT | Q28670 oryctolagus |
| 67 | 121.5 | 7.3 | 360 | 1 | HPL3_HUMAN | Q96886 homo sapien |
| 68 | 121 | 7.3 | 516 | 2 | Q8IWX2 | Q8IWX2 homo sapien |
| 69 | 120.5 | 7.3 | 1570 | 2 | Q75Z13 | Q75Z13 brachydanio |
| 70 | 119.5 | 7.2 | 411 | 2 | Q702X4 | Q702X4 human herpe |
| 71 | 119 | 7.2 | 359 | 2 | Q72X17 | Q72X17 xenopus lae |
| 72 | 118.5 | 7.2 | 3396 | 1 | PGCV_HUMAN | P13611 homo sapien |
| 73 | 118 | 7.1 | 341 | 1 | HPL2_MOUSE | Q9EEM3 mus musculus |
| 74 | 117.5 | 7.1 | 397 | 2 | Q702X3 | Q702X3 human herpe |
| 75 | 117 | 7.1 | 340 | 1 | HPL2_HUMAN | Q9GZV7 homo sapien |
| 76 | 116 | 7.0 | 368 | 2 | Q8BS97 | Q8BS97 mus musculus |
| 77 | 116 | 7.0 | 2738 | 1 | PGCV_RAT | Q9ERB4 rattus norv |
| 78 | 115 | 6.9 | 370 | 2 | Q7M2W7 | Q7M2W7 sus scrofa |
| 79 | 115 | 6.9 | 394 | 2 | Q6DC16 | Q6DC16 xenopus lae |
| 80 | 115 | 6.9 | 3381 | 1 | PGCV_BOVIN | P81282 bos taurus |
| 81 | 114.5 | 6.9 | 1257 | 1 | PGCN_RAT | P55067 rattus norv |
| 82 | 114 | 6.9 | 610 | 2 | Q9N3C0 | Q9N3C0 caenorhabdi |
| 83 | 113.5 | 6.8 | 1290 | 2 | Q9W6E1 | Q9W6E1 gallus gall |
| 84 | 113 | 6.8 | 341 | 1 | HPL2_RAT | Q9EEM2 rattus norv |
| 85 | 113 | 6.8 | 892 | 1 | LDL2_XENLA | Q99088 xenopus lae |
| 86 | 112.5 | 6.8 | 417 | 1 | PGCB_FELCA | P41725 felis silve |
| 87 | 112 | 6.8 | 210 | 2 | Q8C9U7 | Q8C9U7 mus musculus |
| 88 | 112 | 6.8 | 390 | 1 | VGL1_HHV11 | P06487 human herpe |
| 89 | 112 | 6.8 | 390 | 2 | Q702X7 | Q702X7 human herpe |
| 90 | 111.5 | 6.7 | 402 | 1 | ODP2_MYCPN | P75392 mycoplasma |
| 91 | 111 | 6.7 | 354 | 2 | Q86W61 | Q86W61 homo sapien |
| 92 | 110 | 6.6 | 363 | 2 | Q6NV41 | Q6NV41 brachydanio |
| 93 | 109 | 6.6 | 816 | 2 | Q70474 | Q70474 rattus norv |
| 94 | 109 | 6.6 | 1321 | 1 | PGCN_HUMAN | O14594 homo sapien |
| 95 | 108.5 | 6.5 | 397 | 2 | Q702X6 | Q702X6 human herpe |
| 96 | 108 | 6.5 | 354 | 1 | HPL1_HUMAN | P10915 homo sapien |
| 97 | 108 | 6.5 | 359 | 1 | HPL3_MOUSE | Q80W5 mus musculus |
| 98 | 108 | 6.5 | 624 | 2 | Q19780 | Q19780 caenorhabdi |
| 99 | 107.5 | 6.5 | 665 | 2 | Q7Q4E5 | Q7Q4E5 anopheles g |
| 100 | 107.5 | 6.5 | 739 | 2 | O02360 | O02360 caenorhabdi |
| 101 | 107 | 6.5 | 354 | 1 | HPL1_RAT | P03994 rattus norv |
| 102 | 107 | 6.5 | 355 | 1 | HPL1_CHICK | P07354 gallus gall |
| 103 | 107 | 6.5 | 356 | 1 | HPL1_MOUSE | Q9GUP5 mus musculus |
| 104 | 107 | 6.5 | 862 | 2 | Q9UF98 | Q9UF98 homo sapien |

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|-----|-------|-----|------|---|------------|--------|--------------|-----|------|-----|------|---|------------|----------------------|
| 105 | 107 | 6.5 | 1368 | 1 | PGCN_MOUSE | P55066 | mus musculus | 178 | 97.5 | 5.9 | 1403 | 2 | Q81MM4 | Q81mm4 drosophila |
| 106 | 107 | 6.5 | 1368 | 2 | Q6P1E3 | Q6ple3 | mus musculus | 179 | 97 | 5.9 | 316 | 2 | Q9U9J0 | Q9u9j0 toxocara ca |
| 107 | 107 | 6.5 | 1795 | 2 | Q76894 | Q76894 | drosophila | 180 | 97 | 5.9 | 404 | 2 | Q702Y6 | Q702y6 human herpe |
| 108 | 105.5 | 6.4 | 374 | 2 | Q92209 | Q92209 | cricetulus | 181 | 97 | 5.9 | 604 | 2 | Q6E9K8 | Q6e9k8 listeria mo |
| 109 | 105.5 | 6.4 | 573 | 2 | Q8CUD9 | Q8cjd9 | rattus norv | 182 | 97 | 5.9 | 604 | 2 | Q6E9X2 | Q6e9x2 listeria mo |
| 110 | 105.5 | 6.4 | 830 | 2 | Q6CAY0 | Q6cay0 | yarrowia li | 183 | 97 | 5.9 | 604 | 2 | Q6EAI6 | Q6eai6 listeria mo |
| 111 | 105 | 6.3 | 354 | 1 | HPL1_BOVIN | P55252 | bos taurus | 184 | 96.5 | 5.8 | 303 | 2 | Q8R3W0 | Q8r3w0 mus musculus |
| 112 | 105 | 6.3 | 463 | 2 | Q7RNE3 | Q7rne3 | plasmodium | 185 | 96.5 | 5.8 | 385 | 2 | Q9N666 | Q9n666 drosophila |
| 113 | 105 | 6.3 | 612 | 2 | Q6CD44 | Q6cd44 | yarrowia li | 186 | 96.5 | 5.8 | 385 | 2 | Q9NHU6 | Q9nhue drosophila |
| 114 | 104.5 | 6.3 | 862 | 1 | PGCV_MACNE | Q28858 | macaca neme | 187 | 96.5 | 5.8 | 397 | 2 | Q702Y5 | Q702y5 human herpe |
| 115 | 104 | 6.3 | 139 | 2 | Q9S370 | Q9s370 | homo sapien | 188 | 96.5 | 5.8 | 465 | 1 | YHU6_YEAST | P38845 saccharomyc |
| 116 | 104 | 6.3 | 354 | 1 | HPL1_HORSE | Q28381 | equus cabal | 189 | 96.5 | 5.8 | 604 | 2 | Q6GNS1 | Q6gns1 listeria mo |
| 117 | 104 | 6.3 | 354 | 1 | HPL1_PIG | P10859 | sus scrofa | 190 | 96.5 | 5.8 | 731 | 1 | NOG2_CRYBA | Q6t9j8 cryptococcu |
| 118 | 104 | 6.3 | 627 | 2 | Q8MP19 | Q8mpl9 | dictyosteli | 191 | 96.5 | 5.8 | 961 | 2 | Q92223 | Q92223 emaricella |
| 119 | 104 | 6.3 | 1716 | 2 | Q917Q8 | Q917q8 | drosophila | 192 | 96.5 | 5.8 | 1031 | 2 | Q925N8 | Q925n8 mus musculu |
| 120 | 104 | 6.3 | 1512 | 2 | Q9V899 | Q9ve99 | drosophila | 193 | 96.5 | 5.8 | 1031 | 2 | Q9D071 | Q9d071 m mus musculu |
| 121 | 103.5 | 6.2 | 288 | 2 | Q6QPC9 | Q6qpc9 | simian aden | 194 | 96 | 5.8 | 429 | 2 | Q76430 | Q76430 caenorhabdi |
| 122 | 103.5 | 6.2 | 952 | 2 | Q86AH0 | Q86ah0 | dictyosteli | 195 | 96 | 5.8 | 449 | 2 | Q71UN8 | Q71un8 caenorhabdi |
| 123 | 103.5 | 6.2 | 1254 | 2 | Q94185 | Q94185 | caenorhabdi | 196 | 96 | 5.8 | 481 | 2 | Q9XUF4 | Q9xuf4 caenorhabdi |
| 124 | 103 | 6.2 | 80 | 2 | Q86UZ1 | Q86uz1 | homo sapien | 197 | 96 | 5.8 | 555 | 2 | Q95X13 | Q95x13 caenorhabdi |
| 125 | 102.5 | 6.2 | 182 | 2 | Q810D8 | Q810d8 | drosophila | 198 | 96 | 5.8 | 556 | 2 | Q6DEK7 | Q6dek7 brachydantio |
| 126 | 102.5 | 6.2 | 183 | 2 | Q9VT37 | Q9vt37 | drosophila | 199 | 96 | 5.8 | 604 | 2 | Q6E9R2 | Q6e9r2 listeria mo |
| 127 | 102.5 | 6.2 | 497 | 2 | Q8QVC4 | Q8qvc4 | eyach virus | 200 | 96 | 5.8 | 604 | 2 | Q6E9R8 | Q6e9r8 listeria mo |
| 128 | 102.5 | 6.2 | 553 | 2 | Q8F932 | Q8f932 | leptospira | 201 | 96 | 5.8 | 604 | 2 | Q6EAJ7 | Q6eaj7 listeria mo |
| 129 | 102.5 | 6.2 | 557 | 2 | Q72VI3 | Q72vi3 | leptospira | 202 | 96 | 5.8 | 604 | 2 | Q724K9 | Q724k9 listeria mo |
| 130 | 102.5 | 6.2 | 699 | 2 | Q8QVE9 | Q8qve9 | eyach virus | 203 | 96 | 5.8 | 625 | 2 | Q6V6E1 | Q6v6e1 drosophila |
| 131 | 102 | 6.2 | 391 | 2 | Q753G3 | Q753g3 | ashbya goss | 204 | 96 | 5.8 | 1088 | 1 | NCAL_XENLA | P16170 xenopus lae |
| 132 | 102 | 6.2 | 404 | 2 | Q702X0 | Q702x0 | human herpe | 205 | 95.5 | 5.8 | 376 | 1 | MID2_YEAST | P36027 saccharomyc |
| 133 | 102 | 6.2 | 404 | 2 | Q702Y3 | Q702y3 | human herpe | 206 | 95.5 | 5.8 | 385 | 2 | Q9NHU5 | Q9nhu5 drosophila |
| 134 | 101.5 | 6.1 | 380 | 2 | O02343 | O02343 | caenorhabdi | 207 | 95.5 | 5.8 | 385 | 2 | Q9NHU7 | Q9nhu7 drosophila |
| 135 | 101.5 | 6.1 | 768 | 2 | Q6O279 | Q6o279 | homo sapien | 208 | 95.5 | 5.8 | 1259 | 2 | Q869X4 | Q869x4 dictyosteli |
| 136 | 101.5 | 6.1 | 1853 | 2 | Q7KT96 | Q7kt96 | drosophila | 209 | 95.5 | 5.8 | 5374 | 2 | Q99ND0 | Q99nd0 mus musculu |
| 137 | 101.5 | 6.1 | 1893 | 2 | Q9NKC9 | Q9nkc9 | drosophila | 210 | 95 | 5.7 | 273 | 2 | Q61002 | Q61002 mus musculu |
| 138 | 101 | 6.1 | 700 | 2 | Q8TG00 | Q8tg00 | aspergillus | 211 | 95 | 5.7 | 390 | 2 | Q702W9 | Q702w9 human herpe |
| 139 | 101 | 6.1 | 708 | 2 | Q18175 | Q18175 | caenorhabdi | 212 | 95 | 5.7 | 424 | 2 | Q9FGW0 | Q9fgw0 arabidopsis |
| 140 | 101 | 6.1 | 2535 | 2 | Q755B8 | Q755b8 | ashbya goss | 213 | 95 | 5.7 | 538 | 2 | Q69379 | Q69379 listeria mo |
| 141 | 100.5 | 6.1 | 402 | 1 | HPL4_HUMAN | Q86uw8 | homo sapien | 214 | 95 | 5.7 | 604 | 2 | Q6EAD8 | Q6ead8 listeria mo |
| 142 | 100.5 | 6.1 | 411 | 2 | Q702X9 | Q702x9 | human herpe | 215 | 95 | 5.7 | 604 | 2 | Q9RQ13 | Q9rgi3 listeria mo |
| 143 | 100.5 | 6.1 | 1121 | 2 | Q72884 | Q72884 | candida alb | 216 | 95 | 5.7 | 639 | 2 | Q8E904 | Q8e904 listeria mo |
| 144 | 100 | 6.0 | 403 | 2 | Q702W8 | Q702w8 | human herpe | 217 | 95 | 5.7 | 639 | 2 | Q6E982 | Q6e982 listeria mo |
| 145 | 100 | 6.0 | 404 | 2 | Q702W6 | Q702w6 | human herpe | 218 | 95 | 5.7 | 639 | 2 | Q6E9Q6 | Q6e9q6 listeria mo |
| 146 | 100 | 6.0 | 404 | 2 | Q702Y0 | Q702y0 | human herpe | 219 | 95 | 5.7 | 639 | 2 | Q8GNR2 | Q8gnr2 listeria mo |
| 147 | 100 | 6.0 | 486 | 2 | Q8FRY2 | Q8fry2 | corynebacte | 220 | 95 | 5.7 | 753 | 2 | Q6PPF4 | Q6ppf4 brachydantio |
| 148 | 100 | 6.0 | 1240 | 1 | YQU3_CAEEL | Q09550 | caenorhabdi | 221 | 95 | 5.7 | 1203 | 2 | Q6C028 | Q6c028 varrovia li |
| 149 | 99.5 | 6.0 | 478 | 2 | Q7YX15 | Q7yx15 | caenorhabdi | 222 | 94.5 | 5.7 | 345 | 2 | Q691Y8 | Q691y8 anolis sagr |
| 150 | 99.5 | 6.0 | 1092 | 1 | NC42_XENLA | P36335 | xenopus lae | 223 | 94.5 | 5.7 | 383 | 2 | Q702X5 | Q702x5 human herpe |
| 151 | 99 | 6.0 | 178 | 2 | Q8FQU3 | Q8fq3 | corynebacte | 224 | 94.5 | 5.7 | 383 | 2 | Q702Y4 | Q702y4 human herpe |
| 152 | 99 | 6.0 | 410 | 1 | GC5B_MOUSE | Q923z0 | mus musculu | 225 | 94.5 | 5.7 | 395 | 2 | Q702Z0 | Q702z0 human herpe |
| 153 | 99 | 6.0 | 604 | 2 | Q6E9B8 | Q6e9b8 | listeria mo | 226 | 94.5 | 5.7 | 519 | 2 | Q7YTR7 | Q7ytr7 caenorhabdi |
| 154 | 99 | 6.0 | 896 | 2 | Q20253 | Q20253 | caenorhabdi | 227 | 94.5 | 5.7 | 1066 | 2 | Q76NW3 | Q76nw3 dictyosteli |
| 155 | 99 | 6.0 | 1100 | 2 | Q8CCT8 | Q8cct8 | mus musculu | 228 | 94.5 | 5.7 | 1079 | 2 | Q9N4S7 | Q9n4s7 caenorhabdi |
| 156 | 99 | 6.0 | 5376 | 1 | ZAN_MOUSE | Q88799 | mus musculu | 229 | 94.5 | 5.7 | 1390 | 2 | Q17602 | Q17602 caenorhabdi |
| 157 | 98.5 | 5.9 | 204 | 2 | Q9N528 | Q9n528 | caenorhabdi | 230 | 94.5 | 5.7 | 1942 | 2 | Q8GIZ7 | Q8giz7 lactobacill |
| 158 | 98.5 | 5.9 | 346 | 2 | Q7S973 | Q7s973 | neurospora | 231 | 94.5 | 5.7 | 3370 | 2 | Q8I1N9 | Q8i1n9 plasmodium |
| 159 | 98.5 | 5.9 | 397 | 2 | Q702W7 | Q702w7 | human herpe | 232 | 94 | 5.7 | 639 | 2 | Q6E8W8 | Q6e8w8 listeria mo |
| 160 | 98.5 | 5.9 | 397 | 2 | Q702X1 | Q702x1 | human herpe | 233 | 94 | 5.7 | 639 | 2 | Q6E922 | Q6e922 listeria mo |
| 161 | 98.5 | 5.9 | 425 | 2 | Q702W3 | Q702w3 | human herpe | 234 | 94 | 5.7 | 639 | 2 | Q6E9G6 | Q6e9g6 listeria mo |
| 162 | 98.5 | 5.9 | 578 | 2 | Q63ZX6 | Q63zx6 | mus musculu | 235 | 94 | 5.7 | 639 | 2 | Q6EA26 | Q6ea26 listeria mo |
| 163 | 98.5 | 5.9 | 1126 | 2 | Q9VGK5 | Q9vgk5 | drosophila | 236 | 94 | 5.7 | 639 | 2 | Q6EA68 | Q6ea68 listeria mo |
| 164 | 98.5 | 5.9 | 1203 | 2 | Q6ZQ56 | Q6zq56 | mus musculu | 237 | 94 | 5.7 | 639 | 2 | Q6EAF0 | Q6eaf0 listeria mo |
| 165 | 98.5 | 5.9 | 3178 | 1 | YS89_CAEEL | Q09624 | caenorhabdi | 238 | 94 | 5.7 | 639 | 2 | Q8GNR8 | Q8gnr8 listeria mo |
| 166 | 98 | 5.9 | 384 | 2 | Q9DW41 | Q9dw41 | rat cytomeg | 239 | 94 | 5.7 | 769 | 2 | O00816 | O00816 toxoplasma |
| 167 | 98 | 5.9 | 390 | 2 | Q702M4 | Q702m4 | human herpe | 240 | 94 | 5.7 | 776 | 2 | Q7Q5E1 | Q7q5e1 anopheles g |
| 168 | 98 | 5.9 | 604 | 2 | Q6E9T6 | Q6e9t6 | listeria mo | 241 | 94 | 5.7 | 989 | 2 | Q83U76 | Q83u76 chlamydia t |
| 169 | 98 | 5.9 | 604 | 2 | Q8GNR1 | Q8gnr1 | listeria mo | 242 | 94 | 5.7 | 989 | 2 | Q84FU9 | Q84fu9 chlamydia t |
| 170 | 98 | 5.9 | 604 | 2 | Q8GNR7 | Q8gnr7 | listeria mo | 243 | 94 | 5.7 | 1241 | 1 | PER_DROPS | P12348 drosophila |
| 171 | 98 | 5.9 | 771 | 2 | Q22783 | Q22783 | caenorhabdi | 244 | 94 | 5.7 | 1241 | 2 | Q75JCO | Q75jco dictyosteli |
| 172 | 98 | 5.9 | 2112 | 2 | Q9VEL9 | Q9vel9 | drosophila | 245 | 93.5 | 5.6 | 296 | 2 | Q6P9X9 | Q6p9x9 rattus norv |
| 173 | 97.5 | 5.9 | 260 | 2 | Q7PR65 | Q7pr65 | anopheles g | 246 | 93.5 | 5.6 | 359 | 2 | O43656 | O43656 homo sapien |
| 174 | 97.5 | 5.9 | 298 | 2 | Q9Z0P0 | Q9z0p0 | rattus norv | 247 | 93.5 | 5.6 | 383 | 2 | Q702W5 | Q702w5 human herpe |
| 175 | 97.5 | 5.9 | 318 | 2 | Q86HN3 | Q86hn3 | dictyosteli | 248 | 93.5 | 5.6 | 385 | 2 | Q9NHU8 | Q9nhu8 drosophila |
| 176 | 97.5 | 5.9 | 385 | 2 | Q9NHU9 | Q9nhu9 | drosophila | 249 | 93.5 | 5.6 | 498 | 2 | Q6FWR9 | Q6fwr9 candida gia |
| 177 | 97.5 | 5.9 | 909 | 1 | LDL1_XENLA | Q99087 | xenopus lae | 250 | 93.5 | 5.6 | 607 | 2 | Q8GNS0 | Q8gns0 listeria mo |

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|-----|------|-----|------|---|------------|--------------------|-----|------|-----|------|---|------------|--------------------|
| 251 | 93.5 | 5.6 | 626 | 2 | Q9NDD1 | Q9ndd1 leishmania | 324 | 91 | 5.5 | 174 | 2 | Q7YTP1 | Q7ytp1 caenorhabdi |
| 252 | 93 | 5.6 | 261 | 2 | Q70CC2 | Q70cc2 eimeria ten | 325 | 91 | 5.5 | 198 | 2 | Q7X3M4 | Q7x3m4 listeria mo |
| 253 | 93 | 5.6 | 311 | 2 | Q46019 | Q46019 caenorhabdi | 326 | 91 | 5.5 | 246 | 2 | Q9UAV4 | Q9uav4 caenorhabdi |
| 254 | 93 | 5.6 | 364 | 2 | Q96D42 | Q96d42 homo sapien | 327 | 91 | 5.5 | 450 | 2 | Q8CV85 | Q8cv85 oceanobacil |
| 255 | 93 | 5.6 | 385 | 2 | Q8T817 | Q8t817 drosophila | 328 | 91 | 5.5 | 488 | 2 | Q09586 | Q09586 caenorhabdi |
| 256 | 93 | 5.6 | 385 | 2 | Q8T819 | Q8t819 drosophila | 329 | 91 | 5.5 | 596 | 2 | Q6PLT0 | Q6plt0 xenopus tro |
| 257 | 93 | 5.6 | 405 | 2 | Q66HZ2 | Q66hz2 brachydanio | 330 | 91 | 5.5 | 620 | 2 | Q8SVR3 | Q8svr3 encephalito |
| 258 | 93 | 5.6 | 629 | 2 | Q24017 | Q24017 drosophila | 331 | 91 | 5.5 | 639 | 2 | Q6SE94 | Q6se94 listeria mo |
| 259 | 93 | 5.6 | 639 | 2 | Q6E8X4 | Q6e8x4 listeria mo | 332 | 91 | 5.5 | 639 | 2 | Q6EAI0 | Q6eai0 listeria mo |
| 260 | 93 | 5.6 | 639 | 2 | Q8GNR5 | Q8gnr5 listeria mo | 333 | 91 | 5.5 | 701 | 2 | Q8ZMG4 | Q8zmg4 pyrobaculum |
| 261 | 93 | 5.6 | 639 | 2 | Q8GNR6 | Q8gnr6 listeria mo | 334 | 91 | 5.5 | 705 | 2 | Q7PY77 | Q7py77 anopheles g |
| 262 | 93 | 5.6 | 673 | 2 | Q7QJB6 | Q7qjb6 anopheles g | 335 | 91 | 5.5 | 730 | 2 | Q8GAZ8 | Q8gaz8 dictyosteli |
| 263 | 93 | 5.6 | 916 | 2 | Q7YZ10 | Q7yz10 monosiga br | 336 | 91 | 5.5 | 1398 | 2 | Q869T5 | Q869t5 dictyosteli |
| 264 | 93 | 5.6 | 930 | 2 | Q8WBL5 | Q8wbl5 aeropyrum p | 337 | 91 | 5.5 | 2162 | 2 | Q09515 | Q09515 caenorhabdi |
| 265 | 93 | 5.6 | 1349 | 2 | Q8WQ04 | Q8wq04 homo sapien | 338 | 91 | 5.5 | 4262 | 2 | Q685J2 | Q685j2 homo sapien |
| 266 | 92.5 | 5.6 | 247 | 2 | Q8MKY7 | Q8mkv7 drosophila | 339 | 91 | 5.5 | 4493 | 2 | Q685J3 | Q685j3 homo sapien |
| 267 | 92.5 | 5.6 | 248 | 2 | Q9NED0 | Q9ned0 leishmania | 340 | 90.5 | 5.5 | 385 | 2 | Q9NHV0 | Q9nhv0 drosophila |
| 268 | 92.5 | 5.6 | 296 | 2 | Q923D3 | Q923d3 mus musculu | 341 | 90.5 | 5.5 | 385 | 2 | Q9NHV3 | Q9nhv3 drosophila |
| 269 | 92.5 | 5.6 | 300 | 1 | JAM1_MOUSE | Q88792 mus musculu | 342 | 90.5 | 5.5 | 408 | 2 | Q6UDF5 | Q6udf5 psittacid h |
| 270 | 92.5 | 5.6 | 385 | 2 | Q9NHV2 | Q9nhv2 drosophila | 343 | 90.5 | 5.5 | 461 | 2 | Q6C2X8 | Q6c2x8 yarrowia li |
| 271 | 92.5 | 5.6 | 400 | 1 | HPL4_MOUSE | Q80wm4 mus musculu | 344 | 90.5 | 5.5 | 575 | 1 | CH61_CUCMA | Q05045 xenopus lae |
| 272 | 92.5 | 5.6 | 446 | 2 | Q8EMV3 | Q8emv3 oceanobacil | 345 | 90.5 | 5.5 | 662 | 1 | MUC1_XENLA | Q05049 xenopus lae |
| 273 | 92.5 | 5.6 | 569 | 2 | Q9KGV9 | Q9kgv9 listeria mo | 346 | 90.5 | 5.5 | 690 | 2 | Q66S18 | Q66s18 oikopleura |
| 274 | 92.5 | 5.6 | 604 | 2 | Q6EAE4 | Q6eae4 listeria mo | 347 | 90.5 | 5.5 | 966 | 2 | Q9U3P1 | Q9u3p1 caenorhabdi |
| 275 | 92.5 | 5.6 | 623 | 2 | Q57602 | Q57602 ictalurus p | 348 | 90.5 | 5.5 | 1084 | 2 | Q86LA6 | Q86la6 dictyosteli |
| 276 | 92.5 | 5.6 | 708 | 2 | Q73H41 | Q73h41 wobbachia p | 349 | 90.5 | 5.5 | 1175 | 2 | Q9VRL7 | Q9vrl7 drosophila |
| 277 | 92.5 | 5.6 | 784 | 2 | Q7S3V6 | Q7s3v6 neurospora | 350 | 90.5 | 5.5 | 1711 | 1 | N214_DROME | Q9vix4 drosophila |
| 278 | 92.5 | 5.6 | 927 | 2 | Q21811 | Q21811 caenorhabdi | 351 | 90.5 | 5.5 | 1976 | 2 | Q9V9I8 | Q9v9i8 drosophila |
| 279 | 92.5 | 5.6 | 1636 | 1 | BUD3_YEAST | P25558 saccharomyc | 352 | 90.5 | 5.5 | 2300 | 2 | Q7SFP6 | Q7sfp6 neurospora |
| 280 | 92.5 | 5.6 | 2338 | 2 | Q7S9S3 | Q759s3 ashbya goss | 353 | 90 | 5.4 | 388 | 1 | VE2_HPV27 | P36789 human papil |
| 281 | 92 | 5.6 | 347 | 2 | Q8SYW5 | Q8syw5 drosophila | 354 | 90 | 5.4 | 540 | 2 | Q7SF17 | Q7sf17 neurospora |
| 282 | 92 | 5.6 | 429 | 2 | P79046 | P79046 humicola gr | 355 | 90 | 5.4 | 604 | 2 | Q6E9Q0 | Q6e9q0 listeria mo |
| 283 | 92 | 5.6 | 500 | 2 | Q864U4 | Q864u4 bos taurus | 356 | 90 | 5.4 | 626 | 2 | Q81QJ5 | Q81qj5 drosophila |
| 284 | 92 | 5.6 | 604 | 2 | Q9JNA2 | Q9jna2 listeria mo | 357 | 90 | 5.4 | 629 | 2 | Q9V3H7 | Q9v3h7 drosophila |
| 285 | 92 | 5.6 | 639 | 2 | Q6EA92 | Q6ea92 listeria mo | 358 | 90 | 5.4 | 639 | 2 | Q6E8S6 | Q6e8s6 listeria mo |
| 286 | 92 | 5.6 | 644 | 2 | Q6CF33 | Q6cf33 yarrowia li | 359 | 90 | 5.4 | 877 | 2 | Q9H3Q6 | Q9h3q6 homo sapien |
| 287 | 92 | 5.6 | 659 | 2 | Q9SXE2 | Q9sx2 caenorhabdi | 360 | 90 | 5.4 | 878 | 2 | Q9H3Q7 | Q9h3q7 homo sapien |
| 288 | 92 | 5.6 | 741 | 2 | Q6CH88 | Q6ch88 yarrowia li | 361 | 90 | 5.4 | 948 | 2 | Q86AV9 | Q86av9 dictyosteli |
| 289 | 92 | 5.6 | 846 | 2 | O01699 | O01699 caenorhabdi | 362 | 90 | 5.4 | 957 | 2 | O14651 | Q14651 homo sapien |
| 290 | 92 | 5.6 | 907 | 2 | O01699 | O01699 kluveromyc | 363 | 90 | 5.4 | 965 | 2 | Q22286 | Q22286 caenorhabdi |
| 291 | 92 | 5.6 | 966 | 1 | SSN6_YEAST | P14922 saccharomyc | 364 | 90 | 5.4 | 1217 | 2 | Q9UKW9 | Q9ukw9 homo sapien |
| 292 | 92 | 5.6 | 1720 | 2 | Q81486 | Q81486 plasmodium | 365 | 90 | 5.4 | 1367 | 1 | AMYH_YEAST | P08640 saccharomyc |
| 293 | 92 | 5.6 | 2829 | 2 | P70039 | P70039 xenopus lae | 366 | 90 | 5.4 | 1367 | 2 | Q6LCS8 | Q6lcs8 saccharomyc |
| 294 | 91.5 | 5.5 | 161 | 2 | Q6CEP23 | Q6cp23 kluveromyc | 367 | 90 | 5.4 | 1593 | 2 | Q8SX82 | Q8sx82 drosophila |
| 295 | 91.5 | 5.5 | 198 | 2 | Q7WRT1 | Q7wrt1 listeria mo | 368 | 90 | 5.4 | 2282 | 2 | Q9NK56 | Q9nk56 drosophila |
| 296 | 91.5 | 5.5 | 198 | 2 | Q7X384 | Q7x384 listeria mo | 369 | 90 | 5.4 | 2871 | 2 | Q8IM87 | Q8im87 drosophila |
| 297 | 91.5 | 5.5 | 300 | 2 | Q8VC39 | Q8vc39 mus musculu | 370 | 90 | 5.4 | 2871 | 2 | Q9V483 | Q9v483 drosophila |
| 298 | 91.5 | 5.5 | 305 | 2 | Q8RI83 | Q8ri83 mus musculu | 371 | 89.5 | 5.4 | 195 | 2 | Q9QX82 | Q9qx82 rattus norv |
| 299 | 91.5 | 5.5 | 338 | 2 | Q6EAH4 | Q6eah4 listeria mo | 372 | 89.5 | 5.4 | 224 | 2 | Q9CRT7 | Q9crt7 mus musculu |
| 300 | 91.5 | 5.5 | 383 | 2 | Q702X8 | Q702x8 human herpe | 373 | 89.5 | 5.4 | 303 | 2 | Q9D116 | Q9d116 mus musculu |
| 301 | 91.5 | 5.5 | 385 | 2 | Q9NHV1 | Q9nhv1 drosophila | 374 | 89.5 | 5.4 | 305 | 2 | Q8VBM0 | Q8vbm0 mus musculu |
| 302 | 91.5 | 5.5 | 411 | 1 | LMP2_RAT | P17046 rattus norv | 375 | 89.5 | 5.4 | 319 | 2 | Q9D0D7 | Q9dd07 mus musculu |
| 303 | 91.5 | 5.5 | 411 | 2 | Q6P6W1 | Q6p6w1 rattus norv | 376 | 89.5 | 5.4 | 319 | 2 | Q9D4W4 | Q9d4w4 m mus muscu |
| 304 | 91.5 | 5.5 | 497 | 2 | Q8QVC5 | Q8qvc5 eyach virus | 377 | 89.5 | 5.4 | 326 | 2 | Q7SCW5 | Q7scw5 neurospora |
| 305 | 91.5 | 5.5 | 538 | 2 | Q76H84 | Q76h84 streptococc | 378 | 89.5 | 5.4 | 350 | 2 | Q7Q1R0 | Q7q1r0 anopheles g |
| 306 | 91.5 | 5.5 | 573 | 2 | Q69380 | Q69380 listeria mo | 379 | 89.5 | 5.4 | 440 | 2 | Q9P566 | Q9p566 neurospora |
| 307 | 91.5 | 5.5 | 604 | 2 | Q6EBU4 | Q6ebu4 listeria mo | 380 | 89.5 | 5.4 | 443 | 2 | Q6P111 | Q6p111 brachydanio |
| 308 | 91.5 | 5.5 | 604 | 2 | Q8GNR3 | Q8gnr3 listeria mo | 381 | 89.5 | 5.4 | 455 | 2 | Q7VNN0 | Q7vnn0 haemophilus |
| 309 | 91.5 | 5.5 | 627 | 2 | Q7RWT2 | Q7rwt2 neurospora | 382 | 89.5 | 5.4 | 456 | 2 | Q25242 | Q25242 lucilia cup |
| 310 | 91.5 | 5.5 | 633 | 2 | Q9JMY6 | Q9jmy6 listeria mo | 383 | 89.5 | 5.4 | 471 | 2 | Q9VMG7 | Q9vmg7 drosophila |
| 311 | 91.5 | 5.5 | 639 | 1 | ACTA_LISMO | P33379 listeria mo | 384 | 89.5 | 5.4 | 480 | 2 | Q25241 | Q25241 lucilia cup |
| 312 | 91.5 | 5.5 | 639 | 2 | Q6E8V0 | Q6e8v0 listeria mo | 385 | 89.5 | 5.4 | 492 | 2 | Q6CGC6 | Q6cgc6 yarrowia li |
| 313 | 91.5 | 5.5 | 639 | 2 | Q6E914 | Q6e914 listeria mo | 386 | 89.5 | 5.4 | 510 | 2 | Q6SCJ8 | Q6scj8 aspergillus |
| 314 | 91.5 | 5.5 | 639 | 2 | Q6E9X8 | Q6e9x8 listeria mo | 387 | 89.5 | 5.4 | 604 | 2 | Q6E9W0 | Q6e9w0 listeria mo |
| 315 | 91.5 | 5.5 | 639 | 2 | Q6EAS6 | Q6eas6 listeria mo | 388 | 89.5 | 5.4 | 634 | 2 | Q7IT11 | Q7it11 momordica c |
| 316 | 91.5 | 5.5 | 639 | 2 | Q6EAA4 | Q6eaa4 listeria mo | 389 | 89.5 | 5.4 | 659 | 2 | Q86A18 | Q86a18 dictyosteli |
| 317 | 91.5 | 5.5 | 639 | 2 | Q8GNR9 | Q8gnr9 listeria mo | 390 | 89.5 | 5.4 | 1145 | 2 | Q8JKT0 | Q8jkt0 heliothis z |
| 318 | 91.5 | 5.5 | 639 | 2 | Q8GNS2 | Q8gns2 listeria mo | 391 | 89.5 | 5.4 | 1368 | 2 | Q23821 | Q23821 caenorhabdi |
| 319 | 91.5 | 5.5 | 681 | 1 | VGP_MABVP | P35254 marburg vir | 392 | 89.5 | 5.4 | 1403 | 2 | Q9NHN6 | Q9nhn6 drosophila |
| 320 | 91.5 | 5.5 | 681 | 2 | Q71WM1 | Q71wm1 lake victor | 393 | 89 | 5.4 | 307 | 1 | SGS3_DROME | P02840 drosophila |
| 321 | 91.5 | 5.5 | 860 | 2 | Q7RZN3 | Q7rzn3 neurospora | 394 | 89 | 5.4 | 369 | 2 | Q91E39 | Q91e39 phocid herp |
| 322 | 91.5 | 5.5 | 1148 | 2 | Q6CBJ2 | Q6cbj2 yarrowia li | 395 | 89 | 5.4 | 416 | 1 | LMP1_HUMAN | P11279 homo sapien |
| 323 | 91.5 | 5.5 | 1167 | 2 | Q7RWQ7 | Q7rwq7 neurospora | 396 | 89 | 5.4 | 417 | 2 | Q8WU33 | Q8wu33 homo sapien |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|-------------------------|-----|------|-----|------|---|------------|---------------------|
| 397 | 89 | 5.4 | 421 | 2 | Q6KCA6 | Q6kca6 candida dub | 470 | 87.5 | 5.3 | 283 | 2 | Q9FKU2 | Q9fkku2 arabidopsis |
| 398 | 89 | 5.4 | 472 | 2 | Q14887 | Q14887 homo sapien | 471 | 87.5 | 5.3 | 338 | 2 | O6CY50 | O6cy50 kluyveromyc |
| 399 | 89 | 5.4 | 487 | 2 | Q6BSZ9 | Q6bsz9 debaryomyce | 472 | 87.5 | 5.3 | 366 | 2 | O6FSI8 | O6fsi8 candida gla |
| 400 | 89 | 5.4 | 503 | 2 | Q19269 | Q19269 caenorhabdi | 473 | 87.5 | 5.3 | 383 | 2 | Q702Y9 | Q702y9 human herpe |
| 401 | 89 | 5.4 | 603 | 2 | Q6CE49 | Q6ce49 yarrowia li | 474 | 87.5 | 5.3 | 442 | 2 | Q7S2Z3 | Q7s2z3 neurospora |
| 402 | 89 | 5.4 | 666 | 2 | Q7QXK0 | Q7qxx0 giardia lam | 475 | 87.5 | 5.3 | 462 | 2 | Q8TUE0 | Q8tue0 methanosarc |
| 403 | 89 | 5.4 | 714 | 2 | Q9NGW9 | Q9ngw9 dictyosteli | 476 | 87.5 | 5.3 | 498 | 2 | Q6FVC8 | Q6fvc8 candida gla |
| 404 | 89 | 5.4 | 828 | 2 | Q8IRC1 | Q8irc1 drosophila | 477 | 87.5 | 5.3 | 555 | 2 | Q9U6R7 | Q9u6r7 dermatophag |
| 405 | 89 | 5.4 | 846 | 2 | Q9VZ10 | Q9vzi0 drosophila | 478 | 87.5 | 5.3 | 623 | 2 | O6T547 | O6t547 listeria mo |
| 406 | 89 | 5.4 | 882 | 2 | Q917T2 | Q917t2 drosophila | 479 | 87.5 | 5.3 | 634 | 2 | Q7RWB0 | Q7rwb0 neurospora |
| 407 | 89 | 5.4 | 887 | 2 | Q6NQY4 | Q6ngy4 drosophila | 480 | 87.5 | 5.3 | 639 | 2 | Q6T548 | Q6t548 listeria mo |
| 408 | 89 | 5.4 | 893 | 2 | Q8IRCO | Q8irc0 drosophila | 481 | 87.5 | 5.3 | 648 | 2 | O44189 | O44189 caenorhabdi |
| 409 | 89 | 5.4 | 951 | 2 | Q9FVX8 | Q9fvx8 oryza sativ | 482 | 87.5 | 5.3 | 653 | 2 | Q8NK55 | Q8nk55 candida alb |
| 410 | 89 | 5.4 | 978 | 2 | Q8IRB9 | Q8irb9 drosophila | 483 | 87.5 | 5.3 | 717 | 2 | O8NAJ6 | O8naj6 homo sapien |
| 411 | 89 | 5.4 | 1483 | 2 | Q7KWU3 | Q7kwu3 dictyosteli | 484 | 87.5 | 5.3 | 752 | 2 | O8MNE2 | O8mne2 dictyosteli |
| 412 | 89 | 5.4 | 1708 | 2 | Q7XWZ9 | Q7xwz9 oryza sativ | 485 | 87.5 | 5.3 | 785 | 2 | Q7QQI5 | Q7qqi5 giardia lam |
| 413 | 89 | 5.4 | 2273 | 2 | Q63HU2 | Q63hu2 burkholderi | 486 | 87.5 | 5.3 | 825 | 2 | Q9LZA6 | Q9lza6 arabidopsis |
| 414 | 89 | 5.4 | 6994 | 2 | Q17343 | Q17343 caenorhabdi | 487 | 87.5 | 5.3 | 867 | 2 | Q90X49 | Q90x49 brachydanio |
| 415 | 89 | 5.4 | 6994 | 2 | Q17490 | Q17490 caenorhabdi | 488 | 87.5 | 5.3 | 906 | 2 | Q8UUV1 | Q8uvu1 xenopus lae |
| 416 | 88.5 | 5.3 | 193 | 2 | O23366 | O23366 arabidopsis | 489 | 87.5 | 5.3 | 971 | 2 | O6W3C4 | O6w3c4 caenorhabdi |
| 417 | 88.5 | 5.3 | 264 | 2 | O80XS5 | O80xs5 mus musculu | 490 | 87.5 | 5.3 | 989 | 2 | Q19930 | Q19930 caenorhabdi |
| 418 | 88.5 | 5.3 | 321 | 2 | O25939 | O25939 plasmodium | 491 | 87.5 | 5.3 | 997 | 1 | VGNM_APMV | VGNM_APMV |
| 419 | 88.5 | 5.3 | 448 | 2 | Q6AQD8 | Q6aqd8 desulfotale | 492 | 87.5 | 5.3 | 1085 | 1 | CASR_BOVIN | CASR_BOVIN |
| 420 | 88.5 | 5.3 | 481 | 2 | Q9VWK3 | Q9vwk3 drosophila | 493 | 87.5 | 5.3 | 1091 | 1 | NCA1_CHICK | NCA1_CHICK |
| 421 | 88.5 | 5.3 | 518 | 2 | Q8NJS3 | Q8njs3 candida alb | 494 | 87.5 | 5.3 | 1129 | 2 | O6CB75 | O6cb75 yarrowia li |
| 422 | 88.5 | 5.3 | 569 | 2 | O71X10 | O71x10 listeria mo | 495 | 87.5 | 5.3 | 1370 | 2 | O6C3B8 | O6c3b8 yarrowia li |
| 423 | 88.5 | 5.3 | 582 | 2 | O81R74 | O81r74 drosophila | 496 | 87.5 | 5.3 | 1799 | 2 | O7KUI0 | O7kui0 drosophila |
| 424 | 88.5 | 5.3 | 596 | 1 | A1UP_MOUSE | A1up_mouse mus musculu | 497 | 87.5 | 5.3 | 1802 | 1 | HKR1_YEAST | HKR1_YEAST |
| 425 | 88.5 | 5.3 | 598 | 2 | Q9JMY5 | Q9jmy5 listeria mo | 498 | 87.5 | 5.3 | 2817 | 2 | Q7RK42 | Q7rk42 clostridium |
| 426 | 88.5 | 5.3 | 615 | 2 | Q9M6E8 | Q9m6e8 phaseolus v | 499 | 87.5 | 5.3 | 9234 | 2 | Q7KTP5 | Q7ktp5 drosophila |
| 427 | 88.5 | 5.3 | 653 | 2 | O81JX0 | O81jx0 plasmodium | 500 | 87 | 5.3 | 167 | 2 | O65742 | O65742 cicier ariet |
| 428 | 88.5 | 5.3 | 699 | 2 | O6CSM7 | O6csm7 kluyveromyc | 501 | 87 | 5.3 | 235 | 2 | O63349 | O63349 rattus norv |
| 429 | 88.5 | 5.3 | 721 | 2 | O97UG7 | O97ug7 sulfolobus | 502 | 87 | 5.3 | 259 | 2 | O70CD5 | O70cd5 eimeria ten |
| 430 | 88.5 | 5.3 | 722 | 2 | O59644 | O59644 sulfolobus | 503 | 87 | 5.3 | 362 | 2 | Q6CGU2 | Q6cgu2 yarrowia li |
| 431 | 88.5 | 5.3 | 722 | 2 | O6ETP4 | O6etp4 candida gla | 504 | 87 | 5.3 | 363 | 2 | Q91YK8 | Q91yk8 mus musculu |
| 432 | 88.5 | 5.3 | 901 | 2 | Q9H195 | Q9h195 homo sapien | 505 | 87 | 5.3 | 379 | 2 | O823B1 | O823b1 chlamydophi |
| 433 | 88.5 | 5.3 | 980 | 2 | Q84FU8 | Q84fu8 chlamydia t | 506 | 87 | 5.3 | 385 | 2 | O8T8J9 | O8t8j9 drosophila |
| 434 | 88.5 | 5.3 | 980 | 2 | O84FU8 | O84fu8 chlamydia t | 507 | 87 | 5.3 | 442 | 2 | O758Q5 | O758q5 ashbya goss |
| 435 | 88.5 | 5.3 | 981 | 2 | O84FU7 | O84fu7 chlamydia t | 508 | 87 | 5.3 | 453 | 2 | Q9U301 | Q9u301 caenorhabdi |
| 436 | 88.5 | 5.3 | 1101 | 1 | GUNC_CELFI | Gunc_celfi cellulomonas | 509 | 87 | 5.3 | 639 | 2 | Q6E8S0 | Q6e8s0 listeria mo |
| 437 | 88 | 5.3 | 103 | 2 | Q9TTB3 | Q9ttb3 sus scrofa | 510 | 87 | 5.3 | 661 | 2 | O13444 | O13444 cladosporiu |
| 438 | 88 | 5.3 | 161 | 2 | Q9CVT7 | Q9cvt7 mus musculu | 511 | 87 | 5.3 | 689 | 2 | Q724Q0 | Q724q0 listeria mo |
| 439 | 88 | 5.3 | 259 | 2 | Q9N3B9 | Q9n3b9 caenorhabdi | 512 | 87 | 5.3 | 752 | 2 | Q9YC61 | Q9yc61 aeropyrum p |
| 440 | 88 | 5.3 | 319 | 2 | Q7QJAO | Q7qja0 anopheles g | 513 | 87 | 5.3 | 841 | 2 | O6AX88 | O6ax88 xenopus lae |
| 441 | 88 | 5.3 | 345 | 2 | O690W2 | O690w2 anolis sagr | 514 | 87 | 5.3 | 905 | 2 | Q8ESU9 | Q8esu9 homo sapien |
| 442 | 88 | 5.3 | 347 | 2 | Q9TZV4 | Q9tzv4 plasmodium | 515 | 87 | 5.3 | 991 | 2 | Q83UW2 | Q83uw2 chlamydia t |
| 443 | 88 | 5.3 | 362 | 2 | Q9TZV3 | Q9tzv3 plasmodium | 516 | 87 | 5.3 | 991 | 2 | Q84FV0 | Q84fv0 chlamydia t |
| 444 | 88 | 5.3 | 382 | 2 | O6C971 | O6c971 yarrowia li | 517 | 87 | 5.3 | 991 | 1 | PMPH_CHLTR | PMPH_CHLTR |
| 445 | 88 | 5.3 | 385 | 2 | Q8T8I2 | Q8t8i2 drosophila | 518 | 87 | 5.3 | 1016 | 1 | Q9LAU3 | Q9lau3 legionella |
| 446 | 88 | 5.3 | 385 | 2 | O8T8I4 | O8t8i4 drosophila | 519 | 87 | 5.3 | 1048 | 2 | Q9LAU3 | Q9lau3 schizosacch |
| 447 | 88 | 5.3 | 385 | 2 | O8T8I6 | O8t8i6 drosophila | 520 | 87 | 5.3 | 1082 | 1 | YK02_SCHPO | YK02_SCHPO |
| 448 | 88 | 5.3 | 385 | 2 | Q8T8J0 | Q8t8j0 drosophila | 521 | 87 | 5.3 | 1506 | 2 | P79927 | P79927 xenopus lae |
| 449 | 88 | 5.3 | 385 | 2 | Q8T8J1 | Q8t8j1 drosophila | 522 | 87 | 5.3 | 1537 | 1 | FLO1_YEAST | FLO1_YEAST |
| 450 | 88 | 5.3 | 385 | 2 | Q8T8K3 | Q8t8k3 drosophila | 523 | 86.5 | 5.2 | 197 | 2 | Q9Z317 | Q9z317 mus musculu |
| 451 | 88 | 5.3 | 447 | 2 | O6CCR1 | O6ccr1 yarrowia li | 524 | 86.5 | 5.2 | 249 | 2 | Q9R0L9 | Q9r0l9 mus musculu |
| 452 | 88 | 5.3 | 449 | 2 | O6CWZ6 | O6cwz6 kluyveromyc | 525 | 86.5 | 5.2 | 260 | 2 | O7PYX0 | O7pyx0 anopheles g |
| 453 | 88 | 5.3 | 456 | 2 | Q9U2W2 | Q9u2w2 caenorhabdi | 526 | 86.5 | 5.2 | 319 | 2 | Q8BP27 | Q8bp27 mus musculu |
| 454 | 88 | 5.3 | 564 | 2 | O01627 | O01627 caenorhabdi | 527 | 86.5 | 5.2 | 390 | 2 | Q73JV8 | Q73jv8 treponema d |
| 455 | 88 | 5.3 | 577 | 2 | O6FSJ1 | O6fsj1 candida gla | 528 | 86.5 | 5.2 | 400 | 1 | MUAI_XENLA | MUAI_XENLA |
| 456 | 88 | 5.3 | 588 | 2 | Q813F9 | Q813f9 bacillus ce | 529 | 86.5 | 5.2 | 401 | 2 | O6BV71 | O6bv71 debaryomyce |
| 457 | 88 | 5.3 | 601 | 2 | Q6V6S2 | Q6v6s2 drosophila | 530 | 86.5 | 5.2 | 442 | 2 | O7M8Z3 | O7m8z3 wolinnella s |
| 458 | 88 | 5.3 | 602 | 2 | O8YV91 | O8yv91 anabaena sp | 531 | 86.5 | 5.2 | 451 | 2 | Q6DF68 | Q6df68 xenopus tro |
| 459 | 88 | 5.3 | 604 | 2 | O6E916 | O6e916 listeria mo | 532 | 86.5 | 5.2 | 461 | 2 | Q21004 | Q21004 caenorhabdi |
| 460 | 88 | 5.3 | 616 | 2 | Q8R0X0 | Q8r0x0 mus musculu | 533 | 86.5 | 5.2 | 461 | 2 | Q21004 | Q21004 xenopus lae |
| 461 | 88 | 5.3 | 656 | 2 | Q8BUE7 | Q8bue7 mus musculu | 534 | 86.5 | 5.2 | 484 | 1 | PAP2_XENLA | PAP2_XENLA |
| 462 | 88 | 5.3 | 716 | 2 | Q9NYE4 | Q9nye4 homo sapien | 535 | 86.5 | 5.2 | 493 | 2 | Q23330 | Q23330 caenorhabdi |
| 463 | 88 | 5.3 | 761 | 2 | O22271 | O22271 arabidopsis | 536 | 86.5 | 5.2 | 503 | 1 | WSC2_YEAST | WSC2_YEAST |
| 464 | 88 | 5.3 | 995 | 2 | Q91638 | Q91638 xenopus lae | 537 | 86.5 | 5.2 | 601 | 2 | O6V6S4 | O6v6s4 drosophila |
| 465 | 88 | 5.3 | 1051 | 2 | O6CLJ9 | O6clj9 yarrowia li | 538 | 86.5 | 5.2 | 604 | 2 | Q8E8Z8 | Q8e8z8 listeria mo |
| 466 | 88 | 5.3 | 1630 | 1 | MSF1_PLAFK | F04932 plasmodium | 539 | 86.5 | 5.2 | 604 | 2 | Q8E928 | Q8e928 listeria mo |
| 467 | 88 | 5.3 | 1790 | 2 | O81816 | O81816 aplysia cal | 540 | 86.5 | 5.2 | 639 | 2 | Q6E952 | Q6e952 listeria mo |
| 468 | 88 | 5.3 | 5703 | 1 | MUSB_HUMAN | Q9hc84 homo sapien | 541 | 86.5 | 5.2 | 639 | 2 | Q8E976 | Q8e976 listeria mo |
| 469 | 87.5 | 5.3 | 147 | 2 | O61043 | O61043 trypanosoma | 542 | 86.5 | 5.2 | 639 | 2 | Q8GNR0 | Q8gnr0 listeria mo |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|----------------------|-----|------|-----|-------|---|------------|----------------------|
| 543 | 86.5 | 5.2 | 687 | 2 | Q6NHU1 | Q6nhul corynebacte | 616 | 85.5 | 5.2 | 2448 | 2 | Q8WMQ5 | Q8wmq5 homo sapien |
| 544 | 86.5 | 5.2 | 740 | 1 | GAG_SMRVH | P21411 squirrel mo | 617 | 85.5 | 5.2 | 3346 | 2 | Q822X0 | Q822x0 chlamydomophi |
| 545 | 86.5 | 5.2 | 788 | 2 | O18510 | O18510 trichoplusi | 618 | 85.5 | 5.2 | 6995 | 2 | Q86RK2 | Q86rk2 homo sapien |
| 546 | 86.5 | 5.2 | 790 | 2 | Q8TBZ7 | Q8tbz7 homo sapien | 619 | 85 | 5.1 | 172 | 2 | Q8VC95 | Q8vc95 mus musculus |
| 547 | 86.5 | 5.2 | 807 | 2 | O18511 | O18511 trichoplusi | 620 | 85 | 5.1 | 255 | 2 | Q86HS8 | Q86hs8 dictyosteli |
| 548 | 86.5 | 5.2 | 838 | 2 | Q7UNP4 | Q7unp4 rhodopirelli | 621 | 85 | 5.1 | 265 | 2 | Q8GZE5 | Q8gze5 caenorhabditi |
| 549 | 86.5 | 5.2 | 941 | 2 | Q6LRH0 | Q6lrh0 arabidopsis | 622 | 85 | 5.1 | 300 | 2 | Q95XH5 | Q95xh5 caenorhabditi |
| 550 | 86.5 | 5.2 | 1300 | 2 | Q6BZP6 | Q6bzp6 yarrowia li | 623 | 85 | 5.1 | 317 | 2 | Q8BEK4 | Q8bek4 cowpox viru |
| 551 | 86.5 | 5.2 | 1546 | 2 | Q80SS4 | Q80ss4 mus musculus | 624 | 85 | 5.1 | 326 | 2 | Q9VM89 | Q9vm89 drosophila |
| 552 | 86.5 | 5.2 | 1579 | 2 | Q99MP1 | Q99mp1 mus musculus | 625 | 85 | 5.1 | 477 | 2 | Q7MR34 | Q7mr34 wolinnella s |
| 553 | 86.5 | 5.2 | 1683 | 2 | Q810D4 | Q810d4 mus musculus | 626 | 85 | 5.1 | 503 | 2 | Q8VCF0 | Q8vcf0 mus musculus |
| 554 | 86.5 | 5.2 | 1684 | 2 | Q9WTC5 | Q9wtc5 mus musculus | 627 | 85 | 5.1 | 510 | 2 | Q8NUT3 | Q8nut3 kluyveromyc |
| 555 | 86.5 | 5.2 | 1822 | 2 | Q7ROW4 | Q7row4 giardia lam | 628 | 85 | 5.1 | 510 | 2 | Q6CUX5 | Q6cux5 kluyveromyc |
| 556 | 86.5 | 5.2 | 1844 | 2 | Q22579 | Q22579 caenorhabditi | 629 | 85 | 5.1 | 573 | 2 | Q8H7K9 | Q8h7k9 oryza sativ |
| 557 | 86.5 | 5.2 | 1851 | 2 | Q9ESP3 | Q9esp3 rattus norv | 630 | 85 | 5.1 | 576 | 2 | Q66604 | Q66604 saccharomyc |
| 558 | 86.5 | 5.2 | 2781 | 2 | Q9UIG2 | Q9uig2 homo sapien | 631 | 85 | 5.1 | 599 | 2 | Q6C2K2 | Q6c2k2 yarrowia li |
| 559 | 86 | 5.2 | 345 | 2 | Q6UJM5 | Q6ujm5 diploactyl | 632 | 85 | 5.1 | 601 | 2 | Q6V6S1 | Q6v6s1 drosophila |
| 560 | 86 | 5.2 | 347 | 2 | Q9TZV5 | Q9tzv5 plasmodium | 633 | 85 | 5.1 | 627 | 1 | PKNB_LACLA | Q9cst5 lactococcus |
| 561 | 86 | 5.2 | 372 | 2 | Q9TZV6 | Q9tzv6 plasmodium | 634 | 85 | 5.1 | 629 | 2 | Q72TW7 | Q72tw7 brachydanio |
| 562 | 86 | 5.2 | 385 | 2 | Q8T8K4 | Q8t8k4 drosophila | 635 | 85 | 5.1 | 639 | 2 | Q6E9T0 | Q6e9t0 listeria mo |
| 563 | 86 | 5.2 | 390 | 2 | Q66TSS | Q66tss phlebia rad | 636 | 85 | 5.1 | 782 | 2 | Q8GX37 | Q8gx37 arabidopsis |
| 564 | 86 | 5.2 | 390 | 2 | Q70LM3 | Q70lm3 phlebia rad | 637 | 85 | 5.1 | 852 | 2 | Q6CIA5 | Q6cia5 yarrowia li |
| 565 | 86 | 5.2 | 434 | 2 | Q872V2 | Q872v2 neurospora | 638 | 85 | 5.1 | 860 | 1 | VG12_BPB03 | Q37893 bacterioph |
| 566 | 86 | 5.2 | 460 | 2 | O18984 | O18984 cercopithe | 639 | 85 | 5.1 | 911 | 2 | Q7RWL1 | Q7rwl1 dictyosteli |
| 567 | 86 | 5.2 | 476 | 2 | Q03996 | Q03996 plasmodium | 640 | 85 | 5.1 | 989 | 2 | Q9M1E4 | Q9mie4 arabidopsis |
| 568 | 86 | 5.2 | 477 | 2 | Q6AKY5 | Q6aky5 homo sapien | 641 | 85 | 5.1 | 990 | 2 | Q91803 | Q91803 xenopus lae |
| 569 | 86 | 5.2 | 495 | 2 | Q6AK33 | Q6ak33 desulfotale | 642 | 85 | 5.1 | 993 | 2 | Q83TJ6 | Q83tj6 chlamydia t |
| 570 | 86 | 5.2 | 551 | 1 | PODX_RABIT | Q28645 oryctolagus | 643 | 85 | 5.1 | 1013 | 2 | Q6CKC8 | Q6ckc8 kluyveromyc |
| 571 | 86 | 5.2 | 604 | 2 | Q6E9N2 | Q6e9n2 listeria mo | 644 | 85 | 5.1 | 1049 | 2 | Q960E6 | Q960e6 drosophila |
| 572 | 86 | 5.2 | 604 | 2 | Q8GNQ9 | Q8gnq9 listeria mo | 645 | 85 | 5.1 | 1049 | 2 | Q9V6L1 | Q9v6l1 drosophila |
| 573 | 86 | 5.2 | 639 | 2 | Q6E8R4 | Q6e8r4 listeria mo | 646 | 85 | 5.1 | 1170 | 2 | Q95011 | Q95011 caenorhabditi |
| 574 | 86 | 5.2 | 697 | 2 | Q7S009 | Q7s009 neurospora | 647 | 85 | 5.1 | 1225 | 2 | Q9VR49 | Q9vr49 drosophila |
| 575 | 86 | 5.2 | 734 | 2 | Q869R9 | Q869r9 dictyosteli | 648 | 85 | 5.1 | 1354 | 2 | Q9VKA7 | Q9vka7 drosophila |
| 576 | 86 | 5.2 | 750 | 2 | Q9HPZ4 | Q9hpz4 candida alb | 649 | 85 | 5.1 | 1779 | 2 | O52374 | O52374 calicellul |
| 577 | 86 | 5.2 | 780 | 2 | Q9LKT8 | Q9lkt8 arabidopsis | 650 | 85 | 5.1 | 3150 | 2 | Q7PMD5 | Q7pmd5 anopheles g |
| 578 | 86 | 5.2 | 799 | 2 | Q7SFI7 | Q7sfi7 leptospira | 651 | 85 | 5.1 | 17352 | 2 | Q95YM2 | Q95ym2 procamburus |
| 579 | 86 | 5.2 | 799 | 2 | Q8EXF5 | Q8exf5 leptospira | 652 | 84.5 | 5.1 | 220 | 2 | Q9EQG0 | Q9eqg0 mus musculus |
| 580 | 86 | 5.2 | 843 | 2 | Q7XJ06 | Q7xj06 oryza sativ | 653 | 84.5 | 5.1 | 313 | 2 | Q8BEJ1 | Q8bej1 skunkpox vi |
| 581 | 86 | 5.2 | 866 | 2 | O80X18 | O80x18 mus musculus | 654 | 84.5 | 5.1 | 345 | 2 | Q691T8 | Q691t8 anolis sagr |
| 582 | 86 | 5.2 | 1080 | 1 | UBP8_MOUSE | O80u87 mus musculus | 655 | 84.5 | 5.1 | 378 | 2 | Q6FNP6 | Q6fnp6 candida gla |
| 583 | 86 | 5.2 | 1266 | 2 | Q6CAR3 | Q6car3 yarrowia li | 656 | 84.5 | 5.1 | 423 | 2 | Q6CTJ9 | Q6ctj9 kluyveromyc |
| 584 | 86 | 5.2 | 1324 | 2 | Q8MMQ2 | Q8mmq2 dictyosteli | 657 | 84.5 | 5.1 | 456 | 2 | Q8R5M8 | Q8r5m8 mus musculus |
| 585 | 86 | 5.2 | 1674 | 2 | Q80Z18 | Q80z18 mus musculus | 658 | 84.5 | 5.1 | 463 | 2 | Q9JX25 | Q9jx25 rattus norv |
| 586 | 86 | 5.2 | 1785 | 2 | Q255685 | Q255685 plasmodium | 659 | 84.5 | 5.1 | 493 | 1 | TNR8_RAT | P97525 neisseria m |
| 587 | 85.5 | 5.2 | 193 | 2 | Q81B00 | Q81b00 arabidopsis | 660 | 84.5 | 5.1 | 532 | 2 | Q6P7V2 | Q6p7v2 mus musculus |
| 588 | 85.5 | 5.2 | 206 | 2 | Q6LTVK4 | Q6ltvk4 orf virus | 661 | 84.5 | 5.1 | 540 | 1 | CH60_STRAP | Q8k320 streptococc |
| 589 | 85.5 | 5.2 | 224 | 2 | Q8KKT9 | Q8kkt9 rhizobium e | 662 | 84.5 | 5.1 | 562 | 1 | NUPL_HUMAN | P52594 homo sapien |
| 590 | 85.5 | 5.2 | 269 | 2 | Q9USJ2 | Q9usj2 toxocara ca | 663 | 84.5 | 5.1 | 570 | 2 | Q6GMZ9 | Q6gmz9 xenopus lae |
| 591 | 85.5 | 5.2 | 271 | 2 | Q6DG19 | Q6dg19 brachydanio | 664 | 84.5 | 5.1 | 622 | 2 | Q6V6E2 | Q6v6e2 drosophila |
| 592 | 85.5 | 5.2 | 345 | 2 | Q691X0 | Q691x0 anolis sagr | 665 | 84.5 | 5.1 | 624 | 2 | Q675N0 | Q675n0 cornus suec |
| 593 | 85.5 | 5.2 | 370 | 2 | Q7KRX4 | Q7krx4 drosophila | 666 | 84.5 | 5.1 | 636 | 2 | Q66HZ5 | Q66hz5 brachydanio |
| 594 | 85.5 | 5.2 | 378 | 1 | FBSH_MOUSE | Q8r089 mus musculus | 667 | 84.5 | 5.1 | 657 | 2 | Q86ID0 | Q86id0 dictyosteli |
| 595 | 85.5 | 5.2 | 379 | 2 | Q81050 | Q8i050 drosophila | 668 | 84.5 | 5.1 | 658 | 1 | SHK1_SCHPO | P50527 schizosacch |
| 596 | 85.5 | 5.2 | 390 | 2 | Q81GQ0 | Q81gq0 drosophila | 669 | 84.5 | 5.1 | 709 | 2 | O16783 | O16783 caenorhabditi |
| 597 | 85.5 | 5.2 | 429 | 2 | Q95Y50 | Q95y50 caenorhabditi | 670 | 84.5 | 5.1 | 753 | 2 | Q9VCQ7 | Q9vcq7 drosophila |
| 598 | 85.5 | 5.2 | 475 | 1 | CH62_CUCMA | Q05046 cucurbita m | 671 | 84.5 | 5.1 | 773 | 2 | Q8TGH3 | Q8tgh3 malassezia |
| 599 | 85.5 | 5.2 | 525 | 2 | Q7R2J1 | Q7r2j1 giardia lam | 672 | 84.5 | 5.1 | 803 | 1 | IF2_COXBU | Q83bs1 coxiellia bu |
| 600 | 85.5 | 5.2 | 592 | 2 | Q6V6D8 | Q6v6d8 drosophila | 673 | 84.5 | 5.1 | 806 | 2 | Q960Q0 | Q960q0 drosophila |
| 601 | 85.5 | 5.2 | 622 | 2 | Q6V6E4 | Q6v6e4 drosophila | 674 | 84.5 | 5.1 | 814 | 2 | Q6C247 | Q6c247 yarrowia li |
| 602 | 85.5 | 5.2 | 623 | 2 | Q89QR8 | Q89qr8 bradyrhizob | 675 | 84.5 | 5.1 | 834 | 2 | Q877B7 | Q877b7 aspergillus |
| 603 | 85.5 | 5.2 | 625 | 2 | Q9LJC8 | Q9ljc8 staphylococ | 676 | 84.5 | 5.1 | 931 | 2 | Q64YI7 | Q64y17 bacterioides |
| 604 | 85.5 | 5.2 | 649 | 2 | Q49445 | Q49445 arabidopsis | 677 | 84.5 | 5.1 | 1047 | 2 | Q874L3 | Q874l3 candida alb |
| 605 | 85.5 | 5.2 | 734 | 2 | Q7S939 | Q7s939 neurospora | 678 | 84.5 | 5.1 | 1102 | 2 | Q08964 | Q08964 saccharomyc |
| 606 | 85.5 | 5.2 | 781 | 2 | Q96JM7 | Q96jm7 homo sapien | 679 | 84.5 | 5.1 | 1103 | 2 | Q6CA70 | Q6ca70 yarrowia li |
| 607 | 85.5 | 5.2 | 786 | 2 | Q21027 | Q21027 caenorhabditi | 680 | 84.5 | 5.1 | 1161 | 1 | DAN4_YEAST | P47179 saccharomyc |
| 608 | 85.5 | 5.2 | 841 | 2 | Q6RBJ4 | Q6rbj4 brachydanio | 681 | 84.5 | 5.1 | 1355 | 2 | Q86AM1 | Q86am1 dictyosteli |
| 609 | 85.5 | 5.2 | 843 | 2 | Q9VYH8 | Q9vyh8 drosophila | 682 | 84.5 | 5.1 | 1743 | 2 | Q81IL9 | Q81il9 plasmodium |
| 610 | 85.5 | 5.2 | 863 | 2 | Q851G7 | Q851g7 oryza sativ | 683 | 84.5 | 5.1 | 1878 | 2 | Q6CPZ4 | Q6cpz4 kluyveromyc |
| 611 | 85.5 | 5.2 | 895 | 2 | Q80973 | Q80973 arabidopsis | 684 | 84.5 | 5.1 | 1984 | 2 | Q08562 | Q08562 rattus norv |
| 612 | 85.5 | 5.2 | 935 | 2 | Q6R8J3 | Q6r8j3 brachydanio | 685 | 84.5 | 5.1 | 2180 | 2 | Q9VAS8 | Q9vas8 drosophila |
| 613 | 85.5 | 5.2 | 977 | 2 | Q6R8J2 | Q6r8j2 brachydanio | 686 | 84.5 | 5.1 | 2378 | 2 | Q7N7Y6 | Q7n7y6 photorhabdu |
| 614 | 85.5 | 5.2 | 981 | 2 | Q6QG19 | Q6qg19 xenopus lae | 687 | 84.5 | 5.1 | 2481 | 2 | Q99QR6 | Q99qr6 staphylococ |
| 615 | 85.5 | 5.2 | 1052 | 2 | Q91G49 | Q91g49 chilo iride | 688 | 84.5 | 5.1 | 2481 | 2 | Q7A4B1 | Q7a4b1 staphylococ |

| | | | | | | | | | | | | | |
|-----|------|-----|-------|---|------------|-----------------------|-----|------|-----|------|---|------------|------------------------|
| 689 | 84.5 | 5.1 | 2761 | 2 | Q19522 | Q19522 caenorhabdi | 762 | 83.5 | 5.0 | 812 | 2 | Q86AW3 | Q86aw3 dictyosteli |
| 690 | 84.5 | 5.1 | 3443 | 2 | Q8JZM8 | Q8jzm8 mus musculu | 763 | 83.5 | 5.0 | 838 | 2 | Q90YM1 | Q90ym1 brachydanio |
| 691 | 84.5 | 5.1 | 22152 | 2 | Q8WXL7 | Q8wxl7 homo sapien | 764 | 83.5 | 5.0 | 935 | 2 | Q9VGN4 | Q9vgn4 drosophila |
| 692 | 84 | 5.1 | 262 | 2 | P74577 | P74577 synechocyst | 765 | 83.5 | 5.0 | 967 | 2 | Q08294 | Q08294 saccharomyc |
| 693 | 84 | 5.1 | 309 | 2 | Q63549 | Q63549 rattus norv | 766 | 83.5 | 5.0 | 976 | 2 | Q9A531 | Q9a531 caulobacter |
| 694 | 84 | 5.1 | 335 | 2 | Q9C7W2 | Q9c7w2 arabidopsis | 767 | 83.5 | 5.0 | 1001 | 2 | Q05164 | Q05164 saccharomyc |
| 695 | 84 | 5.1 | 359 | 1 | MTD MEDSA | MTD MEDSA medicago sa | 768 | 83.5 | 5.0 | 1043 | 2 | Q97E41 | Q97e41 clostridium |
| 696 | 84 | 5.1 | 385 | 2 | Q8T8I3 | Q8t8i3 drosophila | 769 | 83.5 | 5.0 | 1286 | 2 | Q9TXR6 | Q9txr6 caenorhabdi |
| 697 | 84 | 5.1 | 385 | 2 | Q8T8I5 | Q8t8i5 drosophila | 770 | 83.5 | 5.0 | 1607 | 2 | Q6CDM9 | Q6cdm9 yarrowia li |
| 698 | 84 | 5.1 | 385 | 2 | Q8T8K2 | Q8t8k2 drosophila | 771 | 83.5 | 5.0 | 1713 | 2 | Q8TGE1 | Q8tge1 saccharomyc |
| 699 | 84 | 5.1 | 385 | 2 | Q8T8L0 | Q8t8l0 drosophila | 772 | 83.5 | 5.0 | 2764 | 2 | Q7Z7D6 | Q7z7d6 homo sapien |
| 700 | 84 | 5.1 | 420 | 2 | Q8N7W9 | Q8n7w9 homo sapien | 773 | 83.5 | 5.0 | 3026 | 2 | Q8ILS9 | Q8ils9 plasmodium |
| 701 | 84 | 5.1 | 420 | 2 | Q8N7H1 | Q8n7h1 anabaena sp | 774 | 83.5 | 5.0 | 3175 | 1 | RPOA_EAV | R19811 equine arte |
| 702 | 84 | 5.1 | 456 | 1 | NX3B_BOVIN | NX3B_BOVIN bos tauris | 775 | 83.5 | 5.0 | 3371 | 1 | Q864S8 | Q864s8 felis silve |
| 703 | 84 | 5.1 | 464 | 2 | Q9VX42 | Q9vx42 drosophila | 776 | 83.5 | 5.0 | 5179 | 1 | MUC2_HUMAN | MUC2_HUMAN homo sapien |
| 704 | 84 | 5.1 | 475 | 2 | Q8FQJ1 | Q8fqj1 corynebacte | 777 | 83 | 5.0 | 197 | 2 | Q8JL62 | Q8jl62 christoneu |
| 705 | 84 | 5.1 | 487 | 2 | Q8E1P9 | Q8e1p9 streptococc | 778 | 83 | 5.0 | 217 | 2 | Q7PER9 | Q7per9 anopheles g |
| 706 | 84 | 5.1 | 487 | 2 | Q8E764 | Q8e764 streptococc | 779 | 83 | 5.0 | 221 | 1 | RL1_SULAC | P35024 sulfolobus |
| 707 | 84 | 5.1 | 543 | 2 | Q14879 | Q14879 homo sapien | 780 | 83 | 5.0 | 291 | 2 | Q6QPG5 | Q6qpg5 simian aden |
| 708 | 84 | 5.1 | 625 | 2 | Q7PRT5 | Q7prt5 anopheles g | 781 | 83 | 5.0 | 309 | 2 | Q6IEI3 | Q6iel3 oryza sativ |
| 709 | 84 | 5.1 | 636 | 1 | ENV_MCFP | P15073 mink cell f | 782 | 83 | 5.0 | 309 | 2 | Q7XNY3 | Q7xny3 oryza sativ |
| 710 | 84 | 5.1 | 639 | 2 | Q6E934 | Q6e934 listeria mo | 783 | 83 | 5.0 | 314 | 2 | Q9H8R7 | Q9h8r7 homo sapien |
| 711 | 84 | 5.1 | 641 | 2 | Q6AJU8 | Q6aju8 desulfotale | 784 | 83 | 5.0 | 316 | 2 | Q8TD14 | Q8td14 homo sapien |
| 712 | 84 | 5.1 | 648 | 2 | Q95QX0 | Q95qx0 caenorhabdi | 785 | 83 | 5.0 | 329 | 2 | Q7QB72 | Q7qb72 anopheles g |
| 713 | 84 | 5.1 | 730 | 2 | Q6CPU9 | Q6cpu9 kluyveromyc | 786 | 83 | 5.0 | 337 | 2 | Q7Z5X8 | Q7z5x8 homo sapien |
| 714 | 84 | 5.1 | 793 | 2 | Q8VAG7 | Q8vag7 listeria mo | 787 | 83 | 5.0 | 345 | 2 | Q691Y6 | Q691y6 anolis sagr |
| 715 | 84 | 5.1 | 827 | 2 | Q61WN3 | Q61wn3 ustilago ma | 788 | 83 | 5.0 | 346 | 2 | Q8SHB2 | Q8shb2 rhapholeon |
| 716 | 84 | 5.1 | 864 | 1 | YCL8_HUMAN | Q9ulk2 homo sapien | 789 | 83 | 5.0 | 378 | 2 | Q8SXS5 | Q8sxs5 drosophila |
| 717 | 84 | 5.1 | 880 | 2 | Q7YU85 | Q7yu85 drosophila | 790 | 83 | 5.0 | 382 | 2 | Q9XZ28 | Q9xzz8 litomosoid |
| 718 | 84 | 5.1 | 933 | 2 | Q6ZM25 | Q6zm25 homo sapien | 791 | 83 | 5.0 | 385 | 2 | Q8T8K5 | Q8t8k5 drosophila |
| 719 | 84 | 5.1 | 961 | 1 | BNCL_MOUSE | Q35914 mus musculu | 792 | 83 | 5.0 | 409 | 1 | R23B_HUMAN | P54727 homo sapien |
| 720 | 84 | 5.1 | 996 | 1 | LRP8_MOUSE | Q924x6 mus musculu | 793 | 83 | 5.0 | 419 | 2 | Q8TD11 | Q8td11 homo sapien |
| 721 | 84 | 5.1 | 1021 | 2 | Q6CXI2 | Q6cxy2 kluyveromyc | 794 | 83 | 5.0 | 422 | 2 | Q8TD13 | Q8td13 homo sapien |
| 722 | 84 | 5.1 | 1075 | 1 | FLOS_YEAST | P38894 saccharomyc | 795 | 83 | 5.0 | 463 | 2 | Q4Z665 | Q4z665 schizosacch |
| 723 | 84 | 5.1 | 1153 | 2 | Q6ALQ0 | Q6alq0 drosophila | 796 | 83 | 5.0 | 485 | 2 | Q9V8B0 | Q9v8b0 drosophila |
| 724 | 84 | 5.1 | 1331 | 1 | MANB_CALSA | P22533 caldocellum | 797 | 83 | 5.0 | 559 | 2 | Q9VN36 | Q9vn36 drosophila |
| 725 | 84 | 5.1 | 1343 | 2 | Q9G0V6 | Q9g0v6 drosophila | 798 | 83 | 5.0 | 601 | 1 | A1UP_HUMAN | Q9nrr5 homo sapien |
| 726 | 84 | 5.1 | 1343 | 2 | Q9W2G6 | Q9w2g6 drosophila | 799 | 83 | 5.0 | 605 | 1 | WSC4_YEAST | P38739 saccharomyc |
| 727 | 84 | 5.1 | 1362 | 2 | Q9V294 | Q9v294 pyrococcus | 800 | 83 | 5.0 | 639 | 2 | Q6E8Z2 | Q6e8z2 listeria mo |
| 728 | 84 | 5.1 | 1362 | 2 | Q86AM2 | Q86am2 dictyosteli | 801 | 83 | 5.0 | 653 | 1 | NUMB_MOUSE | Q9qz83 mus musculu |
| 729 | 84 | 5.1 | 1645 | 2 | Q9U263 | Q9u263 caenorhabdi | 802 | 83 | 5.0 | 661 | 2 | Q9V8S2 | Q9v8s2 drosophila |
| 730 | 84 | 5.1 | 1832 | 2 | Q96503 | Q96503 cryptospori | 803 | 83 | 5.0 | 737 | 1 | KNS1_YEAST | P32350 saccharomyc |
| 731 | 84 | 5.1 | 2215 | 2 | Q8I1Z6 | Q8i1z6 plasmodium | 804 | 83 | 5.0 | 738 | 1 | VU47_HHV62 | P52549 human herpe |
| 732 | 83.5 | 5.0 | 216 | 2 | Q28501 | Q28501 macaca mula | 805 | 83 | 5.0 | 762 | 2 | Q86AG3 | Q86ag3 dictyosteli |
| 733 | 83.5 | 5.0 | 274 | 2 | Q9EX24 | Q9ex24 streptomyce | 806 | 83 | 5.0 | 769 | 2 | Q17921 | Q17921 caenorhabdi |
| 734 | 83.5 | 5.0 | 279 | 2 | Q14888 | Q14888 homo sapien | 807 | 83 | 5.0 | 786 | 2 | Q9FDM5 | Q9fdm5 streptococc |
| 735 | 83.5 | 5.0 | 292 | 2 | Q68668 | Q68668 bacillus me | 808 | 83 | 5.0 | 797 | 1 | VGLX_EHVLB | P28968 equine herp |
| 736 | 83.5 | 5.0 | 306 | 2 | Q88V34 | Q88v34 lactobacill | 809 | 83 | 5.0 | 826 | 2 | Q6DLE0 | Q6dle0 equid herpe |
| 737 | 83.5 | 5.0 | 306 | 2 | Q9QVL4 | Q9qvl4 mus musculu | 810 | 83 | 5.0 | 858 | 2 | Q9H8D9 | Q9h8d9 homo sapien |
| 738 | 83.5 | 5.0 | 352 | 2 | Q22685 | Q22685 arabidopsis | 811 | 83 | 5.0 | 866 | 2 | Q39781 | Q39781 equid herpe |
| 739 | 83.5 | 5.0 | 352 | 2 | Q81PH6 | Q81ph6 arabidopsis | 812 | 83 | 5.0 | 866 | 2 | Q39781 | Q39781 equid herpe |
| 740 | 83.5 | 5.0 | 385 | 2 | Q8T8L3 | Q8t8l3 drosophila | 813 | 83 | 5.0 | 866 | 2 | Q6S6W0 | Q6s6w0 equid herpe |
| 741 | 83.5 | 5.0 | 385 | 2 | Q83NC5 | Q83nc5 tropheryma | 814 | 83 | 5.0 | 867 | 2 | Q39782 | Q39782 equid herpe |
| 742 | 83.5 | 5.0 | 405 | 2 | Q95XV0 | Q95xv0 caenorhabdi | 815 | 83 | 5.0 | 963 | 1 | LRP8_HUMAN | Q14114 homo sapien |
| 743 | 83.5 | 5.0 | 446 | 2 | Q6Q008 | Q6cq08 kluyveromyc | 816 | 83 | 5.0 | 1002 | 2 | Q6CBD5 | Q6cbd5 yarrowia li |
| 744 | 83.5 | 5.0 | 446 | 2 | Q9Y849 | Q9y849 kluyveromyc | 817 | 83 | 5.0 | 1030 | 2 | Q7QV30 | Q7qv30 giardia lam |
| 745 | 83.5 | 5.0 | 446 | 2 | Q95QJ6 | Q95qj6 caenorhabdi | 818 | 83 | 5.0 | 1126 | 2 | Q8E6U1 | Q8e6u1 streptococc |
| 746 | 83.5 | 5.0 | 465 | 2 | Q83FT5 | Q83fts tropheryma | 819 | 83 | 5.0 | 1183 | 2 | Q6GCD1 | Q6gcd1 chloroflexu |
| 747 | 83.5 | 5.0 | 465 | 2 | Q84DR0 | Q84dr0 listeria mo | 820 | 83 | 5.0 | 1212 | 2 | Q6QRB1 | Q6qrb1 homo sapien |
| 748 | 83.5 | 5.0 | 476 | 2 | Q7SEJ2 | Q7sej2 neurospora | 821 | 83 | 5.0 | 1265 | 2 | Q9P2G7 | Q9p2g7 homo sapien |
| 749 | 83.5 | 5.0 | 476 | 2 | Q6AYP5 | Q6ayp5 rattus norv | 822 | 83 | 5.0 | 1686 | 2 | Q7RZ6E | Q7rzz6 neurospora |
| 750 | 83.5 | 5.0 | 486 | 2 | Q84DR1 | Q84dr1 listeria mo | 823 | 83 | 5.0 | 2162 | 2 | Q8N3U0 | Q8n3u0 homo sapien |
| 751 | 83.5 | 5.0 | 498 | 1 | TNR8_MOUSE | Q60846 mus musculu | 824 | 83 | 5.0 | 2210 | 2 | Q7Z3E7 | Q7z3e7 homo sapien |
| 752 | 83.5 | 5.0 | 498 | 2 | Q6C977 | Q6c977 yarrowia li | 825 | 83 | 5.0 | 2478 | 2 | Q9LCH2 | Q9lch2 staphylococ |
| 753 | 83.5 | 5.0 | 506 | 2 | Q7PR64 | Q7pr64 anopheles g | 826 | 83 | 5.0 | 2478 | 2 | Q9RL69 | Q9rl69 staphylococ |
| 754 | 83.5 | 5.0 | 516 | 2 | Q7YVC5 | Q7yvc5 cryptospori | 827 | 82.5 | 5.0 | 197 | 2 | Q26878 | Q26878 trypanosoma |
| 755 | 83.5 | 5.0 | 623 | 2 | Q7XND3 | Q7xnd3 oryza sativ | 828 | 82.5 | 5.0 | 231 | 2 | Q86LC2 | Q86lc2 zoanthus sp |
| 756 | 83.5 | 5.0 | 641 | 2 | Q86SD2 | Q86sd2 ciona satis | 829 | 82.5 | 5.0 | 252 | 2 | Q6GZ06 | Q6gz06 avian pneum |
| 757 | 83.5 | 5.0 | 669 | 2 | Q7EZY9 | Q7ezy9 oryza sativ | 830 | 82.5 | 5.0 | 258 | 2 | Q7SGP8 | Q7sgp8 neurospora |
| 758 | 83.5 | 5.0 | 674 | 2 | Q6APL0 | Q6ap10 desulfotale | 831 | 82.5 | 5.0 | 286 | 2 | Q7SAZ7 | Q7saz7 neurospora |
| 759 | 83.5 | 5.0 | 743 | 2 | Q7PQ19 | Q7pq19 anopheles g | 832 | 82.5 | 5.0 | 290 | 1 | LECR_CLAUJ | Q39527 lecrastis |
| 760 | 83.5 | 5.0 | 791 | 2 | Q66VC3 | Q66vc3 equid herpe | 833 | 82.5 | 5.0 | 308 | 2 | Q7XA59 | Q7xa59 lilium long |
| 761 | 83.5 | 5.0 | 800 | 2 | Q8TFG4 | Q8tfg4 schizosacch | 834 | 82.5 | 5.0 | 326 | 2 | Q9NFX5 | Q9nfx5 ceratitis c |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|------------|--------------------|-----|------|-----|-------|---|------------|---------------------|
| 835 | 82.5 | 5.0 | 345 | 2 | Q690V6 | Q690v6 anolis sagr | 908 | 82 | 4.9 | 529 | 2 | Q7PV84 | Q7pv84 anopheles g |
| 836 | 82.5 | 5.0 | 345 | 2 | Q690V7 | Q690v7 anolis sagr | 909 | 82 | 4.9 | 538 | 2 | Q75JS0 | Q75js0 dictyosteli |
| 837 | 82.5 | 5.0 | 345 | 2 | Q690X3 | Q690x3 anolis sagr | 910 | 82 | 4.9 | 544 | 2 | Q8IG67 | Q8ig67 caenorhabdi |
| 838 | 82.5 | 5.0 | 345 | 2 | Q691U6 | Q691u6 anolis sagr | 911 | 82 | 4.9 | 584 | 1 | CEJ1 CAEEL | Q17802 caenorhabdi |
| 839 | 82.5 | 5.0 | 345 | 2 | Q691Z2 | Q691z2 anolis sagr | 912 | 82 | 4.9 | 596 | 2 | Q9UL73 | Q9ult3 homo sapien |
| 840 | 82.5 | 5.0 | 345 | 2 | Q692A4 | Q692a4 anolis sagr | 913 | 82 | 4.9 | 599 | 2 | Q9V680 | Q9ve80 drosophila |
| 841 | 82.5 | 5.0 | 345 | 2 | Q692C2 | Q692c2 anolis quad | 914 | 82 | 4.9 | 601 | 2 | Q9V6S0 | Q9ve60 drosophila |
| 842 | 82.5 | 5.0 | 383 | 1 | VE2 HPV57 | P22155 human papil | 915 | 82 | 4.9 | 630 | 2 | Q6V6H6 | Q6vyh6 sulfolobus |
| 843 | 82.5 | 5.0 | 389 | 2 | Q64BB8 | Q64bb8 uncultured | 916 | 82 | 4.9 | 641 | 2 | Q83363 | Q83363 murine leuk |
| 844 | 82.5 | 5.0 | 389 | 2 | Q6GX00 | Q6gxx0 swine hepat | 917 | 82 | 4.9 | 670 | 2 | Q9VWM0 | Q9vwm0 gibbon ape |
| 845 | 82.5 | 5.0 | 389 | 2 | Q6GX02 | Q6gxx2 swine hepat | 918 | 82 | 4.9 | 673 | 2 | Q91VK6 | Q91vk6 mus musculu |
| 846 | 82.5 | 5.0 | 389 | 2 | Q6GX03 | Q6gxx3 swine hepat | 919 | 82 | 4.9 | 693 | 2 | Q91VK6 | Q91vk6 mus musculu |
| 847 | 82.5 | 5.0 | 400 | 2 | Q9SQF7 | Q9sgf7 brassica ju | 920 | 82 | 4.9 | 720 | 1 | NUP2 YEAST | P32499 saccharomyc |
| 848 | 82.5 | 5.0 | 416 | 2 | Q9K8G4 | Q9k8g4 bacillus ha | 921 | 82 | 4.9 | 746 | 2 | Q82GM0 | Q82gm0 streptomyces |
| 849 | 82.5 | 5.0 | 452 | 2 | Q6CE56 | Q6ce56 yarrowia li | 922 | 82 | 4.9 | 761 | 2 | Q9C9S3 | Q9c9s3 arabidopsis |
| 850 | 82.5 | 5.0 | 456 | 1 | Y883 HAEIN | P44917 haemophilus | 923 | 82 | 4.9 | 771 | 2 | Q86NN7 | Q86nn7 drosophila |
| 851 | 82.5 | 5.0 | 464 | 2 | Q9C247 | Q9c247 neurospora | 924 | 82 | 4.9 | 789 | 2 | Q9VY98 | Q9vy98 drosophila |
| 852 | 82.5 | 5.0 | 508 | 2 | Q6VNX4 | Q6vnx4 drosophila | 925 | 82 | 4.9 | 824 | 2 | Q6CY28 | Q6cy28 kluyveromyc |
| 853 | 82.5 | 5.0 | 540 | 1 | CH60 STRA3 | Q8cx22 streptococc | 926 | 82 | 4.9 | 846 | 2 | Q57577 | Q57577 cynops pyrr |
| 854 | 82.5 | 5.0 | 540 | 1 | CH60 STRAS | Q8cx22 streptococc | 927 | 82 | 4.9 | 847 | 2 | Q6ZQ82 | Q6zq82 mus musculu |
| 855 | 82.5 | 5.0 | 540 | 2 | Q7UPM2 | Q7upm2 rhodopirell | 928 | 82 | 4.9 | 894 | 2 | Q7FL10 | Q7fl10 arabidopsis |
| 856 | 82.5 | 5.0 | 569 | 2 | Q9SL10 | Q9sl10 arabidopsis | 929 | 82 | 4.9 | 894 | 2 | Q9C8I6 | Q9c8i6 arabidopsis |
| 857 | 82.5 | 5.0 | 607 | 2 | Q8GNR4 | Q8gnr4 listeria mo | 930 | 82 | 4.9 | 911 | 2 | Q8GWK9 | Q8gwk9 arabidopsis |
| 858 | 82.5 | 5.0 | 624 | 2 | Q675N1 | Q675n1 cornus suet | 931 | 82 | 4.9 | 911 | 2 | Q9SA18 | Q9sa18 arabidopsis |
| 859 | 82.5 | 5.0 | 635 | 2 | Q66065 | Q66065 fibrobacter | 932 | 82 | 4.9 | 926 | 1 | YIY8 SCHPO | Q9uu18 schizosacch |
| 860 | 82.5 | 5.0 | 639 | 2 | Q6E910 | Q6e910 listeria mo | 933 | 82 | 4.9 | 926 | 2 | Q7LDM3 | Q7ldm3 homo sapien |
| 861 | 82.5 | 5.0 | 639 | 2 | Q6E940 | Q6e940 listeria mo | 934 | 82 | 4.9 | 943 | 1 | YL61 SCHPO | Q8tf99 schizosacch |
| 862 | 82.5 | 5.0 | 686 | 2 | Q8NVE4 | Q8nve4 staphylococ | 935 | 82 | 4.9 | 957 | 2 | Q9UKN0 | Q9ukn0 homo sapien |
| 863 | 82.5 | 5.0 | 698 | 2 | Q74LM8 | Q74lm8 lactobacill | 936 | 82 | 4.9 | 963 | 2 | Q99MX4 | Q99mx4 glaucomya v |
| 864 | 82.5 | 5.0 | 711 | 2 | Q7YX9 | Q7yxx9 cryptospori | 937 | 82 | 4.9 | 971 | 2 | Q6A036 | Q6a036 mus musculu |
| 865 | 82.5 | 5.0 | 726 | 1 | NF11 YEAST | Q12216 saccharomys | 938 | 82 | 4.9 | 973 | 2 | Q7CZHI | Q7czhi agrobacteri |
| 866 | 82.5 | 5.0 | 728 | 2 | Q7NB51 | Q7nb51 mycoplasma | 939 | 82 | 4.9 | 977 | 2 | Q8UFQ8 | Q8ufq8 agrobacteri |
| 867 | 82.5 | 5.0 | 782 | 2 | Q6CNV3 | Q6cnv3 kluyveromyc | 940 | 82 | 4.9 | 1019 | 2 | Q9V6L9 | Q9v6l9 homo sapien |
| 868 | 82.5 | 5.0 | 790 | 1 | AD30 HUMAN | Q9ukf2 homo sapien | 941 | 82 | 4.9 | 1021 | 1 | BUB1 YEAST | P41695 saccharomyc |
| 869 | 82.5 | 5.0 | 808 | 2 | Q81123 | Q81123 caenorhabdi | 942 | 82 | 4.9 | 1023 | 2 | Q7M009 | Q7m009 sinian cyc |
| 870 | 82.5 | 5.0 | 825 | 2 | Q03088 | Q03088 saccharomyc | 943 | 82 | 4.9 | 1074 | 2 | Q8C0P8 | Q8c0p8 mus musculu |
| 871 | 82.5 | 5.0 | 848 | 2 | Q6GP20 | Q6gp20 xenopus lae | 944 | 82 | 4.9 | 1083 | 2 | Q06108 | Q06108 saccharomyc |
| 872 | 82.5 | 5.0 | 871 | 1 | POB1 SCHPO | Q74653 schizosacch | 945 | 82 | 4.9 | 1099 | 2 | Q7TUJ6 | Q7tuj6 prochloroco |
| 873 | 82.5 | 5.0 | 876 | 2 | Q6XLI5 | Q6xli5 brachydanio | 946 | 82 | 4.9 | 1100 | 1 | TCG1 MOUSE | Q8cgf7 mus musculu |
| 874 | 82.5 | 5.0 | 988 | 2 | Q8UVU2 | Q8uvu2 xenopus lae | 947 | 82 | 4.9 | 1126 | 2 | Q9EQJ9 | Q9eqj9 mus musculu |
| 875 | 82.5 | 5.0 | 993 | 2 | Q92JC5 | Q92jc5 rickettsia | 948 | 82 | 4.9 | 1127 | 2 | Q94248 | Q94248 caenorhabdi |
| 876 | 82.5 | 5.0 | 1091 | 2 | Q7SDT8 | Q7sd8 neurospora | 949 | 82 | 4.9 | 1170 | 2 | Q89ZE1 | Q89zel mus musculu |
| 877 | 82.5 | 5.0 | 1163 | 2 | Q7PY32 | Q7py32 anopheles g | 950 | 82 | 4.9 | 1339 | 2 | Q35788 | Q35788 rattus norv |
| 878 | 82.5 | 5.0 | 1206 | 1 | FM14 MOUSE | Q05859 mus musculu | 951 | 82 | 4.9 | 1423 | 2 | Q6CRU1 | Q6crul kluyveromyc |
| 879 | 82.5 | 5.0 | 1258 | 2 | Q86IA2 | Q86ia2 dictyosteli | 952 | 82 | 4.9 | 1564 | 2 | Q95VZ5 | Q95vz5 drosophila |
| 880 | 82.5 | 5.0 | 1261 | 2 | Q7R2F4 | Q7r2f4 giardia lam | 953 | 82 | 4.9 | 1672 | 1 | PMPB CHLMU | Q9pj22 chlamydia m |
| 881 | 82.5 | 5.0 | 1371 | 2 | Q9VU22 | Q9vu22 drosophila | 954 | 82 | 4.9 | 1854 | 2 | Q7ZA78 | Q7za78 candida alb |
| 882 | 82.5 | 5.0 | 1460 | 1 | PMPC CHLMU | Q9pjy1 chlamydia m | 955 | 82 | 4.9 | 2981 | 2 | Q6CEB2 | Q6ceb2 yarrowia li |
| 883 | 82.5 | 5.0 | 1468 | 1 | FMN1 MOUSE | Q05860 mus musculu | 956 | 82 | 4.9 | 3146 | 2 | Q9VUB5 | Q9vub5 drosophila |
| 884 | 82.5 | 5.0 | 1472 | 2 | Q6V9R4 | Q6v9r4 strongyloce | 957 | 82 | 4.9 | 3529 | 2 | Q9GP30 | Q9gp30 theileria p |
| 885 | 82.5 | 5.0 | 1478 | 1 | LHN2 BOVIN | Q97817 bos taurus | 958 | 82 | 4.9 | 26926 | 2 | Q10466 | Q10466 homo sapien |
| 886 | 82.5 | 5.0 | 1969 | 1 | Q7SEZ5 | Q7sezs neurospora | 959 | 81.5 | 4.9 | 171 | 1 | NUOE BUCBP | Q89au3 buchnera ap |
| 887 | 82.5 | 5.0 | 2311 | 1 | KROS CHICK | P08941 gallus gall | 960 | 81.5 | 4.9 | 234 | 2 | Q6FXA6 | Q6fxa6 candida gla |
| 888 | 82.5 | 5.0 | 3295 | 2 | Q6GGT3 | Q6ggt3 rattus norv | 961 | 81.5 | 4.9 | 235 | 2 | Q9M182 | Q9m182 arabidopsis |
| 889 | 82 | 4.9 | 208 | 2 | Q81WS2 | Q81ws2 homo sapien | 962 | 81.5 | 4.9 | 245 | 2 | Q7SBI6 | Q7sbi6 neurospora |
| 890 | 82 | 4.9 | 208 | 2 | Q8N131 | Q8n131 homo sapien | 963 | 81.5 | 4.9 | 273 | 2 | Q6JTK85 | Q6jtk85 neodiprion |
| 891 | 82 | 4.9 | 236 | 2 | Q9LM00 | Q9lm00 pinus taeda | 964 | 81.5 | 4.9 | 345 | 2 | Q690T8 | Q690t8 anolis sagr |
| 892 | 82 | 4.9 | 250 | 2 | Q8FSI6 | Q8fsi6 corynebacte | 965 | 81.5 | 4.9 | 345 | 2 | Q690U2 | Q690u2 anolis sagr |
| 893 | 82 | 4.9 | 255 | 2 | Q81LN1 | Q81ln1 drosophila | 966 | 81.5 | 4.9 | 345 | 2 | Q890U5 | Q890u5 anolis sagr |
| 894 | 82 | 4.9 | 260 | 2 | Q27007 | Q27007 methanobact | 967 | 81.5 | 4.9 | 345 | 2 | Q690U6 | Q690u6 anolis sagr |
| 895 | 82 | 4.9 | 282 | 2 | Q9FSR0 | Q9fsr0 oryza sativ | 968 | 81.5 | 4.9 | 345 | 2 | Q690U8 | Q690u8 anolis sagr |
| 896 | 82 | 4.9 | 323 | 2 | Q8W1I7 | Q8w1i7 drosophila | 969 | 81.5 | 4.9 | 345 | 2 | Q690V1 | Q690v1 anolis sagr |
| 897 | 82 | 4.9 | 328 | 2 | Q8T8J5 | Q8t8j5 drosophila | 970 | 81.5 | 4.9 | 345 | 2 | Q690W8 | Q690w8 anolis sagr |
| 898 | 82 | 4.9 | 339 | 2 | Q9VUX8 | Q9vux8 drosophila | 971 | 81.5 | 4.9 | 345 | 2 | Q690X6 | Q690x6 anolis sagr |
| 899 | 82 | 4.9 | 345 | 2 | Q690W9 | Q690w9 anolis sagr | 972 | 81.5 | 4.9 | 345 | 2 | Q690X8 | Q690x8 anolis sagr |
| 900 | 82 | 4.9 | 345 | 2 | Q691G8 | Q691g8 anolis sagr | 973 | 81.5 | 4.9 | 345 | 2 | Q691Q6 | Q691q6 anolis sagr |
| 901 | 82 | 4.9 | 385 | 2 | Q8T8K9 | Q8t8k9 drosophila | 974 | 81.5 | 4.9 | 345 | 2 | Q691T7 | Q691t7 anolis sagr |
| 902 | 82 | 4.9 | 385 | 2 | Q8T8L2 | Q8t8l2 drosophila | 975 | 81.5 | 4.9 | 345 | 2 | Q691U4 | Q691u4 anolis sagr |
| 903 | 82 | 4.9 | 389 | 2 | Q76573 | Q76573 caenorhabdi | 976 | 81.5 | 4.9 | 345 | 2 | Q691Y0 | Q691y0 anolis sagr |
| 904 | 82 | 4.9 | 410 | 1 | LMP2 HUMAN | P13473 homo sapien | 977 | 81.5 | 4.9 | 345 | 2 | Q691Y1 | Q691y1 anolis sagr |
| 905 | 82 | 4.9 | 411 | 2 | Q6QJG8 | Q6qjg8 homo sapien | 978 | 81.5 | 4.9 | 368 | 2 | Q864C4 | Q864c4 delphinus d |
| 906 | 82 | 4.9 | 477 | 1 | MYPH HUMAN | Q13203 homo sapien | 979 | 81.5 | 4.9 | 369 | 2 | O65249 | O65249 arabidopsis |
| 907 | 82 | 4.9 | 483 | 2 | Q9W4M2 | Q9w4m2 drosophila | 980 | 81.5 | 4.9 | 386 | 2 | Q97G38 | Q97g38 clostridium |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|------------|---------------------|------|------|-----|------|---|------------|---------------------|
| 981 | 81.5 | 4.9 | 388 | 2 | Q7Q1W8 | Q7qlw8 anopheles g | 1054 | 81 | 4.9 | 831 | 2 | Q6BMH2 | Q6bmh2 debaryomyce |
| 982 | 81.5 | 4.9 | 390 | 2 | Q6PND6 | Q6pnd6 emericella | 1055 | 81 | 4.9 | 855 | 1 | CLOC_MOUSE | Q08785 mus musculus |
| 983 | 81.5 | 4.9 | 410 | 2 | Q9UD93 | Q9ud93 homo sapien | 1056 | 81 | 4.9 | 857 | 2 | Q8ZQD6 | Q6zqd6 mus musculus |
| 984 | 81.5 | 4.9 | 412 | 2 | Q9P603 | Q9p603 neurospora | 1057 | 81 | 4.9 | 904 | 2 | Q8IWC1 | Q8iwc1 homo sapien |
| 985 | 81.5 | 4.9 | 432 | 2 | Q6NURO | Q6nuro homo sapten | 1058 | 81 | 4.9 | 911 | 2 | Q7Q143 | Q7q143 anopheles g |
| 986 | 81.5 | 4.9 | 432 | 2 | Q7YU0E4 | Q7yuo04 oryza sativ | 1059 | 81 | 4.9 | 941 | 2 | Q7Q25R7 | Q7z5r7 homo sapien |
| 987 | 81.5 | 4.9 | 438 | 2 | Q6INH8 | Q6inh8 xenopus lae | 1060 | 81 | 4.9 | 948 | 2 | Q8NDA4 | Q8nda4 homo sapien |
| 988 | 81.5 | 4.9 | 463 | 2 | Q9K1H4 | Q9k1h4 neisseria m | 1061 | 81 | 4.9 | 1047 | 2 | Q24019 | Q24019 drosophila |
| 989 | 81.5 | 4.9 | 551 | 2 | Q7S436 | Q7s436 neurospora | 1062 | 81 | 4.9 | 1128 | 1 | BEM3_YEAST | Q28773 saccharomyc |
| 990 | 81.5 | 4.9 | 567 | 2 | Q6PR51 | Q6fr51 candida glia | 1063 | 81 | 4.9 | 1163 | 2 | Q86ARI | Q8ear1 dictyosteli |
| 991 | 81.5 | 4.9 | 599 | 2 | Q9U3W0 | Q9u3w0 drosophila | 1064 | 81 | 4.9 | 1169 | 1 | YK82_YEAST | P36170 saccharomyc |
| 992 | 81.5 | 4.9 | 636 | 1 | YNR6_YEAST | P53882 saccharomyc | 1065 | 81 | 4.9 | 1223 | 2 | Q6ZS17 | Q6zsl7 homo sapien |
| 993 | 81.5 | 4.9 | 687 | 1 | SRB4_YEAST | P32569 saccharomyc | 1066 | 81 | 4.9 | 1322 | 1 | FLO9_YEAST | P39712 saccharomyc |
| 994 | 81.5 | 4.9 | 687 | 2 | Q6B1B4 | Q6bib4 saccharomyc | 1067 | 81 | 4.9 | 1502 | 2 | Q8IS10 | Q8is10 dictyosteli |
| 995 | 81.5 | 4.9 | 838 | 2 | Q7OC91 | Q7oc91 anopheles g | 1068 | 81 | 4.9 | 1569 | 2 | Q8W4X9 | Q8w4x9 homo sapien |
| 996 | 81.5 | 4.9 | 846 | 2 | Q6ZKY0 | Q6zky0 oryza sativ | 1069 | 81 | 4.9 | 1609 | 1 | FIG2_YEAST | P25653 saccharomyc |
| 997 | 81.5 | 4.9 | 860 | 1 | MUTS_LISIN | Q92bv3 listeria in | 1070 | 81 | 4.9 | 1625 | 2 | Q6MVD4 | Q6mvd4 neurospora |
| 998 | 81.5 | 4.9 | 869 | 2 | Q01262 | Q01262 caenorhabdi | 1071 | 81 | 4.9 | 1657 | 2 | Q76NT8 | Q76nt8 dictyosteli |
| 999 | 81.5 | 4.9 | 873 | 2 | Q9W468 | Q9w468 drosophila | 1072 | 81 | 4.9 | 1709 | 2 | Q86L43 | Q86l43 dictyosteli |
| 1000 | 81.5 | 4.9 | 880 | 1 | PHTF_DROME | Q9v9a8 drosophila | 1073 | 81 | 4.9 | 1800 | 2 | Q8IEI9 | Q8ie19 plasmodium |
| 1001 | 81.5 | 4.9 | 913 | 2 | Q7NP28 | Q7np28 gloebacter | 1074 | 81 | 4.9 | 2060 | 2 | Q6MZK8 | Q6mzk8 homo sapien |
| 1002 | 81.5 | 4.9 | 917 | 2 | Q7RA65 | Q7ra65 plasmodium | 1075 | 81 | 4.9 | 2282 | 1 | ZAN_RABIT | P57999 oryctoiaagus |
| 1003 | 81.5 | 4.9 | 976 | 2 | Q6NTV5 | Q6ntv5 xenopus lae | 1076 | 81 | 4.9 | 2727 | 2 | Q6NR00 | Q6nr00 drosophila |
| 1004 | 81.5 | 4.9 | 980 | 1 | SLK3_MOUSE | Q810b9 mus musculus | 1077 | 81 | 4.9 | 2727 | 2 | Q9VL06 | Q9vl06 drosophila |
| 1005 | 81.5 | 4.9 | 980 | 2 | Q9WA13 | Q9ma13 arabidopsis | 1078 | 81 | 4.9 | 2977 | 2 | Q9VAP9 | Q9vap9 drosophila |
| 1006 | 81.5 | 4.9 | 1142 | 2 | Q6CCL7 | Q6ccl7 yarrowia li | 1079 | 81 | 4.9 | 5017 | 2 | Q63DF3 | Q63df3 bacillus ce |
| 1007 | 81.5 | 4.9 | 1151 | 1 | FOG2_MOUSE | Q8ech7 mus musculus | 1080 | 80.5 | 4.9 | 148 | 1 | SY02_RAT | P14844 rattus norv |
| 1008 | 81.5 | 4.9 | 1206 | 1 | BUN2_DROME | Q24523 drosophila | 1081 | 80.5 | 4.9 | 165 | 2 | Q26877 | Q26877 trypanosoma |
| 1009 | 81.5 | 4.9 | 1216 | 1 | YPX5_CAEEL | Q99277 caenorhabdi | 1082 | 80.5 | 4.9 | 242 | 2 | Q86RS8 | Q86rs8 caenorhabdi |
| 1010 | 81.5 | 4.9 | 1320 | 2 | Q9K6F5 | Q96kfs homo sapten | 1083 | 80.5 | 4.9 | 326 | 2 | Q7SCU5 | Q7scj5 neurospora |
| 1011 | 81.5 | 4.9 | 1415 | 1 | ALAI_CANAL | Q13368 candida alb | 1084 | 80.5 | 4.9 | 334 | 2 | Q6VAV6 | Q6vav6 anopheles g |
| 1012 | 81.5 | 4.9 | 1449 | 1 | PTPG_HUMAN | P23470 homo sapten | 1085 | 80.5 | 4.9 | 345 | 2 | Q8WD11 | Q8wd11 anolis sagr |
| 1013 | 81.5 | 4.9 | 1481 | 2 | Q6BW56 | Q6bws6 debaryomyce | 1086 | 80.5 | 4.9 | 345 | 2 | Q690T5 | Q690t5 anolis sagr |
| 1014 | 81.5 | 4.9 | 1500 | 2 | Q6AUV2 | Q6auv2 oryza sativ | 1087 | 80.5 | 4.9 | 345 | 2 | Q690T7 | Q690t7 anolis sagr |
| 1015 | 81.5 | 4.9 | 1536 | 2 | Q86AL7 | Q86al7 dictyosteli | 1088 | 80.5 | 4.9 | 345 | 2 | Q690U0 | Q690u0 anolis sagr |
| 1016 | 81.5 | 4.9 | 2063 | 2 | Q7RQL1 | Q7rgl1 plasmodium | 1089 | 80.5 | 4.9 | 345 | 2 | Q690U1 | Q690u1 anolis sagr |
| 1017 | 81.5 | 4.9 | 2282 | 2 | Q6SNP9 | Q6snp9 mus musculus | 1090 | 80.5 | 4.9 | 345 | 2 | Q690U3 | Q690u3 anolis sagr |
| 1018 | 81.5 | 4.9 | 2338 | 2 | Q629N6 | Q629n6 burkholderi | 1091 | 80.5 | 4.9 | 345 | 2 | Q690V2 | Q690v2 anolis sagr |
| 1019 | 81 | 4.9 | 184 | 2 | Q7BPK1 | Q7bpk1 anopheles g | 1092 | 80.5 | 4.9 | 345 | 2 | Q690W5 | Q690w5 anolis sagr |
| 1020 | 81 | 4.9 | 218 | 2 | Q7Z3K1 | Q7z3k1 homo sapien | 1093 | 80.5 | 4.9 | 345 | 2 | Q691G5 | Q691g5 anolis sagr |
| 1021 | 81 | 4.9 | 267 | 2 | Q6FXC3 | Q6fxc3 candida glia | 1094 | 80.5 | 4.9 | 345 | 2 | Q691M1 | Q691m1 anolis sagr |
| 1022 | 81 | 4.9 | 301 | 2 | Q924G0 | Q924g0 cratogeomys | 1095 | 80.5 | 4.9 | 345 | 2 | Q691R1 | Q691r1 anolis sagr |
| 1023 | 81 | 4.9 | 315 | 2 | Q7VXK11 | Q7vxx11 drosophila | 1096 | 80.5 | 4.9 | 345 | 2 | Q691U7 | Q691u7 anolis sagr |
| 1024 | 81 | 4.9 | 349 | 2 | Q7XEC9 | Q7xec9 oryza sativ | 1097 | 80.5 | 4.9 | 345 | 2 | Q692A0 | Q692a0 anolis sagr |
| 1025 | 81 | 4.9 | 355 | 2 | Q9NP13 | Q9np13 homo sapien | 1098 | 80.5 | 4.9 | 345 | 2 | Q692A2 | Q692a2 anolis sagr |
| 1026 | 81 | 4.9 | 370 | 2 | Q9FN39 | Q9fn39 arabidopsis | 1099 | 80.5 | 4.9 | 345 | 2 | Q692A3 | Q692a3 anolis sagr |
| 1027 | 81 | 4.9 | 370 | 2 | Q9YIT4 | Q9yyt4 mouse endog | 1100 | 80.5 | 4.9 | 356 | 2 | Q6CNP5 | Q6cnp5 kluyveromyc |
| 1028 | 81 | 4.9 | 384 | 2 | Q70Z21 | Q70z21 human herpe | 1101 | 80.5 | 4.9 | 358 | 2 | Q6MRL6 | Q6mr16 drosophila |
| 1029 | 81 | 4.9 | 385 | 2 | Q8T8J7 | Q8t8j7 drosophila | 1102 | 80.5 | 4.9 | 364 | 2 | Q62799 | Q62799 tursiops tr |
| 1030 | 81 | 4.9 | 385 | 2 | Q8T8K0 | Q8t8k0 drosophila | 1103 | 80.5 | 4.9 | 366 | 2 | Q75AD7 | Q75ad7 ashbya goss |
| 1031 | 81 | 4.9 | 411 | 2 | Q8DVK6 | Q8dvx6 streptococc | 1104 | 80.5 | 4.9 | 388 | 2 | Q6CRL0 | Q6crl0 kluyveromyc |
| 1032 | 81 | 4.9 | 413 | 2 | Q53974 | Q53974 streptococc | 1105 | 80.5 | 4.9 | 391 | 1 | VE2_HPV2A | P25482 human papil |
| 1033 | 81 | 4.9 | 422 | 1 | SYT2_RAT | P29101 rattus norv | 1106 | 80.5 | 4.9 | 399 | 2 | Q6CAU7 | Q6cau7 yarrowia li |
| 1034 | 81 | 4.9 | 428 | 2 | Q7SPW2 | Q7spw2 human betar | 1107 | 80.5 | 4.9 | 395 | 2 | Q6SX73 | Q6sx73 human cytom |
| 1035 | 81 | 4.9 | 431 | 1 | MNG1_MACFA | Q95K97 macaca fasc | 1108 | 80.5 | 4.9 | 402 | 2 | Q9N503 | Q9n503 caenorhabdi |
| 1036 | 81 | 4.9 | 437 | 2 | Q7XPL0 | Q7xpl0 oryza sativ | 1109 | 80.5 | 4.9 | 410 | 1 | LWP2_CRIGR | P49130 cricetus |
| 1037 | 81 | 4.9 | 446 | 2 | Q9UL37 | Q9ul37 leishmania | 1110 | 80.5 | 4.9 | 441 | 2 | Q9U2W3 | Q9u2w3 caenorhabdi |
| 1038 | 81 | 4.9 | 489 | 2 | Q9SQ80 | Q9sq80 caenorhabdi | 1111 | 80.5 | 4.9 | 478 | 2 | O61122 | O61122 dictyosteli |
| 1039 | 81 | 4.9 | 495 | 2 | Q6MRG4 | Q6mr94 dellolovibri | 1112 | 80.5 | 4.9 | 487 | 2 | O96601 | O96601 plasmodium |
| 1040 | 81 | 4.9 | 497 | 2 | Q8MY24 | Q8my24 homo sapien | 1113 | 80.5 | 4.9 | 540 | 1 | CH60_STRAG | Q9ame7 streptococc |
| 1041 | 81 | 4.9 | 503 | 2 | Q9SQ82 | Q9sq82 caenorhabdi | 1114 | 80.5 | 4.9 | 541 | 2 | O15681 | O15681 toxoplasma |
| 1042 | 81 | 4.9 | 562 | 2 | Q8IEJ5 | Q8iej5 plasmodium | 1115 | 80.5 | 4.9 | 543 | 2 | Q20720 | Q20720 caenorhabdi |
| 1043 | 81 | 4.9 | 626 | 2 | Q8IGQ7 | Q8igq7 drosophila | 1116 | 80.5 | 4.9 | 547 | 2 | Q8IV81 | Q8iv81 homo sapien |
| 1044 | 81 | 4.9 | 634 | 1 | HWF1_CANAL | P46593 candida alb | 1117 | 80.5 | 4.9 | 552 | 2 | Q69JG4 | Q69jg4 oryza sativ |
| 1045 | 81 | 4.9 | 637 | 2 | Q7TSS5 | Q7tss5 rattus norv | 1118 | 80.5 | 4.9 | 573 | 2 | Q8TOR9 | Q8tor9 drosophila |
| 1046 | 81 | 4.9 | 642 | 2 | Q75JG6 | Q75jg6 dictyosteli | 1119 | 80.5 | 4.9 | 581 | 2 | Q7R0Z5 | Q7r0z5 giardia lam |
| 1047 | 81 | 4.9 | 651 | 1 | VU47_HHV6U | Q06093 human herpe | 1120 | 80.5 | 4.9 | 591 | 2 | Q6K4S0 | Q6k4s0 oryza sativ |
| 1048 | 81 | 4.9 | 668 | 2 | Q6FWR2 | Q6fwr2 candida glia | 1121 | 80.5 | 4.9 | 592 | 2 | Q23036 | Q23036 caenorhabdi |
| 1049 | 81 | 4.9 | 670 | 2 | Q70653 | Q70653 gibbon ape | 1122 | 80.5 | 4.9 | 595 | 1 | DNAK_MYCHO | Q9zej0 mycoplasma |
| 1050 | 81 | 4.9 | 683 | 2 | O24424 | O24424 papaver som | 1123 | 80.5 | 4.9 | 595 | 2 | TNR8_HUMAN | T28908 homo sapien |
| 1051 | 81 | 4.9 | 683 | 2 | Q9SK94 | Q9sk94 arabidopsis | 1124 | 80.5 | 4.9 | 658 | 2 | Q8MQZ8 | Q8mqz8 drosophila |
| 1052 | 81 | 4.9 | 759 | 2 | O05143 | O05143 ruminococcu | 1125 | 80.5 | 4.9 | 668 | 2 | Q75C56 | Q75c56 ashbya goss |
| 1053 | 81 | 4.9 | 802 | 2 | Q7YVP9 | Q7yvp9 trypanosoma | 1126 | 80.5 | 4.9 | 672 | 2 | Q75FD8 | Q75fd8 neurospora |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|------------|---------------------|------|------|-----|-------|---|------------|---------------------|
| 1127 | 80.5 | 4.9 | 676 | 2 | Q9VB94 | Q9vb94 drosophila | 1200 | 80 | 4.8 | 683 | 2 | Q8MRH5 | Q8mrh5 drosophila |
| 1128 | 80.5 | 4.9 | 706 | 2 | Q9VNZ5 | Q9vnz5 drosophila | 1201 | 80 | 4.8 | 688 | 1 | SLP2_CLOTH | Q06953 clostridium |
| 1129 | 80.5 | 4.9 | 747 | 2 | Q7S8F0 | Q7s8f0 neurospora | 1202 | 80 | 4.8 | 698 | 2 | Q8JKG8 | Q8jkg8 heliothis z |
| 1130 | 80.5 | 4.9 | 754 | 2 | Q7NB52 | Q7nb52 mycoplasma | 1203 | 80 | 4.8 | 725 | 1 | AGAL_YEAST | P32223 saccharomyc |
| 1131 | 80.5 | 4.9 | 758 | 2 | Q9T214 | Q9t214 caenorhabdi | 1204 | 80 | 4.8 | 729 | 2 | Q8OWY2 | Q8owY2 mus musculu |
| 1132 | 80.5 | 4.9 | 760 | 2 | Q6RJF7 | Q6rjf7 homo sapien | 1205 | 80 | 4.8 | 732 | 2 | Q8OWY1 | Q8owY1 mus musculu |
| 1133 | 80.5 | 4.9 | 765 | 2 | Q7S127 | Q7s127 oryza sativ | 1206 | 80 | 4.8 | 733 | 2 | Q811D2 | Q811d2 mus musculu |
| 1134 | 80.5 | 4.9 | 805 | 2 | Q6C980 | Q6c980 yarrowia li | 1207 | 80 | 4.8 | 743 | 2 | Q95RK9 | Q95rk9 drosophila |
| 1135 | 80.5 | 4.9 | 832 | 2 | Q8KOC2 | Q8koc2 mus musculu | 1208 | 80 | 4.8 | 743 | 2 | Q8C0S0 | Q960s0 drosophila |
| 1136 | 80.5 | 4.9 | 860 | 2 | Q712R7 | Q712r7 listeria mo | 1209 | 80 | 4.8 | 747 | 2 | Q8CCZ1 | Q8ccz1 mus musculu |
| 1137 | 80.5 | 4.9 | 879 | 2 | Q91SD0 | Q91sd0 canine heyrp | 1210 | 80 | 4.8 | 772 | 2 | Q82YF8 | Q82yf8 streptomyce |
| 1138 | 80.5 | 4.9 | 918 | 1 | GLK1_HUMAN | P39086 homo sapien | 1211 | 80 | 4.8 | 782 | 2 | Q7R2Z3 | Q7r2z3 giardia lam |
| 1139 | 80.5 | 4.9 | 919 | 2 | Q76EQ4 | Q76eq4 streptococc | 1212 | 80 | 4.8 | 787 | 2 | Q9VEY6 | Q9vey6 drosophila |
| 1140 | 80.5 | 4.9 | 951 | 1 | SFRB_HUMAN | Q12872 homo sapien | 1213 | 80 | 4.8 | 789 | 2 | Q7PDP0 | Q7pdp0 plasmodium |
| 1141 | 80.5 | 4.9 | 962 | 1 | Q7PFXG | Q7pxg9 anopheles g | 1214 | 80 | 4.8 | 849 | 2 | P87107 | P87107 saccharomyc |
| 1142 | 80.5 | 4.9 | 983 | 2 | Q8G204 | Q8g204 arabidopsis | 1215 | 80 | 4.8 | 870 | 2 | Q824X2 | Q824x2 chlamyadophi |
| 1143 | 80.5 | 4.9 | 1119 | 1 | ALS3_CANAL | Q74623 candida alb | 1216 | 80 | 4.8 | 873 | 2 | Q9NYU3 | Q9nyu3 homo sapien |
| 1144 | 80.5 | 4.9 | 1124 | 2 | Q92E44 | Q9ze44 rickettsia | 1217 | 80 | 4.8 | 881 | 1 | PRY3_YEAST | P47033 saccharomyc |
| 1145 | 80.5 | 4.9 | 1144 | 2 | Q86AL9 | Q86al9 dictyosteli | 1218 | 80 | 4.8 | 882 | 2 | Q9VA36 | Q9va36 drosophila |
| 1146 | 80.5 | 4.9 | 1155 | 2 | Q7KR63 | Q7kr63 drosophila | 1219 | 80 | 4.8 | 902 | 2 | Q8Q7H5 | Q8q7h5 human immun |
| 1147 | 80.5 | 4.9 | 1159 | 1 | RRPO_ROTGI | P35942 rotavirus (| 1220 | 80 | 4.8 | 916 | 2 | Q9W4A6 | Q9w4a6 drosophila |
| 1148 | 80.5 | 4.9 | 1163 | 1 | COAA_BACTF | Q9x597 bacillus th | 1221 | 80 | 4.8 | 933 | 2 | Q61RA7 | Q61ra7 xenopus lae |
| 1149 | 80.5 | 4.9 | 1179 | 2 | Q9JK71 | Q9jk71 rattus norv | 1222 | 80 | 4.8 | 979 | 2 | Q6B1Q3 | Q6bcq3 debaryomyce |
| 1150 | 80.5 | 4.9 | 1184 | 2 | Q6F3A8 | Q6f3a8 oryza sativ | 1223 | 80 | 4.8 | 982 | 2 | Q6CGV5 | Q6cgv5 yarrowia li |
| 1151 | 80.5 | 4.9 | 1245 | 2 | Q7Q947 | Q7q947 anopheles g | 1224 | 80 | 4.8 | 1008 | 2 | Q6FM15 | Q6fm15 candida gla |
| 1152 | 80.5 | 4.9 | 1297 | 2 | Q8SSS5 | Q8sss5 dictyosteli | 1225 | 80 | 4.8 | 1012 | 1 | PPOL_MOUSE | P11103 mus musculu |
| 1153 | 80.5 | 4.9 | 1342 | 2 | Q8A0H1 | Q8a0h1 bacteroides | 1226 | 80 | 4.8 | 1047 | 2 | Q9VZH2 | Q9vzh2 drosophila |
| 1154 | 80.5 | 4.9 | 1367 | 2 | Q9SFB6 | Q9sfb6 arabidopsis | 1227 | 80 | 4.8 | 1150 | 2 | Q9HBC4 | Q9hbc4 homo sapien |
| 1155 | 80.5 | 4.9 | 1372 | 2 | Q8SX99 | Q8sx99 drosophila | 1228 | 80 | 4.8 | 1153 | 2 | Q9V6J8 | Q9v6j8 drosophila |
| 1156 | 80.5 | 4.9 | 1372 | 2 | Q9VNA6 | Q9vna6 drosophila | 1229 | 80 | 4.8 | 1168 | 2 | Q9VZE8 | Q9vze8 drosophila |
| 1157 | 80.5 | 4.9 | 1743 | 2 | Q811M4 | Q811m4 plasmodium | 1230 | 80 | 4.8 | 1197 | 2 | Q6CDS2 | Q6cds2 yarrowia li |
| 1158 | 80.5 | 4.9 | 1752 | 2 | Q869Q7 | Q869q7 dictyosteli | 1231 | 80 | 4.8 | 1207 | 2 | Q81174 | Q81174 drosophila |
| 1159 | 80.5 | 4.9 | 1984 | 2 | Q7QRS1 | Q7qrs1 giardia lam | 1232 | 80 | 4.8 | 1209 | 2 | Q6SZU2 | Q6szu2 mus musculu |
| 1160 | 80.5 | 4.9 | 2162 | 2 | Q7OPP2 | Q7opp2 drosophila | 1233 | 80 | 4.8 | 1226 | 2 | Q9NZB6 | Q9nzb6 homo sapien |
| 1161 | 80.5 | 4.9 | 2225 | 2 | Q4S881 | Q4s881 caenorhabdi | 1234 | 80 | 4.8 | 1240 | 2 | Q7TQM8 | Q7tqm8 mus musculu |
| 1162 | 80.5 | 4.9 | 3218 | 2 | Q9W3V6 | Q9w3v6 drosophila | 1235 | 80 | 4.8 | 1248 | 2 | Q8BWH3 | Q8bwh3 mus musculu |
| 1163 | 80 | 4.8 | 103 | 2 | Q46380 | Q46380 oryctolagus | 1236 | 80 | 4.8 | 1325 | 2 | Q9BKV7 | Q9bkv7 leishmania |
| 1164 | 80 | 4.8 | 153 | 1 | FTI2_YEAST | Q08906 saccharomyc | 1237 | 80 | 4.8 | 1469 | 2 | Q7S353 | Q7s353 neurospora |
| 1165 | 80 | 4.8 | 174 | 2 | Q64EZ1 | Q64ez1 tenebrio mo | 1238 | 80 | 4.8 | 1486 | 2 | Q9SRE5 | Q9sre5 drosophila |
| 1166 | 80 | 4.8 | 177 | 1 | ARG1_YEAST | P07249 saccharomyc | 1239 | 80 | 4.8 | 1486 | 2 | Q967Y2 | Q967y2 drosophila |
| 1167 | 80 | 4.8 | 231 | 2 | Q9CY44 | Q9cyy4 mus musculu | 1240 | 80 | 4.8 | 1486 | 2 | Q7KRPF | Q7krpf drosophila |
| 1168 | 80 | 4.8 | 242 | 2 | Q9VDN0 | Q9vdn0 drosophila | 1241 | 80 | 4.8 | 1582 | 2 | Q7KRPF | Q7krpf drosophila |
| 1169 | 80 | 4.8 | 250 | 2 | Q9HFS1 | Q9hfs1 candida alb | 1242 | 80 | 4.8 | 1693 | 1 | SAS_DROME | Q04164 drosophila |
| 1170 | 80 | 4.8 | 251 | 2 | Q674L5 | Q674l5 human respi | 1243 | 80 | 4.8 | 1721 | 2 | Q8SSQ0 | Q8ssq0 dictyosteli |
| 1171 | 80 | 4.8 | 257 | 2 | Q77KZ8 | Q77kz8 bovine resp | 1244 | 80 | 4.8 | 1761 | 2 | Q7KTF6 | Q7ktf6 drosophila |
| 1172 | 80 | 4.8 | 257 | 2 | Q9V825 | Q9v825 bovine resp | 1245 | 80 | 4.8 | 1845 | 2 | Q86JH8 | Q86jh8 dictyosteli |
| 1173 | 80 | 4.8 | 261 | 1 | EMCN_HUMAN | Q9ulc0 homo sapien | 1246 | 80 | 4.8 | 2154 | 2 | Q8WZ51 | Q8wz51 homo sapien |
| 1174 | 80 | 4.8 | 272 | 2 | Q6ZSN5 | Q6zen5 homo sapien | 1247 | 80 | 4.8 | 2616 | 1 | NDL_DROME | P98159 drosophila |
| 1175 | 80 | 4.8 | 283 | 2 | Q6C1R8 | Q6c1r8 kluyveromyc | 1248 | 80 | 4.8 | 2828 | 2 | Q6MMK5 | Q6mmk5 bdellovibri |
| 1176 | 80 | 4.8 | 301 | 2 | Q6L4D1 | Q6l4d1 oryza sativ | 1249 | 80 | 4.8 | 3410 | 2 | Q7TN00 | Q7tn00 rattus norv |
| 1177 | 80 | 4.8 | 325 | 2 | Q25936 | Q25936 plasmodium | 1250 | 80 | 4.8 | 3493 | 2 | Q39734 | Q39734 sweet potat |
| 1178 | 80 | 4.8 | 329 | 2 | Q8JFF6 | Q8jff6 xenopus lae | 1251 | 80 | 4.8 | 10791 | 2 | Q7U7M8 | Q7u7m8 synecococc |
| 1179 | 80 | 4.8 | 334 | 2 | Q6VAM0 | Q6vaw0 anopheles g | 1252 | 80 | 4.8 | 26926 | 2 | Q8WZB3 | Q8wzb3 homo sapien |
| 1180 | 80 | 4.8 | 345 | 2 | Q6Z224 | Q6z224 caenorhabdi | 1253 | 80 | 4.8 | 34350 | 2 | Q8WZ42 | Q8wz42 homo sapien |
| 1181 | 80 | 4.8 | 345 | 2 | Q690W7 | Q690w7 anolis sagr | 1254 | 79.5 | 4.8 | 80 | 2 | Q7MSR8 | Q7msr8 wolinnella s |
| 1182 | 80 | 4.8 | 359 | 2 | Q9XZT0 | Q9xzt0 drosophila | 1255 | 79.5 | 4.8 | 123 | 2 | O15773 | O15773 trypanosoma |
| 1183 | 80 | 4.8 | 374 | 2 | Q96NC5 | Q96nc5 homo sapien | 1256 | 79.5 | 4.8 | 129 | 2 | Q5UNH4 | Q5unh4 ictalurus p |
| 1184 | 80 | 4.8 | 415 | 2 | Q8YR34 | Q8yr34 anabaena sp | 1257 | 79.5 | 4.8 | 151 | 2 | Q75QC1 | Q75qc1 locus japon |
| 1185 | 80 | 4.8 | 449 | 2 | Q9VKS4 | Q9vks4 drosophila | 1258 | 79.5 | 4.8 | 152 | 2 | Q81G73 | Q81g73 caenorhabdi |
| 1186 | 80 | 4.8 | 451 | 2 | Q95144 | Q95144 cercopithe | 1259 | 79.5 | 4.8 | 161 | 2 | Q61GP4 | Q61gp4 drosophila |
| 1187 | 80 | 4.8 | 468 | 1 | VAS1_BOVIN | P40682 bos taurus | 1260 | 79.5 | 4.8 | 165 | 1 | H1_TETPY | P12305 tetrahymena |
| 1188 | 80 | 4.8 | 472 | 2 | Q8KWT3 | Q8kwt3 bacillus su | 1261 | 79.5 | 4.8 | 194 | 2 | Q9Y9W0 | Q9y9w0 aeropyrum p |
| 1189 | 80 | 4.8 | 473 | 2 | Q21052 | Q21052 caenorhabdi | 1262 | 79.5 | 4.8 | 199 | 2 | Q6C3G4 | Q6c3g4 yarrowia li |
| 1190 | 80 | 4.8 | 486 | 2 | Q53630 | Q53630 staphylococ | 1263 | 79.5 | 4.8 | 213 | 2 | Q8ZU27 | Q8zu27 homo sapien |
| 1191 | 80 | 4.8 | 486 | 2 | Q6GGT1 | Q6ggt1 staphylococ | 1264 | 79.5 | 4.8 | 232 | 2 | Q69EW2 | Q69ew2 streptococc |
| 1192 | 80 | 4.8 | 521 | 2 | Q04383 | Q04383 saccharomyc | 1265 | 79.5 | 4.8 | 257 | 2 | Q9N5S7 | Q9n5s7 caenorhabdi |
| 1193 | 80 | 4.8 | 549 | 2 | Q8VHX1 | Q8vhx1 mus musculu | 1266 | 79.5 | 4.8 | 269 | 2 | Q7TTU8 | Q7ttu8 synecococc |
| 1194 | 80 | 4.8 | 555 | 2 | Q7REM0 | Q7rem0 plasmodium | 1267 | 79.5 | 4.8 | 272 | 2 | Q8A3G1 | Q8a3g1 bacteroides |
| 1195 | 80 | 4.8 | 600 | 2 | Q8C692 | Q8c692 mus musculu | 1268 | 79.5 | 4.8 | 299 | 2 | Q6EH39 | Q6eh39 respiratory |
| 1196 | 80 | 4.8 | 634 | 2 | Q8JFF5 | Q8jff5 xenopus lae | 1269 | 79.5 | 4.8 | 316 | 2 | Q8BEK1 | Q8bek1 cowpox viru |
| 1197 | 80 | 4.8 | 650 | 2 | Q9U0U5 | Q9uu05 schizosach | 1270 | 79.5 | 4.8 | 326 | 2 | Q6CV42 | Q6cv42 kluyveromyc |
| 1198 | 80 | 4.8 | 657 | 2 | Q6AM00 | Q6am00 desulfotale | 1271 | 79.5 | 4.8 | 328 | 2 | Q9TXC7 | Q9txc7 drosophila |
| 1199 | 80 | 4.8 | 667 | 1 | CYL1_BOVIN | P35662 bos taurus | 1272 | 79.5 | 4.8 | 333 | 2 | Q6VAV7 | Q6vav7 anopheles g |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|------------|---------------------|------|------|-----|------|---|------------|--------------------|
| 1273 | 79.5 | 4.8 | 344 | 2 | Q691Z8 | Q691z8 anolis sagr | 1346 | 79.5 | 4.8 | 1441 | 2 | Q8S628 | Q8s628 oryza sativ |
| 1274 | 79.5 | 4.8 | 345 | 2 | Q690W1 | Q690w1 anolis sagr | 1347 | 79.5 | 4.8 | 1441 | 2 | Q8GU94 | Q8gu94 oryza sativ |
| 1275 | 79.5 | 4.8 | 345 | 2 | Q690X0 | Q690x0 anolis sagr | 1348 | 79.5 | 4.8 | 1443 | 2 | Q9Y8P2 | Q9y8f2 candida alb |
| 1276 | 79.5 | 4.8 | 345 | 2 | Q691G9 | Q691g9 anolis sagr | 1349 | 79.5 | 4.8 | 1444 | 2 | Q94KE2 | Q94ke2 arabidopsis |
| 1277 | 79.5 | 4.8 | 345 | 2 | Q691U8 | Q691u8 anolis sagr | 1350 | 79.5 | 4.8 | 1445 | 2 | Q94HN8 | Q94hn8 oryza sativ |
| 1278 | 79.5 | 4.8 | 345 | 2 | Q692A8 | Q692a8 anolis sagr | 1351 | 79.5 | 4.8 | 1445 | 2 | Q7XGK2 | Q7xgk2 oryza sativ |
| 1279 | 79.5 | 4.8 | 354 | 2 | Q25402 | Q25402 litomoeide | 1352 | 79.5 | 4.8 | 1459 | 1 | LHN2_HUMAN | Q95490 homo sapien |
| 1280 | 79.5 | 4.8 | 373 | 2 | Q76810 | Q76810 litomoeide | 1353 | 79.5 | 4.8 | 1532 | 2 | Q9LJW1 | Q91uw1 arabidopsis |
| 1281 | 79.5 | 4.8 | 384 | 2 | Q882D3 | Q882d3 lactobacill | 1354 | 79.5 | 4.8 | 1707 | 2 | Q6PMR4 | Q6pmr4 swine hepat |
| 1282 | 79.5 | 4.8 | 385 | 2 | Q8T8L4 | Q8t8l4 drosophila | 1355 | 79.5 | 4.8 | 1806 | 2 | Q869R4 | Q869r4 dictyosteli |
| 1283 | 79.5 | 4.8 | 403 | 2 | Q8MVA9 | Q8mva9 ixodes scap | 1356 | 79.5 | 4.8 | 1873 | 2 | Q6S003 | Q6s003 dictyosteli |
| 1284 | 79.5 | 4.8 | 425 | 2 | Q7RSR5 | Q7r5r5 plasmodium | 1357 | 79.5 | 4.8 | 2359 | 2 | Q81519 | Q81519 plasmodium |
| 1285 | 79.5 | 4.8 | 429 | 2 | Q93ZM7 | Q93zm7 arabidopsis | 1358 | 79.5 | 4.8 | 2623 | 2 | Q6WRI0 | Q6wri0 homo sapien |
| 1286 | 79.5 | 4.8 | 433 | 2 | Q88VC0 | Q88vc0 lactobacill | 1359 | 79.5 | 4.8 | 3365 | 2 | Q6XHA7 | Q6xha7 dictyosteli |
| 1287 | 79.5 | 4.8 | 457 | 2 | Q81VS6 | Q81vs6 homo sapien | 1360 | 79.5 | 4.8 | 3550 | 2 | Q66GT4 | Q66gt4 rattus norv |
| 1288 | 79.5 | 4.8 | 461 | 1 | TR1B_HUMAN | P20333 h tumor nec | 1361 | 79.5 | 4.8 | 5017 | 2 | Q6HKW5 | Q6hkw5 bacillus th |
| 1289 | 79.5 | 4.8 | 480 | 2 | Q84DS4 | Q84ds4 listeria mo | 1362 | 79.5 | 4.8 | 6458 | 2 | Q7QZ9A | Q7qza9 giardia lam |
| 1290 | 79.5 | 4.8 | 480 | 2 | Q84DS5 | Q84ds5 listeria mo | 1363 | 79.5 | 4.8 | 2015 | 2 | Q81QI8 | Q81qi8 drosophila |
| 1291 | 79.5 | 4.8 | 495 | 2 | Q9CV82 | Q9cv82 mus musculu | 1364 | 79 | 4.8 | 146 | 2 | Q6FIU3 | Q6fiu3 candida gla |
| 1292 | 79.5 | 4.8 | 504 | 2 | Q8VYJ6 | Q8vyj6 arabidopsis | 1365 | 79 | 4.8 | 195 | 2 | Q9W4V3 | Q9w4v3 drosophila |
| 1293 | 79.5 | 4.8 | 509 | 1 | AIOL_HUMAN | Q9ukt9 homo sapien | 1366 | 79 | 4.8 | 202 | 2 | Q7XLD8 | Q7xld8 oryza sativ |
| 1294 | 79.5 | 4.8 | 510 | 2 | Q9JUS7 | Q9j577 chlamydia p | 1367 | 79 | 4.8 | 204 | 2 | Q7M5K8 | Q7m5k8 smian aden |
| 1295 | 79.5 | 4.8 | 510 | 2 | Q84DS4 | Q9z6n9 chlamydia p | 1368 | 79 | 4.8 | 211 | 2 | Q6DF90 | Q6df90 xenopus lae |
| 1296 | 79.5 | 4.8 | 511 | 2 | Q8UYA8 | Q8uya8 human herpe | 1369 | 79 | 4.8 | 214 | 1 | H11_HUMAN | Q02539 homo sapien |
| 1297 | 79.5 | 4.8 | 511 | 2 | Q8UZ60 | Q8uz60 human herpe | 1370 | 79 | 4.8 | 215 | 2 | Q98TQ9 | Q98tq9 gallus gall |
| 1298 | 79.5 | 4.8 | 511 | 2 | Q8UZ61 | Q8uz61 human herpe | 1371 | 79 | 4.8 | 249 | 2 | Q9SJQ4 | Q9sjq4 arabidopsis |
| 1299 | 79.5 | 4.8 | 511 | 2 | Q8UZ66 | Q8uz66 human herpe | 1372 | 79 | 4.8 | 267 | 2 | Q8R0H4 | Q8r0h4 mus musculu |
| 1300 | 79.5 | 4.8 | 511 | 2 | Q8UZ66 | Q8uz66 human herpe | 1373 | 79 | 4.8 | 308 | 2 | Q74KF4 | Q74kf4 lactobacill |
| 1301 | 79.5 | 4.8 | 511 | 2 | Q8UZ67 | Q8uz67 human herpe | 1374 | 79 | 4.8 | 317 | 2 | Q8BEK2 | Q8bek2 cowpox viru |
| 1302 | 79.5 | 4.8 | 530 | 2 | Q6F107 | Q6f107 mesoplasma | 1375 | 79 | 4.8 | 333 | 2 | Q6VAV8 | Q6vav8 anopheles g |
| 1303 | 79.5 | 4.8 | 534 | 2 | Q80853 | Q80853 arabidopsis | 1376 | 79 | 4.8 | 340 | 2 | Q82KQ1 | Q82kq1 salmonella |
| 1304 | 79.5 | 4.8 | 540 | 1 | CH60_STRSA | Q8kj16 streptococc | 1377 | 79 | 4.8 | 345 | 2 | Q91V5 | Q91v5 anolis sagr |
| 1305 | 79.5 | 4.8 | 545 | 2 | Q8BEX1 | Q8eex1 shewanella | 1378 | 79 | 4.8 | 352 | 2 | Q49782 | Q49782 arabidopsis |
| 1306 | 79.5 | 4.8 | 552 | 2 | Q9LJJB0 | Q9ljjb0 arabidopsis | 1379 | 79 | 4.8 | 353 | 2 | Q8VPM3 | Q8vpm3 micrococcu |
| 1307 | 79.5 | 4.8 | 552 | 1 | NFL_BOVIN | P02548 bos taurus | 1380 | 79 | 4.8 | 374 | 2 | Q8TAY8 | Q8tay8 homo sapien |
| 1308 | 79.5 | 4.8 | 560 | 2 | Q87LX9 | Q87lx9 vibrio para | 1381 | 79 | 4.8 | 374 | 2 | Q96NF3 | Q96nf3 homo sapien |
| 1309 | 79.5 | 4.8 | 572 | 2 | Q9LRW0 | Q9lrw0 arabidopsis | 1382 | 79 | 4.8 | 382 | 2 | Q6UX15 | Q6ux15 homo sapien |
| 1310 | 79.5 | 4.8 | 580 | 2 | Q19315 | Q19315 caenorhabdi | 1383 | 79 | 4.8 | 392 | 2 | Q82JV1 | Q82jv1 streptomyce |
| 1311 | 79.5 | 4.8 | 581 | 2 | Q9VVG9 | Q9vv99 drosophila | 1384 | 79 | 4.8 | 417 | 2 | Q15828 | Q15828 leishmania |
| 1312 | 79.5 | 4.8 | 602 | 2 | Q8SY16 | Q8sy16 drosophila | 1385 | 79 | 4.8 | 447 | 2 | Q8BIY6 | Q8biy6 mus musculu |
| 1313 | 79.5 | 4.8 | 612 | 2 | Q9NVJ6 | Q9nvj6 homo sapien | 1386 | 79 | 4.8 | 459 | 2 | Q9H915 | Q9h915 homo sapien |
| 1314 | 79.5 | 4.8 | 689 | 2 | Q7QN60 | Q7qn60 anopheles g | 1387 | 79 | 4.8 | 461 | 2 | Q9LH91 | Q9lh91 arabidopsis |
| 1315 | 79.5 | 4.8 | 689 | 2 | Q8HYW1 | Q8hyw1 bos taurus | 1388 | 79 | 4.8 | 482 | 2 | Q76740 | Q76740 dictyosteli |
| 1316 | 79.5 | 4.8 | 693 | 2 | O01600 | O01600 caenorhabdi | 1389 | 79 | 4.8 | 492 | 2 | Q94HR9 | Q94hr9 arabidopsis |
| 1317 | 79.5 | 4.8 | 721 | 2 | Q86171 | Q86171 clostridium | 1390 | 79 | 4.8 | 534 | 2 | Q94317 | Q94317 schizosacch |
| 1318 | 79.5 | 4.8 | 729 | 2 | Q95RU5 | Q95ru5 drosophila | 1391 | 79 | 4.8 | 534 | 2 | Q86AL2 | Q86al2 dictyosteli |
| 1319 | 79.5 | 4.8 | 752 | 2 | Q640L3 | Q640l3 mus musculu | 1392 | 79 | 4.8 | 549 | 2 | Q8VBY3 | Q8vby3 mus musculu |
| 1320 | 79.5 | 4.8 | 756 | 2 | Q62985 | Q62985 rattus norv | 1393 | 79 | 4.8 | 554 | 2 | Q8CCJ9 | Q8ccj9 mus musculu |
| 1321 | 79.5 | 4.8 | 796 | 2 | Q8MRG9 | Q8mr99 drosophila | 1394 | 79 | 4.8 | 555 | 2 | Q9VH46 | Q9vh46 drosophila |
| 1322 | 79.5 | 4.8 | 796 | 2 | Q9VTR4 | Q9vtr4 drosophila | 1395 | 79 | 4.8 | 559 | 1 | NUPL_MOUSE | Q8k2k6 mus musculu |
| 1323 | 79.5 | 4.8 | 827 | 2 | Q9SZ08 | Q9sz08 arabidopsis | 1396 | 79 | 4.8 | 575 | 2 | Q62223 | Q62223 caenorhabdi |
| 1324 | 79.5 | 4.8 | 860 | 1 | MUTS_LISMO | Q8y789 listeria mo | 1397 | 79 | 4.8 | 594 | 2 | Q6PAN1 | Q6pan1 mus musculu |
| 1325 | 79.5 | 4.8 | 867 | 2 | Q6BTV1 | Q6bty1 debaryomyce | 1398 | 79 | 4.8 | 608 | 2 | Q6F3B7 | Q6f3b7 oryza sativ |
| 1326 | 79.5 | 4.8 | 873 | 2 | Q9Y076 | Q9y076 leishmania | 1399 | 79 | 4.8 | 611 | 2 | Q92EE6 | Q92ee6 listeria in |
| 1327 | 79.5 | 4.8 | 887 | 2 | Q6XD56 | Q6xd56 gallus gall | 1400 | 79 | 4.8 | 626 | 2 | Q8KUUS | Q8kuus synechococc |
| 1328 | 79.5 | 4.8 | 972 | 2 | Q9VFU8 | Q9vfus drosophila | 1401 | 79 | 4.8 | 644 | 2 | Q817L0 | Q817l0 caenorhabdi |
| 1329 | 79.5 | 4.8 | 980 | 2 | Q6NZM5 | Q6nzm5 mus musculu | 1402 | 79 | 4.8 | 644 | 2 | Q85510 | Q85510 xenotrophic |
| 1330 | 79.5 | 4.8 | 985 | 2 | Q67643 | Q67643 gallid herp | 1403 | 79 | 4.8 | 648 | 2 | Q895B6 | Q895b6 clostridium |
| 1331 | 79.5 | 4.8 | 998 | 1 | PPOL_XENLA | P31669 xenopus lae | 1404 | 79 | 4.8 | 649 | 2 | Q7JGN6 | Q7jgn6 xenopus lae |
| 1332 | 79.5 | 4.8 | 1011 | 2 | Q9XVR0 | Q9xvr0 caenorhabdi | 1405 | 79 | 4.8 | 692 | 1 | FIS2_ARATH | Q9ant9 arabidopsis |
| 1333 | 79.5 | 4.8 | 1125 | 2 | Q9H2V6 | Q9h2v6 homo sapien | 1406 | 79 | 4.8 | 702 | 2 | Q6BHB3 | Q6bbb3 debaryomyce |
| 1334 | 79.5 | 4.8 | 1137 | 2 | Q6CEC1 | Q6cec1 yarrowia li | 1407 | 79 | 4.8 | 710 | 1 | Y026_YEAST | P39744 saccharomyc |
| 1335 | 79.5 | 4.8 | 1212 | 2 | Q42347 | Q42347 gallus gall | 1408 | 79 | 4.8 | 712 | 2 | Q7Q2L5 | Q7q2l5 anopheles g |
| 1336 | 79.5 | 4.8 | 1237 | 2 | Q7WYN2 | Q7wyn2 acetivibrio | 1409 | 79 | 4.8 | 718 | 2 | Q94HGI | Q94hgi oryza sativ |
| 1337 | 79.5 | 4.8 | 1258 | 2 | Q8R458 | Q8r458 rattus norv | 1410 | 79 | 4.8 | 727 | 2 | Q817L1 | Q817l1 caenorhabdi |
| 1338 | 79.5 | 4.8 | 1280 | 2 | Q97SQ07 | Q97sq07 streptococc | 1411 | 79 | 4.8 | 729 | 2 | Q8BW38 | Q8bw38 mus musculu |
| 1339 | 79.5 | 4.8 | 1301 | 2 | Q7L7Z7 | Q7l7z7 homo sapien | 1412 | 79 | 4.8 | 738 | 2 | Q9WT23 | Q9wt23 human herpe |
| 1340 | 79.5 | 4.8 | 1306 | 2 | Q7TT18 | Q7tt18 mus musculu | 1413 | 79 | 4.8 | 748 | 2 | Q9Y6E1 | Q9y6e1 homo sapien |
| 1341 | 79.5 | 4.8 | 1306 | 2 | Q9UK31 | Q9jk31 mus musculu | 1414 | 79 | 4.8 | 780 | 2 | Q7PR05 | Q7pr05 anopheles g |
| 1342 | 79.5 | 4.8 | 1329 | 2 | Q9HCE3 | Q9hce3 homo sapien | 1415 | 79 | 4.8 | 784 | 2 | Q9H5A0 | Q9h5a0 homo sapien |
| 1343 | 79.5 | 4.8 | 1346 | 2 | Q7KR62 | Q7kr62 drosophila | 1416 | 79 | 4.8 | 801 | 2 | Q6P2S1 | Q6p2s1 homo sapien |
| 1344 | 79.5 | 4.8 | 1365 | 1 | SUZ2_DROME | P25172 drosophila | 1417 | 79 | 4.8 | 822 | 1 | DEXT_STREL | Q59979 streptococc |
| 1345 | 79.5 | 4.8 | 1368 | 2 | Q9V6J0 | Q9v6j0 drosophila | 1418 | 79 | 4.8 | 836 | 1 | NOT3_YEAST | P06102 saccharomyc |

| | | | | | | | | | | | | | | | |
|------|------|-----|------|---|------------|--------------------|--------|--------------|------|------|-----|-----|---|-----------|--------------------|
| 1419 | 79 | 4.8 | 836 | 2 | Q6B233 | saccharomyc | Q6b233 | saccharomyc | 1492 | 78.5 | 4.7 | 371 | 2 | O46052 | O46052 drosophila |
| 1420 | 79 | 4.8 | 864 | 2 | Q8ZTU7 | pyrobaculum | Q8ztu7 | pyrobaculum | 1493 | 78.5 | 4.7 | 387 | 1 | PAB_PEPMA | Q51911 peptostrept |
| 1421 | 79 | 4.8 | 878 | 2 | Q6W8T0 | pichia angu | Q6w8t0 | pichia angu | 1494 | 78.5 | 4.7 | 407 | 2 | Q8REG3 | Q8reg3 fusobacteri |
| 1422 | 79 | 4.8 | 893 | 2 | Q9LHT1 | arabidopsis | Q9lht1 | arabidopsis | 1495 | 78.5 | 4.7 | 420 | 2 | Q8IER5 | Q8ier5 plasmodium |
| 1423 | 79 | 4.8 | 900 | 2 | Q8C9A0 | mus musculus | Q8c9a0 | mus musculus | 1496 | 78.5 | 4.7 | 422 | 2 | Q69BM2 | Q69bm2 homo sapien |
| 1424 | 79 | 4.8 | 903 | 2 | Q8BRQ3 | mus musculus | Q8brq3 | mus musculus | 1497 | 78.5 | 4.7 | 423 | 2 | Q04429 | Q04429 saccharomyc |
| 1425 | 79 | 4.8 | 921 | 2 | Q6CB10 | yarrowia li | Q6cb10 | yarrowia li | 1498 | 78.5 | 4.7 | 430 | 2 | Q9N4F8 | Q9n4f8 caenorhabdi |
| 1426 | 79 | 4.8 | 921 | 2 | Q9P496 | mus musculus | Q9p496 | mus musculus | 1499 | 78.5 | 4.7 | 453 | 2 | Q7TOR8 | Q7tor8 xenopus lae |
| 1427 | 79 | 4.8 | 934 | 2 | Q8BRT2 | mus musculus | Q8brt2 | mus musculus | 1500 | 78.5 | 4.7 | 456 | 2 | Q84DS8 | Q84ds8 listeria mo |
| 1428 | 79 | 4.8 | 949 | 1 | GLK1_RAT | rattus norv | P22756 | rattus norv | | | | | | | |
| 1429 | 79 | 4.8 | 951 | 2 | Q9VQ36 | drosophila | Q9vq36 | drosophila | | | | | | | |
| 1430 | 79 | 4.8 | 969 | 2 | Q81UJ7 | debarryomyce | Q81uj7 | debarryomyce | | | | | | | |
| 1431 | 79 | 4.8 | 1067 | 2 | Q6BUL7 | debarryomyce | Q6bul7 | debarryomyce | | | | | | | |
| 1432 | 79 | 4.8 | 1098 | 1 | TCG1_HUMAN | homo sapien | O14776 | homo sapien | | | | | | | |
| 1433 | 79 | 4.8 | 1155 | 2 | Q874L2 | candida alb | Q874l2 | candida alb | | | | | | | |
| 1434 | 79 | 4.8 | 1238 | 2 | Q9V8B6 | drosophila | Q9v8b6 | drosophila | | | | | | | |
| 1435 | 79 | 4.8 | 1260 | 2 | Q9XDB6 | streptococ | Q9xdb6 | streptococ | | | | | | | |
| 1436 | 79 | 4.8 | 1287 | 2 | Q9F930 | streptococ | Q9f930 | streptococ | | | | | | | |
| 1437 | 79 | 4.8 | 1340 | 2 | Q8B274 | sweet potat | Q8b274 | sweet potat | | | | | | | |
| 1438 | 79 | 4.8 | 1351 | 2 | Q7YU89 | drosophila | Q7yu89 | drosophila | | | | | | | |
| 1439 | 79 | 4.8 | 1378 | 2 | Q8SQ12 | sarcophaga | Q8sq12 | sarcophaga | | | | | | | |
| 1440 | 79 | 4.8 | 1492 | 2 | Q86JC7 | dictyosteli | Q86jc7 | dictyosteli | | | | | | | |
| 1441 | 79 | 4.8 | 1689 | 2 | Q8Q2F4 | crimean-con | Q8q2f4 | crimean-con | | | | | | | |
| 1442 | 79 | 4.8 | 1689 | 2 | Q8Q2F5 | crimean-con | Q8q2f5 | crimean-con | | | | | | | |
| 1443 | 79 | 4.8 | 1689 | 2 | Q99LH9 | crimean-con | Q99lh9 | crimean-con | | | | | | | |
| 1444 | 79 | 4.8 | 1736 | 2 | Q81IM6 | plasmodium | Q81im6 | plasmodium | | | | | | | |
| 1445 | 79 | 4.8 | 1752 | 2 | Q81IK8 | plasmodium | Q81ik8 | plasmodium | | | | | | | |
| 1446 | 79 | 4.8 | 1752 | 2 | Q9AE52 | ruminococcu | Q9ae52 | ruminococcu | | | | | | | |
| 1447 | 79 | 4.8 | 1849 | 1 | IGA4_HAEIN | haemophilus | P45386 | haemophilus | | | | | | | |
| 1448 | 79 | 4.8 | 1904 | 2 | Q38319 | lactococcus | Q38319 | lactococcus | | | | | | | |
| 1449 | 79 | 4.8 | 2217 | 2 | Q6FNY7 | candida gla | Q6fny7 | candida gla | | | | | | | |
| 1450 | 79 | 4.8 | 2880 | 2 | Q65XZ9 | tomato spot | Q65xz9 | tomato spot | | | | | | | |
| 1451 | 78.5 | 4.7 | 94 | 2 | Q61030 | trypanosoma | Q61030 | trypanosoma | | | | | | | |
| 1452 | 78.5 | 4.7 | 142 | 2 | Q26943 | trypanosoma | Q26943 | trypanosoma | | | | | | | |
| 1453 | 78.5 | 4.7 | 152 | 2 | Q9GVS3 | caenorhabdi | Q9gvs3 | caenorhabdi | | | | | | | |
| 1454 | 78.5 | 4.7 | 164 | 2 | Q14851 | homo sapten | Q14851 | homo sapten | | | | | | | |
| 1455 | 78.5 | 4.7 | 216 | 2 | Q8CTD8 | staphylococ | Q8ctd8 | staphylococ | | | | | | | |
| 1456 | 78.5 | 4.7 | 231 | 2 | Q8EZW6 | leptospira | Q8ezw6 | leptospira | | | | | | | |
| 1457 | 78.5 | 4.7 | 232 | 2 | Q27423 | drosophila | Q27423 | drosophila | | | | | | | |
| 1458 | 78.5 | 4.7 | 232 | 2 | Q69EV5 | streptococ | Q69ev5 | streptococ | | | | | | | |
| 1459 | 78.5 | 4.7 | 232 | 2 | Q69EV7 | streptococ | Q69ev7 | streptococ | | | | | | | |
| 1460 | 78.5 | 4.7 | 232 | 2 | Q69EV8 | streptococ | Q69ev8 | streptococ | | | | | | | |
| 1461 | 78.5 | 4.7 | 232 | 2 | Q69EX1 | streptococ | Q69ex1 | streptococ | | | | | | | |
| 1462 | 78.5 | 4.7 | 251 | 2 | Q8K201 | mus musculus | Q8k201 | mus musculus | | | | | | | |
| 1463 | 78.5 | 4.7 | 252 | 2 | Q7PND6 | anopheles g | Q7pnd6 | anopheles g | | | | | | | |
| 1464 | 78.5 | 4.7 | 252 | 2 | Q8OG93 | avian pneum | Q8og93 | avian pneum | | | | | | | |
| 1465 | 78.5 | 4.7 | 258 | 2 | Q6TV72 | bovine papu | Q6tv72 | bovine papu | | | | | | | |
| 1466 | 78.5 | 4.7 | 262 | 2 | Q9JMF0 | mus musculus | Q9jmf0 | mus musculus | | | | | | | |
| 1467 | 78.5 | 4.7 | 270 | 2 | Q9YN72 | vaccinia vi | Q9yn72 | vaccinia vi | | | | | | | |
| 1468 | 78.5 | 4.7 | 271 | 2 | Q71DD6 | drosophila | Q71dd6 | drosophila | | | | | | | |
| 1469 | 78.5 | 4.7 | 284 | 2 | Q91U83 | human respi | Q91u83 | human respi | | | | | | | |
| 1470 | 78.5 | 4.7 | 285 | 2 | Q86H76 | dictyosteli | Q86h76 | dictyosteli | | | | | | | |
| 1471 | 78.5 | 4.7 | 293 | 2 | Q714W8 | homo sapten | Q714w8 | homo sapten | | | | | | | |
| 1472 | 78.5 | 4.7 | 294 | 2 | Q99322 | homo sapten | Q99322 | homo sapten | | | | | | | |
| 1473 | 78.5 | 4.7 | 300 | 2 | Q6CCZ0 | Q6ccz0 yarrowia li | Q6ccz0 | yarrowia li | | | | | | | |
| 1474 | 78.5 | 4.7 | 308 | 2 | Q91C17 | vaccinia vi | Q91c17 | vaccinia vi | | | | | | | |
| 1475 | 78.5 | 4.7 | 308 | 2 | Q91ZR9 | Q91zr9 cantagalo o | Q91zr9 | cantagalo o | | | | | | | |
| 1476 | 78.5 | 4.7 | 314 | 1 | HENA_VACCV | vaccinia vi | Q01218 | vaccinia vi | | | | | | | |
| 1477 | 78.5 | 4.7 | 314 | 2 | Q6L4S2 | oryza sativ | Q6l4s2 | oryza sativ | | | | | | | |
| 1478 | 78.5 | 4.7 | 314 | 2 | Q76ZM3 | vaccinia vi | Q76zm3 | vaccinia vi | | | | | | | |
| 1479 | 78.5 | 4.7 | 314 | 2 | Q8BE19 | vaccinia vi | Q8bei9 | vaccinia vi | | | | | | | |
| 1480 | 78.5 | 4.7 | 320 | 2 | Q741D6 | mycobacteri | Q741d6 | mycobacteri | | | | | | | |
| 1481 | 78.5 | 4.7 | 322 | 2 | Q67RB1 | mycobacteri | Q67rb1 | mycobacteri | | | | | | | |
| 1482 | 78.5 | 4.7 | 322 | 2 | Q62605 | rattus norv | Q62605 | rattus norv | | | | | | | |
| 1483 | 78.5 | 4.7 | 334 | 1 | MO15_HUMAN | homo sapten | Q8nj87 | homo sapten | | | | | | | |
| 1484 | 78.5 | 4.7 | 334 | 2 | Q6VAV5 | anopheles g | Q6vav5 | anopheles g | | | | | | | |
| 1485 | 78.5 | 4.7 | 334 | 2 | Q6VAV9 | anopheles g | Q6vav9 | anopheles g | | | | | | | |
| 1486 | 78.5 | 4.7 | 338 | 2 | Q43420 | homo sapten | Q43420 | homo sapten | | | | | | | |
| 1487 | 78.5 | 4.7 | 338 | 2 | Q95Y19 | caenorhabdi | Q95y19 | caenorhabdi | | | | | | | |
| 1488 | 78.5 | 4.7 | 345 | 2 | Q690X9 | anolis sagr | Q690x9 | anolis sagr | | | | | | | |
| 1489 | 78.5 | 4.7 | 345 | 2 | Q691N0 | anolis sagr | Q691n0 | anolis sagr | | | | | | | |
| 1490 | 78.5 | 4.7 | 345 | 2 | Q691T6 | anolis sagr | Q691t6 | anolis sagr | | | | | | | |
| 1491 | 78.5 | 4.7 | 361 | 2 | Q6BWL2 | debarryomyce | Q6bw12 | debarryomyce | | | | | | | |

RESULT 1

Q9UNF4

ID Q9UNF4 PRELIMINARY; PRT; 322 AA.

AC Q9UNF4;

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Hyaluronic acid receptor (XLK01).

GN Name=HAR; ORFNames=UNQ230;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Winkelmann J.C., Basu S., Ozdemir E., Blough R.I.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

EX MEDLINE=23887296; PubMed=12975309; DOI=10.1101/gr.1293003;

RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,

RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,

RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,

RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,

RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,

RA Seehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,

RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,

RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,

Godowski P.;

"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";

RL Genome Res. 13:2265-2270(2003).

DR EMBL; AF127670; AAD49220.2; -.

DR EMBL; AY358925; AAQ89284.1; -.

DR HSSP; P98066; 107B.

DR GO; GO:0005540; F:hyaluronic acid binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR000538; Link.

DR Pfam; PF00193; Xlink; 1.

DR PRINTS; PR01265; LINKMODULE.

 DR ProDom; PD000918; Link; 1. | DR PROSITE; PS50963; LINK_2; 1. | KW Receptor. | SQ SEQUENCE 322 AA; 35213 MW; 8B4D6D623F52D559 CRC64; | Query Match 100.0%; Score 1657; DB 2; Length 322; | Best Local Similarity 100.0%; Pred.No. 9.8e-126; | Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0; |

QY 1 MARCFSLVLLTSTWTTTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQLNFTAEKEA 60

DB 1 MARCFSLVLLTSTWTTTLLVQGSRLAEELSIQVSCRIMGITLVSKKANQLNFTAEKEA 60

QY 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120

DB 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120

QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
 Db |||||
 QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
 Db |||||
 QY 161 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPVENKAAAFKNEAAGFGVPTAL 240
 Db |||||
 QY 161 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPVENKAAAFKNEAAGFGVPTAL 240
 Db |||||
 QY 241 LVLALLFPGAAGLGFVCYVKRVKAFPTNKNQOKEMIEITKVVEEKANDSNPNESKKT 300
 Db |||||
 QY 241 LVLALLFPGAAGLGFVCYVKRVKAFPTNKNQOKEMIEITKVVEEKANDSNPNESKKT 300
 Db |||||
 QY 301 DKNPEESKSPSKTTVRCLEAEV 322
 Db |||||
 QY 301 DKNPEESKSPSKTTVRCLEAEV 322
 Db |||||

RESULT 2

Q8TC18 PRELIMINARY; PRT; 322 AA.
 AC Q8TC18;
 DT 01-JUN-2002 (TremBLrel. 21, Created)
 DT 01-JUN-2002 (TremBLrel. 21, Last sequence update)
 DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
 DE Extracellular link domain containing 1.
 GN Name=XLKDI;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026231; AAH26231.1;
 DR HSSP; P98066; 107B.
 DR Genew; HGNC:14687; XLKDI.
 DR GO; GO:0005540; F:hyalurononic acid binding; IEA.
 DR GO; GO:0007155; P:cell adhesion; IEA.
 DR InterPro; IPR000538; Link.
 DR Pfam; PF00193; Xlink; 1.
 DR PRINTS; PD01265; LINKMODULE.
 DR ProDom; PD000918; Link; 1.
 DR SMART; SM00445; LINK; 1.
 DR PROSITE; PSS0963; LINK_2; 1.
 SQ SEQUENCE 322 AA; 35183 MW; 0B1EDBD76CE4610A CRC64;

Query Match 99.2%; Score 1643; DB 2; Length 322;

Best Local Similarity 99.7%; Pred. No. 1.3e-124;
 Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MARCFSLVLLTSTIWTTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60
 Db |||||
 QY 1 MARCFSLVLLTSTIWTTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60
 Db |||||
 QY 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVWISRIQSPNPKCGKNGVGLIWKVPV 120
 Db |||||
 QY 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVWISRIQSPNPKCGKNGVGLIWKVPV 120
 Db |||||
 QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
 Db |||||
 QY 121 SRQFAAYCYNSSDTWTNSCIPEIITTKOPIFNTQTATQTEFIVSDSYSPYSTIPA 180
 Db |||||
 QY 181 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPVENKAAAFKNEAAGFGVPTAL 240
 Db |||||
 QY 181 PTTTTPAPASTSIIPRKKLICVTEVFMETSTMTSTETEPVENKAAAFKNEAAGFGVPTAL 240
 Db |||||
 QY 241 LVLALLFPGAAGLGFVCYVKRVKAFPTNKNQOKEMIEITKVVEEKANDSNPNESKKT 300
 Db |||||
 QY 241 LVLALLFPGAAGLGFVCYVKRVKAFPTNKNQOKEMIEITKVVEEKANDSNPNESKKT 300
 Db |||||
 QY 301 DKNPEESKSPSKTTVRCLEAEV 322
 Db |||||
 QY 301 DKNPEESKSPSKTTVRCLEAEV 322
 Db |||||

RESULT 3

Q9Y5Y7 PRELIMINARY; PRT; 322 AA.
 AC Q9Y5Y7;
 DT 01-NOV-1999 (TremBLrel. 12, Created)
 DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
 DE 01-MAR-2004 (TremBLrel. 26, Last annotation update)
 DE Lymphatic endothelium-specific hyaluronan receptor LYVE-1.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99156989; PubMed=10037799; DOI=10.1083/jcb.144.4.789;
 RA Banerji S., Ni J., Wang S.X., Clasper S., Su J., Tammi R., Jones M.,
 RA Jackson D.G.;
 RA "LYVE-1, a new homologue of the CD44 glycoprotein, is a lymph-specific
 RT receptor for hyaluronan."
 RL J. Cell Biol. 144:789-801 (1999).
 DR EMBL; AF118108; AAD42764.1; -.
 DR HSSP; P98066; 107B.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005624; C:membrane fraction; TAS.
 DR GO; GO:0004872; F:receptor activity; TAS.
 DR GO; GO:0006928; P:cell motility; TAS.
 DR GO; GO:0007160; P:cell-matrix adhesion; TAS.
 DR GO; GO:0009653; P:morphogenesis; TAS.
 DR GO; GO:0009611; P:response to wounding; TAS.
 DR InterPro; IPR000538; Link.
 DR Pfam; PF00193; Xlink; 1.
 DR PRINTS; PR01265; LINKMODULE.
 DR ProDom; PD000918; Link; 1.
 DR SMART; SM00445; LINK; 1.
 DR PROSITE; PSS0963; LINK_2; 1.
 KW Receptor.
 SQ SEQUENCE 322 AA; 35238 MW; 0EBEA56729CEFF7 CRC64;

Query Match 98.9%; Score 1638; DB 2; Length 322;
 Best Local Similarity 99.1%; Pred. No. 3.4e-124;
 Matches 319; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARCFSLVLLTSTIWTTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60
 Db |||||
 QY 1 MARCFSLVLLTSTIWTTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTAEKAA 60
 Db |||||

QY 61 CRLGLSLAGKQOVETALKASSETCSYGWGDFVVISRISPNPKGKNGVGLIWKVPV 120
DB 61 CRLGLSLAGKQOVETALKASSETCSYGWGDFVVISRISPNPKGKNGVGLIWKVPV 120
QY 121 SRQFAAYCYNSSDWTNSCIPIIITTKDPIFNQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDWTNSCIPIIITTKDPIFNQTATOTTEFIVSDSTYSVASPYSTIPA 180
QY 181 PTTTPPAPASTSIPIRKKLICVTEVFEMETSTMSTETEPVENKAAPKNEAAGFGVPTAL 240
DB 181 PTTTPPAPASTSIPIRKKLICVTEVFEMETSTMSTETEPVENKAAPKNEAAGFGVPTAL 240
QY 241 LVALLFFGAAGLFCYVKRYVKAFFPTNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
DB 241 LVALLFFGAAGLFCYVKRYVKAFFPTNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
QY 301 DKNPESKSPSKTTVRCLEAEV 322
DB 301 DKNPESKSPSKTTVRCLEAEV 322
RESULT 4
Q6UC88
ID Q6UC88 PRELIMINARY; PRT; 322 AA.
AC Q6UC88;
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DE Cell surface retention sequence binding protein-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22940027; PubMed=12912978; DOI=10.1074/jbc.M306411200;
RA Huang S.S., Tang F.M., Huang Y.H., Liu I.H., Hsu S.C., Chen S.T.,
RA Huang J.S.;
RT "Cloning, expression, characterization and role in autocrine cell
RT growth of cell surface retention sequence binding protein-1.";
RL J. Biol. Chem. 278:43855-43869 (2003).
DR EMBL; AY372937; AAQ85130.1; -
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR000538; Link.
DR PRINTS; PR01265; LINKMODULE.
DR PRODOM; PD000918; Link; 1.
DR SMART; SM00445; Link; 1.
DR PROSITE; PS01241; LINK_1; UNKNOWN_1.
DR PROSITE; PS0963; LINK_2; 1.
SQ SEQUENCE 322 AA; 35561 MW; 4901DALBF92648AE CRC64;
Query Match 70.9%; Score 1174; DB 2; Length 322;
Best Local Similarity 71.1%; Pred. No. 1.1e-86;
Matches 229; Conservative 34; Mismatches 59; Indels 0; Gaps 0;
QY 1 MARCESLVLLTISWTRLLVGGSRABEELSQVSCRIMGITLVSKKANQINFTEAKEA 60
DB 1 MAKFSGLGLLASIWTRLLVGGSRSEISILGPCRIMGVTLVTKTQPLNFTAEQEA 60
QY 61 CRLGLSLAGKQOVETALKASSETCSYGWGDFVVISRISPNPKGKNGVGLIWKVPV 120
DB 61 CRLVGLTLASQOVVEARKEFGTCSYGNVKNQVFIPIISNPKGSGVGVWIRSSL 120
QY 121 SRQFAAYCYNSSDWTNSCIPIIITTKDPIFNQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 121 SSRHRSYCHNSSDIWNSCLPIIITDPLFNFTETATVTKLWVSDSTHSELSTGPDV 180
QY 181 PTTTPPAPASTSIPIRKKLICVTEVFEMETSTMSTETEPVENKAAPKNEAAGFGVPTAL 240
DB 181 TTTVAPPLASTSTPRKKLICITEAFMDTSAVATERESDIQNRPAFKNEAVFGVGPVPTAL 240

QY 241 LVALLFFGAAGLFCYVKRYVKAFFPTNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
DB 241 LVALLFFGAAGLFCYVKRYVKAFFPTNKNQKQKEMIETKVVKBEKANDSNPNESKKT 300
QY 301 DKNPESKSPSKTTVRCLEAEV 322
DB 301 NKTPEPKSPKTTVRCLEAEV 322
RESULT 5
Q8BHC0
ID Q8BHC0 PRELIMINARY; PRT; 318 AA.
AC Q8BHC0;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TremBLrel. 28, Last annotation update)
DE Extra cellular link domain-containing 1 (Mus musculus adult male lung
DE cDNA, RIKEN full-length enriched library, clone:1200012G08
DE product:extra cellular link domain-containing 1, full insert
DE sequence).
GN Name=Xlkdl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CZSCH II; TISSUE=Lung, and Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Moore T., Max S.J., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=CZSCH II; TISSUE=Lung, and Mammary gland;
RX Strausberg R.;
RN Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44 (1999).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690 (2001).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Lung;
RA The FANTOM Consortium,

QY 94 FVVISRPNPKCGKNGVGLWIKVPSRQFAAYCYNSSDTWTNSCIPBI----- 143
Db 92 -VLIPRIKPNCAANYTGILGNNEISLRVDYVCYNASETEKSLPVLNNEYDFSHN 150
QY 144 -TTTKDPIFNTQTATOTTEFIVSDSYVASVSTIPATPTTTPAP 188
Db 151 TIDSYPDTLDTIQNSDKSGYQGSV-----TDPAPAMITPDP 188
RESULT 9
CD44_CRIGR STANDARD; PRT; 362 AA.
AC P20944;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-I) (HUTCH-I)
DE (Extracellular matrix receptor-III) (ECMR-III) (GP90 lymphocyte
DE homing/adhesion receptor) (Hermes antigen) (Hyaluronate receptor).
GN Name=CD44;
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90304889; PubMed=1694723; DOI=10.1016/0092-8674(90)90694-A;
RA Aruffo A., Stamenkovic I., Melnick M., Underhill C.B., Seed B.;
RT "CD44 is the principal cell surface receptor for hyaluronate.";
RL Cell 61:1303-1313(1990).
CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to
CC mucosal high endothelial venule and to types I and VI collagen.
CC Probably involved in matrix adhesion, lymphocyte activation and
CC lymph node homing.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- INDUCTION: By EBV.
CC -!- PTM: Extensively modified including N- and O-linked glycosylation,
CC addition of the glycosaminoglycan chondroitin sulfate, of sulfate,
CC of phosphate to cytoplasmic domain serine residues.
CC -!- SIMILARITY: Contains 1 Link domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M33827; AAA36967.1; -.
CC FIR; A35616; A35616.
CC HSSP; P98066; ITSG.
CC InterPro; IPR001231; CD44 antigen.
CC InterPro; IPR000538; Link.
CC Pfam; PF00193; Xlink; 1.
CC PRINTS; PR00658; CD44.
CC PRINTS; PR01265; LINKMODULE.
CC ProDom; PD000918; Link; 1.
CC PROSITE; PS01241; Link; 1.
CC PROSITE; PS00963; LINK 2; 1.
KW Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;
KW Proteoglycan; Pyrrolidone carboxylic acid; Receptor; Signal;
KW Transmembrane.
FT SIGNAL 1 22 By similarity.
FT CHAIN 23 362 CD44 antigen.
FT DOMAIN 23 269 Extracellular (Potential).
FT TRANSMEM 270 290 Potential.
FT DOMAIN 291 322 Cytoplasmic (Potential).
FT DOMAIN 34 122 Link.
FT DOMAIN 152 160 Arg/Lys-rich (basic).
FT DOMAIN 226 269 Stem.

FT MOD_RES 23 23 Pyrrolidone carboxylic acid (By
FT similarity).
FT DISULFID 55 120 By similarity.
FT DISULFID 79 99 By similarity.
FT MOD_RES 292 292 Phosphoserine (by PKC) (By similarity).
FT MOD_RES 326 326 Phosphoserine (By similarity).
FT CARBOHYD 27 27 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 59 59 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 102 102 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 112 112 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 122 122 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 174 174 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 256 256 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 362 AA; 39775 MW; E89EB434E9EC948 CRC64;
Query Match 14.1%; Score 233.5; DB 1; Length 362;
Best Local Similarity 26.3%; Pred. No. 1.6e-10;
Matches 91; Conservative 45; Mismatches 147; Indels 63; Gaps 12;
QY 24 SIRAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEACRLGLSLAGKQDVETALKASPE 83
Db 18 SLAHEQIDNITCRVAGVHVEKNGRYSIRTEAADLCOAFNSTLPTWQDMVMALSKGFE 77
QY 84 TCSYGVGDGFVVISRISPNPKCGKNGVGLWIKVPSRQFAAYCYNSSDTWTNSCIPBI 143
Db 78 TCRYGFI-EGHVIPRIQPNALCAANHTGVILTSNTS-HVDTYCFNASAPLEEDC--- 131
QY 144 ITTKDPIFNTQTATOTTEFIVSDST-YVASVYST-----IPATPTTPAPAS----- 190
Db 132 -TSVTDLNSPEGPVTITIVNRDGRYKKGERTHQEDIDASNTTDDVDSSGSSEKST 190
QY 191 -----TSIPRRKKLICVTEFVEMETSTMSTE-----TSPFVEN 222
Db 191 SGYVHYTHLTIHSTADQDPYFGSTWATRDQDSSMDPRGNSLITVDGSKLTHSSGN 250
QY 223 KAAFKNEAAGFGG---VPTALLVLALLFFGAAGLFCYKRVYKAFPTTKNQKQEMIE 279
Db 251 QDSGLNSTSRPGKPRVFWLVLASL-LALAILAVC-----IAVNRRRRCQKKLVI 304
QY 280 TKVVKVEKANDSNPNNEESKTKDNPE-----ESKSPSKTIVTRCLEAE 321
Db 305 NS--GNGKVEDRKPSLNGEASKQEMVHLVNKEPSETPDQPMFTAD 348
RESULT 10
Q6P8A2 PRELIMINARY; PRT; 437 AA.
AC Q6P8A2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75816.
GN Name=MGC75816;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RP [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RT "CD44 variant exon v5 encodes a tyrosine that is sulphated.";

RL Eur. J. Biochem. 255:74-80(1998).

CC -!- FUNCTION: Main cell surface receptor for hyaluronate. Adhesion to

CC mucosal high endothelial venule and to types I and VI collagen.

CC Probably involved in matrix adhesion, lymphocyte activation and

CC lymph node homing.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=2; Synonyms=Long, Meta-1;

CC IsoId=P26051-1; Sequence=Displayed;

CC Name=1; Synonyms=Short;

CC IsoId=P26051-2; Sequence=VSP_005330;

CC -!- PTM: N-glycosylated (By similarity).

CC -!- PTM: O-glycosylated; contains chondroitin sulfate glycans which

CC can be more or less sulfated (By similarity).

CC -!- PTM: Phosphorylated; activation of PKC results in the

CC dephosphorylation of Ser-467 (constitutive phosphorylation site),

CC and the phosphorylation of Ser-433 (By similarity).

CC -!- SIMILARITY: Contains 1 Link domain.

CC -----

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CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; M61875; AAA53532.1; -;

DR EMBL; M61874; AAA53534.1; -;

DR EMBL; U52179; AAA97915.1; -;

DR EMBL; U46957; AAA92920.1; -;

DR PIR; B38745; B38745.

DR HSP; P98066; LTSG.

DR InterPro; IPR001231; CD44 antigen.

DR InterPro; IPR000538; Link.

DR Pfam; PF00193; XLink; 1.

DR PRINTS; PR00658; CD44.

DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 1.

DR PROSITE; PS01241; LINK_1; 1.

DR PROSITE; PS0963; LINK_2; 1.

DR Alternative splicing; Cell adhesion; Glycoprotein; Phosphorylation;

KW Proteoglycan; Pyrrolidone carboxylic acid; receptor; signal;

KW Sulfation; Transmembrane.

FT SIGNAL 1 21

FT CHAIN 22 503

FT DOMAIN 22 410

FT TRANSMEM 411 431

FT DOMAIN 432 503

FT DOMAIN 35 124

FT DOMAIN 154 162

FT DOMAIN 228 410

FT MOD_RES 22 22

FT DISULFID 56 122

FT DISULFID 80 100

FT MOD_RES 288 288

FT MOD_RES 433 433

FT MOD_RES 467 467

FT CARBOHYD 28 28

FT CARBOHYD 60 60

FT CARBOHYD 103 103

FT CARBOHYD 114 114

FT CARBOHYD 124 124

FT CARBOHYD 266 266

FT CARBOHYD 274 274

FT CARBOHYD 306 306

FT VARSPIC 224 385

FT --> SDGSSMDPRGGFDVTVTHGSELA (in isoform

FT 1).

FT /FTId=VSP_005330.

FT R -> S (in Ref. 2).

FT CONFLICT 74 74

FT SEQUENCE 503 AA; 55945 MW; FB489D009BD4EE22 CRC64;

Query Match 13.4%; Score 222; DB 1; Length 503;

Best Local Similarity 25.7%; Pred. No. 2e-09;

Matches 84; Conservative 40; Mismatches 165; Indels 38; Gaps 11;

QY 15 WTRLLVQSLPAEELSQVSCRMIGITLVSKANQQLNFTKEACRLLGLSLACKDQV 74

DB 10 WGLLCLQLSLAQOQIDLNITCYAGVFHVEKNGRYSISRTBAADLCEAFNTTLPMTQM 69

QY 75 ETALKASFETCSYGMVGDGVVISRISPNPKCKGKGVGLIWKVPVSRQFAAYCYNSSDT 134

DB 70 ELALRKGFTCYGFI-EGHVVIPIHHPNAICAAANTGVYILLASNTSHDYDYCFNASAP 128

QY 135 WTNSCIPEIITTKDPIFNTQTATQTFEIVSDST-YSVASPYST----IPAPT----- 182

DB 129 LEEDC-----TSVTDLPSFDGPVITITVNRDGTTRYKKGEYRTHQEDIDASNIDEDVS 183

QY 183 -----TTPPA-PASTSIPRKKLICVTEVPMETSTMST-BTEPFVENKAAPKNEAGF 233

DB 184 SGSTIEKSTPEGYILHDLPTSQPTGDRDDAFIGSTLATIATTPWVSAHTKQNBQRTQM 243

QY 234 GGV---PTALLVLALLFFGAAAGLGFVYKRVK--APPFTNKKQKEMIEKVVKEEKA 288

DB 244 NPIHNPVLLQTTTRMTDIDRNSTSANGENWTQEPQPFNNHYYQDER-ETPHATSTTW 302

QY 289 NDSNPNEESKTKDK-----NPNEESKSP 310

DB 303 ADPNSTTBEAATQKEKWFENWQGNP 329

RESULT 14

OD8779

ID O08779 PRELIMINARY; PRT; 780 AA.

AC O08779;

DT 01-JUL-1997 (TREMELrel. 04, Created)

DT 01-JUL-1997 (TREMELrel. 04, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE CD44 protein.

GN Name=CD44;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BDX; TISSUE=Pancreas;

RA Hofmann M.;

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U96138; AAB54002.1; -;

DR HSSP; P98066; 1078.

DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005540; F:hyaluronic acid binding; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

DR InterPro; IPR001231; CD44 antigen.

DR InterPro; IPR000538; Link.

DR Pfam; PF00193; XLink; 1.

DR PRINTS; PR00658; CD44.

DR PRINTS; PR01265; LINKMODULE.

DR ProDom; PD000918; Link; 1.

DR SMART; SM00445; Link; 1.

DR PROSITE; PS01241; LINK_1; 1.

DR PROSITE; PS0963; LINK_2; 1.

SQ SEQUENCE 780 AA; 85917 MW; CC4D35AB1EA7377C CRC64;

Query Match 13.2%; Score 219.5; DB 2; Length 780;

Best Local Similarity 24.9%; Pred. No. 5.4e-09;

Matches 86; Conservative 45; Mismatches 144; Indels 71; Gaps 13;

IAITPWSAHTKQNBQRTQNTQNTPIHNPVLLQTTTRMTDID

RNSTSANGENWTQEPQPFNNHYYQDEETPHATSTTWADP

NTTEEAATQKEKWFENWQGNPPTPSDSHVTEGTASA

HNNHPSQRMSTQSDVSWTDFDPFISHPMQGGHQTESK

QY 15 WTRLLVQSLRAEELSIQVSCRMGITLVSKKANQOLNFTAEKACRLLGLSLAGKQOV 74
Db 10 WGLLCLQLSLAQOQIDNITCRYAGVFHVEKNGRYSISRTEAADLCEAFNTTLPTMAQM 69
QY 75 ETALKAFTCTSYGVWGDGFVVISRISPNPKCGKGVGLIWKVPVSRQFAAYCYNSSDT 134
Db 70 ELALRKGFCTCRYGFI-EGHVIPRIHPNAICAANNNTGVILLASNTSHDYTCFNASAP 128
QY 135 WNSCIPELIITTKDPINFNTQTATQTFEIVSDST-YSVASPYST-----IPAPT----- 182
Db 129 LEEDC-----TSVTDLPNSFDGPEVITITVNRDGTYSKKGEYRTHQEDIDASNIIDEDVS 183
QY 183 -----TTPPA-PASTSIPRKKKLCVTEVFMETSTMSTETEPFVENKAAAFKNEAAG-- 232
Db 184 SGSTIEKSTPEGVILHTDLPSTQPTGDRDDAFPIGSTLAT-----IASTVYSKSHATAOK 238
QY 233 -----FGG-----VPTALLVLALLFGAA-----AGLGFCYVKRYVKAPPT 269
Db 239 QNNWISWFGNSQSITQTQDSPTTTATTALMTTPETPPKQEAQNWFSW-----PF 289
QY 270 NKNOQKEMETKVVKEEKANDSN-----PNEESK-KTDKNPEESKS 309
Db 290 QPSEKSHLHTTKMPGTESENTNPTGKWPNEENEDETDKYPNFGS 335

RESULT 15

Q98SR5 PRELIMINARY; PRT; 265 AA.
AC Q98SR5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE T cell antigen CD44 isoform b.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Pekin;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332869; AAK18277.1; -
DR HSSP; P98066; 107B.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005540; F:hyaluronic acid binding; IEA.
DR GO; GO:0007155; P:cell adhesion; IEA.
DR InterPro; IPR001231; CD44_antigen.
DR InterPro; IPR000538; Link.
DR Pfam; PF00193; Xlink; 1.
DR PRINTS; PR00658; CD44.
DR PRINTS; PR01265; LINKMODULE.
DR ProDom; PD000918; Link; 1.
DR SMART; SM00445; LINK; 1.
DR PROSITE; PS01241; LINK 1; UNKNOWN_1.
DR PROSITE; PS0963; LINK 2; 1.
SQ SEQUENCE 265 AA; 29215 MW; 77C176E0A998D081 CRC64;

Query Match 13.2%; Score 219; DB 2; Length 265;
Best Local Similarity 28.3%; Pred. No. 1.6e-09;
Matches 66; Conservative 32; Mismatches 103; Indels 32; Gaps 5;

QY 14 IWTRLLVQSLRAEELSIQVSCRMGITLVSKKANQOLNFTAEKACRLLGLSLAGKQOV 73
Db 6 VVATFGLCLLKLCTETQPNVSCRVGPHVEKNGRYSLTRTEAADLCLALNSTLSTLEQ 65
QY 74 VETALKAFTCTSYGVWGDGFVVISRISPNPKCGKGVGLIWKVPVSRQFAAYCYNSSD 133
Db 66 LEKAHELGFCTCRYGFV-VGYIVIPRINYPHLCAANHGTGIYKLSANTTGRYDAYCYNATE 124
QY 134 TWNSCIP-----EITTKDP-----IPNTQTATQTFEIVSDSTYSVASPY 175
Db 125 TRDKACEPIERTDTSFLSNQGEIVDNEGSRYNADGTRHSGDSTSGVDENVGSGSSH 184

QY 176 STIPAPTTTPPAPAS-----TSIPR-----RKKLICVTEVFMETSTMSTE 215
Db 185 DTTTPVDTSIRKSSPSYSGSVTPVPHLSHDHSGGGGKEKFPVINSDDDEISFTSTD 237

Search completed: October 5, 2005, 17:31:31
Job time : 183.744 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 17:16:37 ; Search time 30.4111 Seconds
(without alignments)
1018.766 Million cell updates/sec

Title: US-10-063-510-6

Perfect score: 1657

Sequence: 1 MARCPSLVLLTSTWTRILL.....NPESKSPSTTVRCLEAEV 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 229.5 | 13.9 | 363 | 2 | A37009 |
| 2 | 222.5 | 13.4 | 362 | 2 | A30901 |
| 3 | 222.5 | 13.4 | 365 | 2 | A34424 |
| 4 | 222.5 | 13.4 | 365 | 2 | B38745 |
| 5 | 217.5 | 13.1 | 362 | 2 | A35616 |
| 6 | 208.5 | 12.6 | 366 | 2 | A53286 |
| 7 | 205 | 12.4 | 361 | 2 | JH0417 |
| 8 | 202.5 | 12.2 | 351 | 2 | S45305 |
| 9 | 202 | 12.2 | 742 | 2 | A47195 |
| 10 | 199.5 | 12.0 | 426 | 2 | JH0518 |
| 11 | 199.5 | 12.0 | 493 | 2 | S13530 |
| 12 | 198 | 11.9 | 395 | 2 | I77371 |
| 13 | 196.5 | 11.9 | 699 | 2 | I37369 |
| 14 | 186 | 11.2 | 359 | 2 | S24240 |
| 15 | 148.5 | 9.0 | 2109 | 1 | I50421 |
| 16 | 145.5 | 8.8 | 3562 | 2 | A47171 |
| 17 | 145 | 8.8 | 277 | 2 | A41735 |
| 18 | 145 | 8.8 | 1069 | 2 | J42681 |
| 19 | 144 | 8.7 | 275 | 2 | JC6506 |
| 20 | 143 | 8.6 | 2327 | 2 | T42630 |
| 21 | 137 | 8.3 | 276 | 2 | A47290 |
| 22 | 131.5 | 7.9 | 2124 | 2 | A28452 |
| 23 | 131 | 7.9 | 2132 | 1 | A55182 |
| 24 | 130.5 | 7.9 | 883 | 2 | S57653 |
| 25 | 130.5 | 7.9 | 883 | 2 | S49126 |
| 26 | 130.5 | 7.9 | 2415 | 2 | A39086 |
| 27 | 128.5 | 7.8 | 912 | 2 | A54423 |
| 28 | 121 | 7.3 | 1340 | 2 | A39808 |
| 29 | 117 | 7.1 | 340 | 2 | JC7505 |
| 30 | 116 | 7.0 | 2397 | 1 | A55535 |
| 31 | 115 | 6.9 | 370 | 2 | S29139 |
| 32 | 115 | 6.9 | 1643 | 2 | T14274 |
| 33 | 115 | 6.9 | 3381 | 2 | T42389 |
| 34 | 114.5 | 6.9 | 1257 | 2 | S28764 |
| 35 | 112 | 6.8 | 390 | 1 | Q8BE77 |
| 36 | 111.5 | 6.7 | 402 | 2 | S73773 |
| 37 | 111.5 | 6.7 | 909 | 1 | QRXL2 |
| 38 | 111 | 6.7 | 2409 | 1 | A60979 |
| 39 | 108 | 6.5 | 354 | 1 | LKHU |
| 40 | 108 | 6.5 | 645 | 2 | T29818 |
| 41 | 107.5 | 6.5 | 739 | 2 | T21769 |
| 42 | 107 | 6.5 | 355 | 1 | LKCH |
| 43 | 107 | 6.5 | 371 | 2 | A53908 |
| 44 | 107 | 6.5 | 408 | 1 | LKRT2 |
| 45 | 107 | 6.5 | 1268 | 2 | S52781 |
| 46 | 105.5 | 6.4 | 113 | 2 | A55885 |
| 47 | 104.5 | 6.3 | 862 | 2 | S43922 |
| 48 | 104 | 6.3 | 354 | 1 | S04243 |
| 49 | 104 | 6.3 | 354 | 1 | S42938 |
| 50 | 103.5 | 6.2 | 1229 | 2 | T25697 |
| 51 | 101.5 | 6.1 | 380 | 2 | T28081 |
| 52 | 101.5 | 6.1 | 768 | 2 | T00073 |
| 53 | 101 | 6.1 | 708 | 2 | T19474 |
| 54 | 100 | 6.0 | 378 | 2 | I46268 |
| 55 | 100 | 6.0 | 1251 | 2 | T21389 |
| 56 | 99.5 | 6.0 | 1092 | 1 | JN0635 |
| 57 | 99 | 6.0 | 896 | 2 | T22061 |
| 58 | 99 | 6.0 | 5376 | 2 | T42215 |
| 59 | 98.5 | 5.9 | 796 | 2 | T21460 |
| 60 | 98 | 5.9 | 771 | 2 | T34376 |
| 61 | 97.5 | 5.9 | 909 | 1 | QRXL1 |
| 62 | 96.5 | 5.8 | 465 | 2 | S46759 |
| 63 | 96.5 | 5.8 | 660 | 2 | JH0067 |
| 64 | 96 | 5.8 | 449 | 2 | T33257 |
| 65 | 96 | 5.8 | 1088 | 1 | IUXLNL |
| 66 | 95.5 | 5.8 | 376 | 2 | S52137 |
| 67 | 95.5 | 5.8 | 1471 | 2 | B48218 |
| 68 | 94.5 | 5.7 | 1272 | 2 | S26180 |
| 69 | 94.5 | 5.7 | 1390 | 2 | T18883 |
| 70 | 94 | 5.7 | 1241 | 2 | S01827 |
| 71 | 93 | 5.6 | 930 | 2 | B72537 |
| 72 | 92.5 | 5.6 | 477 | 2 | S53362 |
| 73 | 92.5 | 5.6 | 569 | 2 | A11347 |
| 74 | 92.5 | 5.6 | 851 | 2 | T22696 |
| 75 | 92.5 | 5.6 | 927 | 2 | T24031 |
| 76 | 92.5 | 5.6 | 1367 | 2 | S74285 |
| 77 | 92 | 5.6 | 429 | 1 | JC5861 |
| 78 | 92 | 5.6 | 846 | 2 | T21700 |
| 79 | 92 | 5.6 | 966 | 2 | S25365 |
| 80 | 91.5 | 5.5 | 411 | 2 | A33664 |
| 81 | 91.5 | 5.5 | 639 | 2 | S20887 |
| 82 | 91.5 | 5.5 | 639 | 2 | A81100 |
| 83 | 91.5 | 5.5 | 672 | 2 | T32557 |
| 84 | 91.5 | 5.5 | 681 | 2 | S33316 |
| 85 | 91 | 5.5 | 246 | 2 | T33965 |
| 86 | 91 | 5.5 | 747 | 2 | T34329 |
| 87 | 91 | 5.5 | 2172 | 2 | T20145 |
| 88 | 90.5 | 5.5 | 575 | 2 | S29315 |
| 89 | 90.5 | 5.5 | 662 | 2 | A45155 |
| 90 | 90 | 5.4 | 388 | 2 | S36500 |
| 91 | 90 | 5.4 | 1007 | 2 | T24643 |
| 92 | 90 | 5.4 | 1367 | 1 | S48478 |
| 93 | 89.5 | 5.4 | 518 | 2 | T49778 |
| 94 | 89.5 | 5.4 | 1369 | 2 | S70713 |
| 95 | 89 | 5.4 | 307 | 1 | G8FF3 |
| 96 | 89 | 5.4 | 416 | 1 | A31959 |
| 97 | 89 | 5.4 | 517 | 2 | T20658 |
| 98 | 89 | 5.4 | 5170 | 2 | T15348 |
| 99 | 88.5 | 5.3 | 193 | 2 | A71415 |
| 100 | 88.5 | 5.3 | 721 | 2 | B90487 |
| 101 | 88.5 | 5.3 | 770 | 2 | T22808 |
| 102 | 88.5 | 5.3 | 1101 | 2 | S15271 |

versican precursor
aggreccan - pig (fr
versican precursor
versican precursor
versican precursor
glycoprotein 1 pre
diolipolipamide a
LDL receptor 2 pre
versican precursor
proteoglycan link
hypothetical prote
hypothetical prote
proteoglycan link
brevican precursor
proteoglycan link
neurocan - mouse
chondroitin sulfat
versican - pig-tal
proteoglycan link
proteoglycan link
hypothetical prote
hypothetical prote
hypothetical prote
brevican precursor
hypothetical prote
neural cell adhesi
hypothetical prote
zonadhesin - mouse
hypothetical prote
hypothetical prote
LDL receptor 1 pre
hypothetical prote
chitinase (EC 3.2.
hypothetical prote
neural cell adhesi
MID2 protein - yea
neurexin III-alpha
neurofascin - chic
hypothetical prote
period clock prote
hypothetical prote
mucin 5AC (clone J
hypothetical prote
hypothetical prote
BUD3 protein - yea
endo-1,4-beta-xyla
hypothetical prote
CYC8 protein - yea
96K lysosomal memb
acta protein precu
actin-assembly ind
hypothetical prote
structural protein
hypothetical prote
hypothetical prote
hypothetical prote
chaperonin 60 - cu
mucin PIM-C.1 - Af
E2 protein - human
glucan 1,4-alpha-g
hypothetical prote
protein-tyrosine k
salivary glue prot
lysosome-associate
probable zinc meta
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
endoglucanase C (E

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|--------------------|-----|------|-----|------|---|--------|--------------------|
| 103 | 88 | 5.3 | 456 | 2 | T31483 | hypothetical prote | 176 | 83 | 5.0 | 738 | 2 | T44194 | hypothetical prote |
| 104 | 88 | 5.3 | 564 | 2 | T25945 | hypothetical prote | 177 | 83 | 5.0 | 797 | 1 | VGBEX1 | glycoprotein X pre |
| 105 | 88 | 5.3 | 602 | 2 | AD2067 | hypothetical prote | 178 | 83 | 5.0 | 866 | 2 | T45462 | membrane glycoprot |
| 106 | 88 | 5.3 | 761 | 2 | T00940 | hypothetical prote | 179 | 83 | 5.0 | 867 | 2 | T45463 | membrane glycoprot |
| 107 | 88 | 5.3 | 1631 | 1 | SAZQK1 | major merozoit su | 180 | 83 | 5.0 | 970 | 2 | T16232 | hypothetical prote |
| 108 | 88 | 5.3 | 3507 | 2 | T34513 | hypothetical prote | 181 | 82.5 | 5.0 | 290 | 2 | S66355 | lectin-related sto |
| 109 | 88 | 5.3 | 3570 | 2 | T45025 | mucin MUC9B, trach | 182 | 82.5 | 5.0 | 383 | 1 | S15624 | E2 protein - human |
| 110 | 87.5 | 5.3 | 825 | 2 | T48431 | hypothetical prote | 183 | 82.5 | 5.0 | 416 | 2 | B84030 | stage VI sporulati |
| 111 | 87.5 | 5.3 | 1085 | 2 | S40476 | Ca(2+)-sensing rec | 184 | 82.5 | 5.0 | 456 | 1 | H64099 | probable amino aci |
| 112 | 87.5 | 5.3 | 1891 | 1 | IUCGNL | neural cell adhesi | 185 | 82.5 | 5.0 | 569 | 2 | B84470 | Mutator-like trans |
| 113 | 87.5 | 5.3 | 1802 | 2 | S69703 | HKRI protein precu | 186 | 82.5 | 5.0 | 726 | 2 | S67044 | NF1 protein - yea |
| 114 | 87.5 | 5.3 | 2817 | 2 | B97033 | uncharacterized pr | 187 | 82.5 | 5.0 | 825 | 2 | S62042 | probable membrane |
| 115 | 87 | 5.3 | 235 | 2 | PC2022 | mucin like protein | 188 | 82.5 | 5.0 | 871 | 2 | T43427 | pob1 protein - fis |
| 116 | 87 | 5.3 | 752 | 2 | H72616 | hypothetical prote | 189 | 82.5 | 5.0 | 993 | 2 | F97717 | hypothetical prote |
| 117 | 87 | 5.3 | 1016 | 2 | H71460 | probable outer mem | 190 | 82.5 | 5.0 | 1206 | 2 | S24407 | formin isoform IV |
| 118 | 87 | 5.3 | 1506 | 2 | T30886 | integumentary muc | 191 | 82.5 | 5.0 | 1407 | 2 | T18381 | latrophilin-2 (spl |
| 119 | 87 | 5.3 | 1537 | 2 | S53465 | flocculation prote | 192 | 82.5 | 5.0 | 1420 | 2 | T18385 | latrophilin-2 (spl |
| 120 | 86.5 | 5.2 | 400 | 1 | A28172 | spasmolysin precu | 193 | 82.5 | 5.0 | 1422 | 2 | T18383 | latrophilin-2, spl |
| 121 | 86.5 | 5.2 | 461 | 2 | T22946 | hypothetical prote | 194 | 82.5 | 5.0 | 1435 | 2 | T18387 | latrophilin-2 (spl |
| 122 | 86.5 | 5.2 | 503 | 2 | S63257 | probable membrane | 195 | 82.5 | 5.0 | 1450 | 2 | T18382 | latrophilin-2 (spl |
| 123 | 86.5 | 5.2 | 550 | 2 | T29919 | hypothetical prote | 196 | 82.5 | 5.0 | 1460 | 2 | D81675 | polymorphic membra |
| 124 | 86.5 | 5.2 | 740 | 1 | FOJLHD | gag polypeptide - | 197 | 82.5 | 5.0 | 1463 | 2 | T18386 | latrophilin-2 (spl |
| 125 | 86.5 | 5.2 | 1777 | 2 | T34369 | hypothetical prote | 198 | 82.5 | 5.0 | 1465 | 2 | T18384 | latrophilin-2 (spl |
| 126 | 86.5 | 5.2 | 2616 | 2 | A57096 | nudel protein proc | 199 | 82.5 | 5.0 | 1468 | 2 | S11515 | formin - mouse |
| 127 | 86 | 5.2 | 333 | 2 | T27883 | hypothetical prote | 200 | 82.5 | 5.0 | 1478 | 2 | T18388 | latrophilin-2 (spl |
| 128 | 86 | 5.2 | 1785 | 2 | A45546 | major merozoit su | 201 | 82.5 | 5.0 | 2311 | 1 | TVCHSR | kinase-related pro |
| 129 | 85.5 | 5.2 | 575 | 2 | S23216 | chaperonin 60 - cu | 202 | 82 | 4.9 | 260 | 1 | G89223 | molybdate-binding |
| 130 | 85.5 | 5.2 | 649 | 2 | T04606 | protein kinase hom | 203 | 82 | 4.9 | 389 | 2 | T33340 | hypothetical prote |
| 131 | 85.5 | 5.2 | 786 | 2 | T16509 | hypothetical prote | 204 | 82 | 4.9 | 410 | 1 | B31959 | lysosome-associate |
| 132 | 85.5 | 5.2 | 895 | 2 | T02597 | Mutator-like trans | 205 | 82 | 4.9 | 410 | 1 | JC4317 | lysosome-associate |
| 133 | 85 | 5.1 | 265 | 2 | T33695 | hypothetical prote | 206 | 82 | 4.9 | 476 | 2 | A46118 | myosin-binding pro |
| 134 | 85 | 5.1 | 576 | 2 | S59829 | hypothetical prote | 207 | 82 | 4.9 | 544 | 2 | T15175 | hypothetical prote |
| 135 | 85 | 5.1 | 627 | 2 | G88860 | serine/threonine p | 208 | 82 | 4.9 | 577 | 2 | G89430 | protein K02E2.3 li |
| 136 | 85 | 5.1 | 989 | 2 | T47503 | hypothetical prote | 209 | 82 | 4.9 | 584 | 2 | T19061 | hypothetical prote |
| 137 | 85 | 5.1 | 990 | 2 | T15618 | nucleolar phosphop | 210 | 82 | 4.9 | 693 | 2 | T19551 | mucin-like protein |
| 138 | 85 | 5.1 | 1162 | 2 | T21557 | hypothetical prote | 211 | 82 | 4.9 | 720 | 2 | S51340 | nucleoporin NUP2 - |
| 139 | 85 | 5.1 | 1779 | 2 | T31085 | xylanase - Caldice | 212 | 82 | 4.9 | 761 | 2 | A96810 | probable Mutator-1 |
| 140 | 84.5 | 5.1 | 463 | 2 | B82001 | probable amino-aci | 213 | 82 | 4.9 | 894 | 2 | B96557 | probable receptor |
| 141 | 84.5 | 5.1 | 493 | 2 | JC5486 | membrane glycoprot | 214 | 82 | 4.9 | 911 | 2 | E86438 | hypothetical prote |
| 142 | 84.5 | 5.1 | 562 | 2 | A57088 | nucleoporin-like p | 215 | 82 | 4.9 | 926 | 2 | T38198 | COP1 coated vesic |
| 143 | 84.5 | 5.1 | 658 | 2 | T39500 | serine/threonine-s | 216 | 82 | 4.9 | 973 | 2 | A97522 | ribonuclease E, RN |
| 144 | 84.5 | 5.1 | 658 | 2 | S60170 | protein kinase Pak | 217 | 82 | 4.9 | 977 | 2 | AC2741 | ribonuclease E [im |
| 145 | 84.5 | 5.1 | 709 | 2 | T28712 | hypothetical prote | 218 | 82 | 4.9 | 1021 | 2 | S64506 | protein kinase RUB |
| 146 | 84.5 | 5.1 | 1102 | 2 | S65235 | probable membrane | 219 | 82 | 4.9 | 1023 | 2 | JC4013 | major acidic nucle |
| 147 | 84.5 | 5.1 | 1161 | 2 | S57180 | probable membrane | 220 | 82 | 4.9 | 1083 | 2 | S59780 | hypothetical prote |
| 148 | 84.5 | 5.1 | 2481 | 2 | D90011 | FmcB protein [impo | 221 | 82 | 4.9 | 1127 | 2 | T25804 | hypothetical prote |
| 149 | 84.5 | 5.1 | 2761 | 2 | T21064 | hypothetical prote | 222 | 82 | 4.9 | 1672 | 2 | C81675 | polymorphic membra |
| 150 | 84 | 5.1 | 262 | 2 | S76772 | hypothetical prote | 223 | 82 | 4.9 | 2738 | 2 | E88320 | protein F07A11.6 [|
| 151 | 84 | 5.1 | 335 | 2 | H96667 | AP2-containing DNA | 224 | 82 | 4.9 | 2926 | 1 | I38344 | titin, cardiac mus |
| 152 | 84 | 5.1 | 420 | 2 | AB2426 | hypothetical prote | 225 | 81.5 | 4.9 | 235 | 2 | T47379 | hypothetical prote |
| 153 | 84 | 5.1 | 426 | 2 | B53580 | neurexin III beta | 226 | 81.5 | 4.9 | 369 | 2 | T01196 | transcription fact |
| 154 | 84 | 5.1 | 543 | 2 | S35047 | mucin JUL7 - human | 227 | 81.5 | 4.9 | 386 | 2 | B97212 | protein containing |
| 155 | 84 | 5.1 | 636 | 1 | VCWVFS | env polypeptide - | 228 | 81.5 | 4.9 | 463 | 2 | B81228 | sodium/alanine sym |
| 156 | 84 | 5.1 | 793 | 2 | AH1094 | probable peptidogl | 229 | 81.5 | 4.9 | 636 | 2 | S63131 | probable membrane |
| 157 | 84 | 5.1 | 996 | 2 | JE0237 | apolipoprotein E r | 230 | 81.5 | 4.9 | 687 | 2 | A40711 | RNA polymerase II |
| 158 | 84 | 5.1 | 1075 | 2 | S48992 | flocculation prote | 231 | 81.5 | 4.9 | 860 | 2 | AG1612 | DNA mismatch repai |
| 159 | 84 | 5.1 | 1331 | 2 | A48954 | mannan endo-1,4-be | 232 | 81.5 | 4.9 | 869 | 2 | T22422 | hypothetical prote |
| 160 | 84 | 5.1 | 1362 | 2 | A75207 | amyloglucanase P | 233 | 81.5 | 4.9 | 1151 | 2 | T18297 | zinc-finger protei |
| 161 | 84 | 5.1 | 1832 | 2 | T31113 | mucin-like glycopr | 234 | 81.5 | 4.9 | 1212 | 2 | T13804 | shs protein - frui |
| 162 | 84 | 5.1 | 3020 | 2 | A43932 | mucin 2 precursor, | 235 | 81.5 | 4.9 | 1216 | 2 | F88473 | protein F40H6.5 [i |
| 163 | 83.5 | 5.0 | 216 | 2 | I51920 | mucin - rhesus mac | 236 | 81.5 | 4.9 | 1419 | 2 | T30531 | agglutinin-like ad |
| 164 | 83.5 | 5.0 | 279 | 2 | S53363 | mucin SAC (Clone J | 237 | 81.5 | 4.9 | 1445 | 1 | A48148 | protein-tyrosine-p |
| 165 | 83.5 | 5.0 | 446 | 2 | T43525 | WSCA homolog [impo | 238 | 81.5 | 4.9 | 1513 | 2 | T23681 | hypothetical prote |
| 166 | 83.5 | 5.0 | 967 | 2 | S66852 | hypothetical prote | 239 | 81.5 | 4.9 | 2282 | 2 | T42717 | DNA-binding protei |
| 167 | 83.5 | 5.0 | 976 | 2 | A87576 | peptidase, M16 fam | 240 | 81 | 4.9 | 339 | 2 | T25562 | plasma protein rec |
| 168 | 83.5 | 5.0 | 1043 | 2 | F97302 | hypothetical prote | 241 | 81 | 4.9 | 413 | 2 | S55890 | hypothetical prote |
| 169 | 83.5 | 5.0 | 1286 | 2 | AR8396 | protein M01E10.2 [| 242 | 81 | 4.9 | 422 | 1 | BMRT2V | synaptotagmin II - |
| 170 | 83.5 | 5.0 | 3175 | 1 | RRWVEV | genome polypeptin | 243 | 81 | 4.9 | 651 | 2 | C56653 | membrane glycoprot |
| 171 | 83 | 5.0 | 221 | 2 | S53649 | ribosomal protein | 244 | 81 | 4.9 | 683 | 2 | T10720 | NADPH-ferrihemopro |
| 172 | 83 | 5.0 | 409 | 2 | T44346 | RAD23 protein homo | 245 | 81 | 4.9 | 683 | 2 | E86358 | Flxk8.13 protein - |
| 173 | 83 | 5.0 | 463 | 2 | T38444 | hypothetical prote | 246 | 81 | 4.9 | 911 | 2 | S46497 | aspartate kinase (|
| 174 | 83 | 5.0 | 605 | 2 | S48940 | hypothetical prote | 247 | 81 | 4.9 | 1047 | 2 | A55617 | masquerade precurs |
| 175 | 83 | 5.0 | 737 | 1 | S64767 | probable serine/th | 248 | 81 | 4.9 | 1128 | 2 | A49960 | bud emergence prot |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|---------------------|-----|------|-----|------|---|--------|---------------------|
| 249 | 81 | 4.9 | 1169 | 2 | S38181 | flocculation prote | 322 | 78.5 | 4.7 | 423 | 2 | S69583 | hypothetical prote |
| 250 | 81 | 4.9 | 1367 | 2 | S51959 | hypothetical prote | 323 | 78.5 | 4.7 | 542 | 1 | S64030 | probable membrane |
| 251 | 81 | 4.9 | 1609 | 2 | S25345 | probable membrane | 324 | 78.5 | 4.7 | 591 | 1 | WMBPQ2 | gene P2 protein - |
| 252 | 81 | 4.9 | 1726 | 2 | A39401 | merozoite surface | 325 | 78.5 | 4.7 | 599 | 2 | S46630 | hypothetical prote |
| 253 | 80.5 | 4.9 | 6642 | 2 | T29757 | protein UNC-89 - C | 326 | 78.5 | 4.7 | 688 | 2 | B42161 | CGMP-gated cation |
| 254 | 80.5 | 4.9 | 148 | 1 | S07723 | immediate-early se | 327 | 78.5 | 4.7 | 815 | 2 | JG0197 | myosin-light chain |
| 255 | 80.5 | 4.9 | 391 | 1 | S15617 | E2 protein - human | 328 | 78.5 | 4.7 | 825 | 2 | T29634 | hypothetical prote |
| 256 | 80.5 | 4.9 | 441 | 2 | T31482 | hypothetical prote | 329 | 78.5 | 4.7 | 919 | 1 | PX2P1P | H+-exporting ATPase |
| 257 | 80.5 | 4.9 | 543 | 2 | T22585 | hypothetical prote | 330 | 78.5 | 4.7 | 1011 | 1 | JH0581 | NAD ADP-ribosyltra |
| 258 | 80.5 | 4.9 | 592 | 2 | T34446 | hypothetical prote | 331 | 78.5 | 4.7 | 1356 | 2 | T16754 | hypothetical prote |
| 259 | 80.5 | 4.9 | 595 | 2 | A42086 | CD30 antigen precu | 332 | 78.5 | 4.7 | 1420 | 2 | T17158 | CL2AB protein - ra |
| 260 | 80.5 | 4.9 | 742 | 2 | T33514 | hypothetical prote | 333 | 78.5 | 4.7 | 1435 | 2 | T46611 | CL2BB protein - ra |
| 261 | 80.5 | 4.9 | 798 | 2 | T34248 | hypothetical prote | 334 | 78.5 | 4.7 | 1452 | 2 | T17157 | CL2AA protein - ra |
| 262 | 80.5 | 4.9 | 918 | 2 | I58178 | glutamate receptor | 335 | 78.5 | 4.7 | 1463 | 2 | T17159 | CL2BA protein - ra |
| 263 | 80.5 | 4.9 | 1124 | 2 | F71719 | inner layer protei | 336 | 78.5 | 4.7 | 1467 | 2 | T17160 | CL2BC protein - ra |
| 264 | 80.5 | 4.9 | 1159 | 1 | A44280 | hypothetical prote | 337 | 78.5 | 4.7 | 1478 | 2 | T17185 | alpha-latrotoxin r |
| 265 | 80.5 | 4.9 | 2225 | 2 | T26063 | hypothetical prote | 338 | 78.5 | 4.7 | 1487 | 2 | T14324 | zinc metalloprotei |
| 266 | 80 | 4.8 | 153 | 2 | S67294 | hypothetical prote | 339 | 78.5 | 4.7 | 1876 | 2 | E97944 | Ran-binding protei |
| 267 | 80 | 4.8 | 177 | 1 | RGBVGI | regulatory protein | 340 | 78.5 | 4.7 | 3224 | 1 | S58884 | hypothetical prote |
| 268 | 80 | 4.8 | 345 | 2 | T21776 | hypothetical prote | 341 | 78 | 4.7 | 253 | 2 | S76719 | hypothetical prote |
| 269 | 80 | 4.8 | 359 | 2 | T13478 | hypothetical prote | 342 | 78 | 4.7 | 260 | 2 | AG2238 | hypothetical prote |
| 270 | 80 | 4.8 | 415 | 2 | AE2237 | hypothetical prote | 343 | 78 | 4.7 | 266 | 2 | T30919 | hypothetical prote |
| 271 | 80 | 4.8 | 451 | 2 | S71754 | cellular hepatitis | 344 | 78 | 4.7 | 287 | 2 | T12471 | hypothetical prote |
| 272 | 80 | 4.8 | 468 | 2 | A55116 | vacuolar ATPase (E | 345 | 78 | 4.7 | 293 | 2 | G87018 | probable membrane |
| 273 | 80 | 4.8 | 521 | 2 | S69359 | hypothetical prote | 346 | 78 | 4.7 | 321 | 2 | T26152 | hypothetical prote |
| 274 | 80 | 4.8 | 650 | 2 | T41681 | probable serine/th | 347 | 78 | 4.7 | 340 | 2 | AH0940 | probable ABC trans |
| 275 | 80 | 4.8 | 667 | 2 | A40713 | cyclicin I - bovine | 348 | 78 | 4.7 | 372 | 2 | T48660 | heat shock protein |
| 276 | 80 | 4.8 | 698 | 2 | T18263 | S-layer protein - | 349 | 78 | 4.7 | 373 | 2 | F81333 | chaperone DnaJ Cj1 |
| 277 | 80 | 4.8 | 702 | 2 | T34313 | hypothetical prote | 350 | 78 | 4.7 | 384 | 2 | T21929 | hypothetical prote |
| 278 | 80 | 4.8 | 725 | 2 | A41258 | a-agglutinin core | 351 | 78 | 4.7 | 425 | 2 | T48724 | hypothetical prote |
| 279 | 80 | 4.8 | 891 | 2 | S56032 | probable membrane | 352 | 78 | 4.7 | 434 | 2 | B84684 | hypothetical prote |
| 280 | 80 | 4.8 | 1013 | 1 | S04200 | NAD ADP-ribosyltra | 353 | 78 | 4.7 | 530 | 2 | A45690 | transactivator EBN |
| 281 | 80 | 4.8 | 1348 | 2 | S27812 | probable epidermal | 354 | 78 | 4.7 | 627 | 1 | VCVM2 | env polyprotein - |
| 282 | 79.5 | 4.8 | 152 | 2 | T15170 | hypothetical prote | 355 | 78 | 4.7 | 655 | 2 | T30044 | hypothetical prote |
| 283 | 79.5 | 4.8 | 165 | 2 | A27195 | histone H1 - Tetra | 356 | 78 | 4.7 | 786 | 1 | A47544 | serine proteinase |
| 284 | 79.5 | 4.8 | 184 | 2 | F72525 | hypothetical prote | 357 | 78 | 4.7 | 1050 | 2 | T31853 | hypothetical prote |
| 285 | 79.5 | 4.8 | 354 | 2 | T46740 | microfilarial shea | 358 | 78 | 4.7 | 1337 | 2 | T30291 | dextranase - Strept |
| 286 | 79.5 | 4.8 | 461 | 1 | A35356 | tumor necrosis fac | 359 | 78 | 4.7 | 1360 | 2 | T33922 | hypothetical prote |
| 287 | 79.5 | 4.8 | 510 | 2 | B72007 | conserved hypotet | 360 | 78 | 4.7 | 1442 | 1 | B48148 | protein-tyrosine-p |
| 288 | 79.5 | 4.8 | 510 | 2 | A86618 | CT861 hypothetical | 361 | 78 | 4.7 | 1634 | 2 | T28517 | hypothetical prote |
| 289 | 79.5 | 4.8 | 534 | 2 | G84713 | hypothetical prote | 362 | 78 | 4.7 | 1723 | 2 | H85557 | polymorphic membra |
| 290 | 79.5 | 4.8 | 554 | 2 | JW0094 | neurofilament prot | 363 | 78 | 4.7 | 1732 | 2 | E72067 | polymorphic membra |
| 291 | 79.5 | 4.8 | 580 | 2 | T20716 | hypothetical prote | 364 | 78 | 4.7 | 1955 | 1 | AGCH | agrin precursor - |
| 292 | 79.5 | 4.8 | 693 | 2 | T25878 | hypothetical prote | 365 | 78 | 4.7 | 1995 | 2 | T08166 | probable membrane |
| 293 | 79.5 | 4.8 | 827 | 2 | T04789 | hypothetical prote | 366 | 78 | 4.7 | 5327 | 2 | T13564 | microtubule-associ |
| 294 | 79.5 | 4.8 | 860 | 2 | AC1250 | DNA mismatch repai | 367 | 78 | 4.7 | 5275 | 2 | T21933 | hypothetical prote |
| 295 | 79.5 | 4.8 | 998 | 2 | S31735 | NAD ADP-ribosyltra | 368 | 77.5 | 4.7 | 396 | 2 | F83130 | probable MFS trans |
| 296 | 79.5 | 4.8 | 1011 | 2 | T20785 | hypothetical prote | 369 | 77.5 | 4.7 | 401 | 2 | AG3552 | branched-chain ami |
| 297 | 79.5 | 4.8 | 1280 | 2 | E95031 | alkaline amylopul | 370 | 77.5 | 4.7 | 474 | 1 | BMFFSY | synaptotagmin - fr |
| 298 | 79.5 | 4.8 | 1365 | 2 | S14871 | suppressor two of | 371 | 77.5 | 4.7 | 476 | 2 | T32032 | hypothetical prote |
| 299 | 79 | 4.8 | 215 | 2 | S26363 | histone H1.1 - hum | 372 | 77.5 | 4.7 | 496 | 2 | B41322 | N-acetyluramoyl-L |
| 300 | 79 | 4.8 | 249 | 2 | G84781 | hypothetical prote | 373 | 77.5 | 4.7 | 514 | 2 | JQ1317 | activin receptor p |
| 301 | 79 | 4.8 | 352 | 2 | T51659 | myb-related transc | 374 | 77.5 | 4.7 | 519 | 2 | T45764 | hypothetical prote |
| 302 | 79 | 4.8 | 534 | 2 | T39903 | serine-rich protei | 375 | 77.5 | 4.7 | 526 | 2 | A56573 | nuclear pore compl |
| 303 | 79 | 4.8 | 575 | 2 | T21775 | hypothetical prote | 376 | 77.5 | 4.7 | 607 | 2 | S01939 | hypothetical prote |
| 304 | 79 | 4.8 | 611 | 2 | AB1497 | internalin protein | 377 | 77.5 | 4.7 | 623 | 2 | T18892 | hypothetical prote |
| 305 | 79 | 4.8 | 710 | 2 | S67098 | probable membrane | 378 | 77.5 | 4.7 | 816 | 2 | S64439 | hypothetical prote |
| 306 | 79 | 4.8 | 738 | 2 | T44007 | hypothetical prote | 379 | 77.5 | 4.7 | 860 | 2 | JC4566 | chitinase (EC 3.2. |
| 307 | 79 | 4.8 | 739 | 2 | T49456 | hypothetical prote | 380 | 77.5 | 4.7 | 906 | 2 | G90281 | conserved hypotet |
| 308 | 79 | 4.8 | 822 | 2 | JC4076 | cell division cont | 381 | 77.5 | 4.7 | 938 | 2 | A56731 | chromatin assembly |
| 309 | 79 | 4.8 | 836 | 2 | S49940 | glutamate receptor | 382 | 77.5 | 4.7 | 975 | 2 | T08606 | protein phosphatas |
| 310 | 79 | 4.8 | 949 | 2 | S19808 | probable transcrip | 383 | 77.5 | 4.7 | 993 | 1 | PIVXTA | RNA 1 protein - to |
| 311 | 79 | 4.8 | 1098 | 2 | T08599 | IGA-specific metal | 384 | 77.5 | 4.7 | 1127 | 2 | E86386 | probable mutator-1 |
| 312 | 79 | 4.8 | 1849 | 2 | C41859 | tail-host specific | 385 | 77.5 | 4.7 | 1156 | 2 | T23748 | hypothetical prote |
| 313 | 79 | 4.8 | 1904 | 2 | T13256 | hypothetical prote | 386 | 77.5 | 4.7 | 1312 | 2 | A97879 | beta-N-acetylhexos |
| 314 | 78.5 | 4.7 | 152 | 2 | T28759 | mucin SAC - human | 387 | 77.5 | 4.7 | 1475 | 2 | S42718 | nuclear pore compl |
| 315 | 78.5 | 4.7 | 164 | 2 | I53641 | larval glue protei | 388 | 77.5 | 4.7 | 3968 | 2 | A44265 | trichorax homolog |
| 316 | 78.5 | 4.7 | 232 | 2 | A60095 | mucin, tracheal (A | 389 | 77.5 | 4.7 | 257 | 2 | G72690 | probable spermidin |
| 317 | 78.5 | 4.7 | 294 | 2 | A37232 | hemagglutinin prec | 390 | 77 | 4.6 | 350 | 2 | E75341 | env polyprotein - |
| 318 | 78.5 | 4.7 | 314 | 1 | HNZVZW | apomucin precursor | 391 | 77 | 4.6 | 352 | 2 | S22805 | peptidyl-prolyl ci |
| 319 | 78.5 | 4.7 | 314 | 1 | JQ1793 | albumin-binding pr | 392 | 77 | 4.6 | 453 | 2 | F75206 | maltose-binding pe |
| 320 | 78.5 | 4.7 | 322 | 2 | A53586 | | 393 | 77 | 4.6 | 528 | 2 | S69589 | hypothetical prote |
| 321 | | | 387 | 2 | | | 394 | | | | | | |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|--------------------|-----|------|-----|------|---|--------|--------------------|
| 395 | 77 | 4.6 | 553 | 2 | T19894 | hypothetical prote | 468 | 76 | 4.6 | 1014 | 1 | A39725 | NAD ADP-ribosyltra |
| 396 | 77 | 4.6 | 598 | 2 | T22610 | hypothetical prote | 469 | 76 | 4.6 | 1041 | 2 | H71617 | SERA antigen/papai |
| 397 | 77 | 4.6 | 623 | 2 | A48123 | cell cycle regulat | 470 | 76 | 4.6 | 1046 | 2 | T29776 | hypothetical prote |
| 398 | 77 | 4.6 | 639 | 2 | T33166 | hypothetical prote | 471 | 76 | 4.6 | 1216 | 2 | B90580 | hypothetical prote |
| 399 | 77 | 4.6 | 669 | 1 | VCWEK | env polyprotein - | 472 | 76 | 4.6 | 1263 | 2 | AH2011 | heterocyst glycoli |
| 400 | 77 | 4.6 | 734 | 2 | B42680 | nucleolus-cytoplas | 473 | 76 | 4.6 | 1338 | 2 | S09982 | protein-tyrosine k |
| 401 | 77 | 4.6 | 750 | 2 | T42614 | probable envelope | 474 | 76 | 4.6 | 1348 | 2 | A43917 | probable epidermal |
| 402 | 77 | 4.6 | 771 | 2 | JC7388 | M83 protein - huma | 475 | 76 | 4.6 | 1388 | 2 | A53317 | collagen alpha 1(X |
| 403 | 77 | 4.6 | 861 | 2 | T23810 | hypothetical prote | 476 | 76 | 4.6 | 1401 | 2 | T17452 | werner syndrome pr |
| 404 | 77 | 4.6 | 862 | 2 | B36786 | hypothetical prote | 477 | 76 | 4.6 | 1422 | 2 | T42636 | protein-tyrosine-p |
| 405 | 77 | 4.6 | 892 | 2 | T09193 | ataxin 7 - human | 478 | 76 | 4.6 | 1438 | 2 | B71610 | WD40 WEB-1 homolog |
| 406 | 77 | 4.6 | 897 | 2 | S05050 | SINI-associated pr | 479 | 76 | 4.6 | 1489 | 2 | G71406 | probable retroviro |
| 407 | 77 | 4.6 | 967 | 2 | G86229 | hypothetical prote | 480 | 76 | 4.6 | 1513 | 2 | T44045 | hypothetical prote |
| 408 | 77 | 4.6 | 977 | 2 | S49004 | tyrosine kinase Mp | 481 | 76 | 4.6 | 1890 | 2 | T04556 | hypothetical prote |
| 409 | 77 | 4.6 | 1016 | 2 | T41720 | hypothetical prote | 482 | 76 | 4.6 | 2570 | 2 | T17451 | fimbriae-associate |
| 410 | 77 | 4.6 | 1237 | 2 | T14633 | hypothetical prote | 483 | 75.5 | 4.6 | 261 | 2 | T30170 | hypothetical prote |
| 411 | 77 | 4.6 | 1401 | 2 | T30247 | werner syndrome pr | 484 | 75.5 | 4.6 | 273 | 1 | T44657 | protein GP80 [impo |
| 412 | 77 | 4.6 | 1513 | 2 | A54895 | mucin 2, intestina | 485 | 75.5 | 4.6 | 319 | 1 | A35163 | carbonate dehydrat |
| 413 | 77 | 4.6 | 2187 | 2 | T30826 | nascent polypeptid | 486 | 75.5 | 4.6 | 343 | 2 | T40306 | hypothetical prote |
| 414 | 76.5 | 4.6 | 284 | 2 | T42367 | a-agglutinin core | 487 | 75.5 | 4.6 | 348 | 1 | B46216 | transcription fact |
| 415 | 76.5 | 4.6 | 349 | 2 | T43457 | hypothetical prote | 488 | 75.5 | 4.6 | 364 | 1 | OHUG | opsin, green-sensi |
| 416 | 76.5 | 4.6 | 382 | 2 | S27388 | neuropeptide Y rec | 489 | 75.5 | 4.6 | 387 | 2 | A86302 | hypothetical prote |
| 417 | 76.5 | 4.6 | 391 | 2 | C69673 | penicillin-binding | 490 | 75.5 | 4.6 | 411 | 2 | T03154 | DNA polymerase pro |
| 418 | 76.5 | 4.6 | 421 | 2 | A60058 | neural cell adhesi | 491 | 75.5 | 4.6 | 412 | 2 | E97279 | TPR-repeat-contain |
| 419 | 76.5 | 4.6 | 433 | 2 | H84120 | methyl-accepting c | 492 | 75.5 | 4.6 | 430 | 1 | A46216 | transcription fact |
| 420 | 76.5 | 4.6 | 482 | 2 | AG1147 | P60 extracellular | 493 | 75.5 | 4.6 | 435 | 2 | S40993 | hypothetical prote |
| 421 | 76.5 | 4.6 | 484 | 2 | A41487 | protein P60 precur | 494 | 75.5 | 4.6 | 443 | 2 | D72383 | NADH oxidase - The |
| 422 | 76.5 | 4.6 | 505 | 2 | B46629 | mucin 6, gastric (| 495 | 75.5 | 4.6 | 445 | 2 | I38521 | inwardly rectifyin |
| 423 | 76.5 | 4.6 | 518 | 2 | G88961 | protein F59A7.8 [i | 496 | 75.5 | 4.6 | 448 | 2 | S17370 | DNA-binding protei |
| 424 | 76.5 | 4.6 | 542 | 2 | I39540 | chitinase (EC 3.2. | 497 | 75.5 | 4.6 | 468 | 2 | S70297 | SPS2 protein homol |
| 425 | 76.5 | 4.6 | 549 | 2 | SC4845 | IG heavy chain pre | 498 | 75.5 | 4.6 | 511 | 1 | VGBEF4 | glycoprotein C - h |
| 426 | 76.5 | 4.6 | 640 | 1 | VCVWML | env polyprotein - | 499 | 75.5 | 4.6 | 609 | 2 | G87496 | peptidase, M23/M37 |
| 427 | 76.5 | 4.6 | 679 | 2 | S64258 | hypothetical prote | 500 | 75.5 | 4.6 | 639 | 2 | T13151 | adapter protein CM |
| 428 | 76.5 | 4.6 | 718 | 2 | T29708 | hypothetical prote | 501 | 75.5 | 4.6 | 665 | 2 | G97213 | probable membrane- |
| 429 | 76.5 | 4.6 | 727 | 2 | A88131 | protein F10G7.9 [i | 502 | 75.5 | 4.6 | 709 | 2 | T32089 | hypothetical prote |
| 430 | 76.5 | 4.6 | 749 | 2 | B86403 | probable mutator-1 | 503 | 75.5 | 4.6 | 778 | 2 | T43223 | hypothetical prote |
| 431 | 76.5 | 4.6 | 773 | 2 | T00502 | hypothetical prote | 504 | 75.5 | 4.6 | 780 | 2 | A48143 | HF-1 regulatory el |
| 432 | 76.5 | 4.6 | 806 | 2 | E69424 | hypothetical prote | 505 | 75.5 | 4.6 | 963 | 2 | T40290 | hypothetical prote |
| 433 | 76.5 | 4.6 | 990 | 2 | T16554 | hypothetical prote | 506 | 75.5 | 4.6 | 1131 | 2 | T41144 | hypothetical serin |
| 434 | 76.5 | 4.6 | 1154 | 1 | VGJHIB | E2 glycoprotein pr | 507 | 75.5 | 4.6 | 1166 | 2 | S37692 | probable tumor sup |
| 435 | 76.5 | 4.6 | 1379 | 2 | T45119 | FIM protein [impor | 508 | 75.5 | 4.6 | 1235 | 2 | T13710 | protein-tyrosine k |
| 436 | 76.5 | 4.6 | 1736 | 2 | F86178 | hypothetical prote | 509 | 75.5 | 4.6 | 1237 | 2 | E86457 | probable RNA helic |
| 437 | 76.5 | 4.6 | 1946 | 2 | JC6032 | lactocepin (EC 3.4 | 510 | 75.5 | 4.6 | 1473 | 2 | T31422 | C-terminal domain- |
| 438 | 76.5 | 4.6 | 3869 | 2 | A48205 | All-1 protein +GPE | 511 | 75.5 | 4.6 | 1655 | 2 | T32633 | hypothetical prote |
| 439 | 76.5 | 4.6 | 5037 | 2 | B35041 | ryanodine receptor | 512 | 75.5 | 4.6 | 1737 | 2 | A59235 | unconventional myo |
| 440 | 76 | 4.6 | 167 | 2 | A33532 | mucin SMUC-40 - hu | 513 | 75.5 | 4.6 | 1881 | 2 | H95076 | zinc metalloprotei |
| 441 | 76 | 4.6 | 172 | 2 | T21753 | hypothetical prote | 514 | 75.5 | 4.6 | 2526 | 2 | T20531 | hypothetical prote |
| 442 | 76 | 4.6 | 243 | 2 | B41710 | promastigote surfa | 515 | 75.5 | 4.6 | 3176 | 2 | CGHU3A | collagen alpha 3(V |
| 443 | 76 | 4.6 | 356 | 2 | D89979 | protein F37B4.9 [i | 516 | 75 | 4.5 | 94 | 2 | S53365 | mucin 5AC (clone C |
| 444 | 76 | 4.6 | 368 | 2 | S36564 | E2 protein - human | 517 | 75 | 4.5 | 128 | 2 | T05035 | hypothetical prote |
| 445 | 76 | 4.6 | 378 | 2 | A12180 | hypothetical prote | 518 | 75 | 4.5 | 205 | 2 | S55670 | hypothetical prote |
| 446 | 76 | 4.6 | 382 | 2 | B88561 | protein F58A4.7b [| 519 | 75 | 4.5 | 248 | 2 | AF1914 | carbon dioxide con |
| 447 | 76 | 4.6 | 384 | 2 | A41710 | promastigote surfa | 520 | 75 | 4.5 | 256 | 2 | T09034 | hypothetical prote |
| 448 | 76 | 4.6 | 389 | 2 | A47013 | butanol dehydrogen | 521 | 75 | 4.5 | 295 | 2 | T28078 | hypothetical prote |
| 449 | 76 | 4.6 | 389 | 2 | E97305 | NADH-dependent bu | 522 | 75 | 4.5 | 310 | 1 | H71054 | hypothetical prote |
| 450 | 76 | 4.6 | 499 | 2 | T47722 | probable protein k | 523 | 75 | 4.5 | 313 | 2 | AH0734 | probable bacteriop |
| 451 | 76 | 4.6 | 515 | 2 | AD1162 | flagellar motor sw | 524 | 75 | 4.5 | 353 | 2 | S33322 | (S)-2-hydroxy-acid |
| 452 | 76 | 4.6 | 532 | 2 | T28784 | hypothetical prote | 525 | 75 | 4.5 | 388 | 2 | T16861 | hypothetical prote |
| 453 | 76 | 4.6 | 536 | 2 | T37544 | hypothetical serin | 526 | 75 | 4.5 | 390 | 2 | A72108 | hypothetical prote |
| 454 | 76 | 4.6 | 539 | 2 | T02512 | hypothetical prote | 527 | 75 | 4.5 | 390 | 2 | B86514 | hypothetical prote |
| 455 | 76 | 4.6 | 549 | 2 | T49298 | hypothetical prote | 528 | 75 | 4.5 | 418 | 2 | T16713 | hypothetical prote |
| 456 | 76 | 4.6 | 592 | 2 | T16725 | hypothetical prote | 529 | 75 | 4.5 | 425 | 1 | A26431 | nerve growth facto |
| 457 | 76 | 4.6 | 615 | 2 | T47395 | hypothetical prote | 530 | 75 | 4.5 | 453 | 2 | C40511 | hypothetical prote |
| 458 | 76 | 4.6 | 687 | 2 | A49636 | soluble vascular e | 531 | 75 | 4.5 | 475 | 2 | E84745 | probable splicing |
| 459 | 76 | 4.6 | 699 | 2 | I38073 | nucleolar phospho | 532 | 75 | 4.5 | 477 | 2 | T32938 | hypothetical prote |
| 460 | 76 | 4.6 | 700 | 2 | A54641 | interspersed seque | 533 | 75 | 4.5 | 481 | 2 | T38149 | pre-mrna splicing |
| 461 | 76 | 4.6 | 763 | 2 | T08929 | hypothetical prote | 534 | 75 | 4.5 | 554 | 2 | A56596 | chitinase (EC 3.2. |
| 462 | 76 | 4.6 | 766 | 2 | B85440 | receptor kinase-li | 535 | 75 | 4.5 | 604 | 2 | T37994 | probable splicing |
| 463 | 76 | 4.6 | 824 | 2 | T23923 | hypothetical prote | 536 | 75 | 4.5 | 607 | 2 | S63395 | probable membrane |
| 464 | 76 | 4.6 | 929 | 2 | G72677 | hypothetical prote | 537 | 75 | 4.5 | 651 | 2 | T16450 | hypothetical prote |
| 465 | 76 | 4.6 | 940 | 2 | AD1374 | internalin protein | 538 | 75 | 4.5 | 679 | 2 | T19703 | hypothetical prote |
| 466 | 76 | 4.6 | 960 | 1 | JN0677 | protein-tyrosine k | 539 | 75 | 4.5 | 739 | 2 | I56187 | transcription fact |
| 467 | 76 | 4.6 | 994 | 1 | MNWVM | nonstructural prot | 540 | 75 | 4.5 | 775 | 1 | WNBE19 | ribonucleoside-dip |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|---------------------|-----|------|-----|------|---|--------|--------------------|
| 541 | 75 | 4.5 | 778 | 2 | T45221 | DNA damage checkpo | 614 | 74 | 4.5 | 621 | 2 | T20307 | hypothetical prote |
| 542 | 75 | 4.5 | 796 | 2 | E96654 | hypothetical prote | 615 | 74 | 4.5 | 622 | 2 | AC1236 | acyltransferase (c |
| 543 | 75 | 4.5 | 858 | 1 | IJRTNC | neural cell adhesi | 616 | 74 | 4.5 | 665 | 1 | VCWVKA | env polyprotein pr |
| 544 | 75 | 4.5 | 904 | 2 | T03806 | hypothetical prote | 617 | 74 | 4.5 | 672 | 2 | T20310 | hypothetical prote |
| 545 | 75 | 4.5 | 916 | 2 | T20909 | hypothetical prote | 618 | 74 | 4.5 | 681 | 2 | A45705 | type I transembra |
| 546 | 75 | 4.5 | 940 | 2 | D89723 | protein F39D8.1b [| 619 | 74 | 4.5 | 689 | 2 | B43491 | env polyprotein - |
| 547 | 75 | 4.5 | 948 | 2 | T21998 | hypothetical prote | 620 | 74 | 4.5 | 731 | 2 | T04455 | hypothetical prote |
| 548 | 75 | 4.5 | 1048 | 1 | S61388 | dotA protein - Leg | 621 | 74 | 4.5 | 739 | 1 | A34873 | transcription fact |
| 549 | 75 | 4.5 | 1118 | 2 | A48292 | mucin, tracheobron | 622 | 74 | 4.5 | 775 | 2 | A32494 | transposable eleme |
| 550 | 75 | 4.5 | 1253 | 2 | T18528 | probable pyruvate | 623 | 74 | 4.5 | 823 | 2 | G90848 | probable exonuclea |
| 551 | 75 | 4.5 | 1741 | 2 | T13610 | parallel sister ch | 624 | 74 | 4.5 | 823 | 2 | E85706 | hypothetical prote |
| 552 | 75 | 4.5 | 1768 | 2 | T13349 | parallel sister ch | 625 | 74 | 4.5 | 852 | 2 | T06310 | hypothetical prote |
| 553 | 75 | 4.5 | 1838 | 1 | CGHU1V | collagen alpha 1(V | 626 | 74 | 4.5 | 862 | 2 | S51493 | major nitrogen reg |
| 554 | 75 | 4.5 | 1979 | 2 | T17622 | hypothetical prote | 627 | 74 | 4.5 | 903 | 2 | T00705 | N-chimerin homolog |
| 555 | 75 | 4.5 | 3122 | 2 | T17202 | DNA-directed DNA p | 628 | 74 | 4.5 | 1016 | 2 | T19006 | ankyrin related pr |
| 556 | 75 | 4.5 | 3375 | 2 | T19821 | hypothetical prote | 629 | 74 | 4.5 | 1099 | 2 | T40253 | hypothetical prote |
| 557 | 74.5 | 4.5 | 148 | 2 | S50653 | hypothetical prote | 630 | 74 | 4.5 | 1104 | 2 | G90546 | conserved hypothet |
| 558 | 74.5 | 4.5 | 211 | 2 | S28046 | TUB8 protein - pot | 631 | 74 | 4.5 | 1104 | 2 | S59310 | probable membrane |
| 559 | 74.5 | 4.5 | 254 | 2 | D88560 | protein F58A4.1 [l | 632 | 74 | 4.5 | 1110 | 2 | I51116 | hypothetical prote |
| 560 | 74.5 | 4.5 | 262 | 2 | T33597 | hypothetical prote | 633 | 74 | 4.5 | 1115 | 1 | IUNSNL | neural cell adhesi |
| 561 | 74.5 | 4.5 | 276 | 2 | T51685 | myb-related transc | 634 | 74 | 4.5 | 1159 | 2 | S62562 | probable nuclear p |
| 562 | 74.5 | 4.5 | 281 | 2 | T49537 | hypothetical prote | 635 | 74 | 4.5 | 1164 | 2 | B71429 | phytochrome D - Ar |
| 563 | 74.5 | 4.5 | 294 | 2 | AI2016 | hypothetical prote | 636 | 74 | 4.5 | 1390 | 2 | T14004 | trfA protein - sli |
| 564 | 74.5 | 4.5 | 310 | 1 | YAZQ31 | 300K antigen Ag231 | 637 | 74 | 4.5 | 1694 | 2 | H64106 | IgA-specific metal |
| 565 | 74.5 | 4.5 | 321 | 2 | T50966 | hypothetical prote | 638 | 74 | 4.5 | 1828 | 2 | A40115 | microtubule-associ |
| 566 | 74.5 | 4.5 | 382 | 2 | T25280 | hypothetical prote | 639 | 74 | 4.5 | 1938 | 1 | MWK1 | myosin heavy chain |
| 567 | 74.5 | 4.5 | 396 | 2 | T50229 | probable transmem | 640 | 74 | 4.5 | 2414 | 2 | A54277 | transcription adap |
| 568 | 74.5 | 4.5 | 407 | 2 | T26938 | hypothetical prote | 641 | 73.5 | 4.4 | 168 | 2 | A31196 | prespore-specific |
| 569 | 74.5 | 4.5 | 416 | 2 | T20448 | hypothetical prote | 642 | 73.5 | 4.4 | 182 | 2 | T30078 | hypothetical prote |
| 570 | 74.5 | 4.5 | 429 | 2 | S29044 | endoglucanase A pr | 643 | 73.5 | 4.4 | 253 | 2 | T32879 | hypothetical prote |
| 571 | 74.5 | 4.5 | 432 | 2 | T08771 | hypothetical prote | 644 | 73.5 | 4.4 | 263 | 2 | T38003 | hypothetical prote |
| 572 | 74.5 | 4.5 | 478 | 2 | A32555 | major merozoite su | 645 | 73.5 | 4.4 | 292 | 2 | S24169 | hypothetical ser-t |
| 573 | 74.5 | 4.5 | 482 | 2 | T22754 | hypothetical prote | 646 | 73.5 | 4.4 | 305 | 2 | A44661 | mucin - rat |
| 574 | 74.5 | 4.5 | 520 | 2 | S14598 | B2 glycoprotein - | 647 | 73.5 | 4.4 | 335 | 2 | AE3000 | ZK353.4 protein - |
| 575 | 74.5 | 4.5 | 531 | 2 | S09859 | hypothetical prote | 648 | 73.5 | 4.4 | 335 | 2 | D98283 | cell division prot |
| 576 | 74.5 | 4.5 | 551 | 2 | S52287 | urbain - silkworm | 649 | 73.5 | 4.4 | 345 | 2 | D91201 | hypothetical prote |
| 577 | 74.5 | 4.5 | 636 | 2 | T23232 | hypothetical prote | 650 | 73.5 | 4.4 | 345 | 2 | H86047 | type III secretion |
| 578 | 74.5 | 4.5 | 713 | 2 | JE0230 | NADPH-cytochrome P | 651 | 73.5 | 4.4 | 358 | 2 | AD2378 | escu [imported] - |
| 579 | 74.5 | 4.5 | 802 | 2 | T21315 | hypothetical prote | 652 | 73.5 | 4.4 | 371 | 2 | S20075 | hypothetical prote |
| 580 | 74.5 | 4.5 | 808 | 2 | T23129 | hypothetical prote | 653 | 73.5 | 4.4 | 376 | 2 | T48245 | promastigote surfa |
| 581 | 74.5 | 4.5 | 884 | 2 | AE3166 | ATP-dependent DNA | 654 | 73.5 | 4.4 | 381 | 2 | E69862 | hypothetical prote |
| 582 | 74.5 | 4.5 | 998 | 2 | S37627 | protein-tyrosine k | 655 | 73.5 | 4.4 | 397 | 2 | G69287 | hypothetical prote |
| 583 | 74.5 | 4.5 | 1042 | 2 | T48801 | hypothetical prote | 656 | 73.5 | 4.4 | 405 | 2 | A60534 | P2B/LAMP-1 precurs |
| 584 | 74.5 | 4.5 | 1595 | 2 | T31082 | endo-1,4-beta-xyla | 657 | 73.5 | 4.4 | 445 | 2 | A54852 | potassium rectifie |
| 585 | 74.5 | 4.5 | 1630 | 2 | A53577 | ascites stialoglyco | 658 | 73.5 | 4.4 | 447 | 2 | A39321 | mucin - rat (fragm |
| 586 | 74.5 | 4.5 | 1902 | 2 | C97702 | cell surface antig | 659 | 73.5 | 4.4 | 457 | 2 | T20884 | hypothetical prote |
| 587 | 74.5 | 4.5 | 1965 | 2 | T33216 | hypothetical prote | 660 | 73.5 | 4.4 | 458 | 2 | T31631 | hypothetical prote |
| 588 | 74.5 | 4.5 | 2688 | 2 | I49477 | alpha-A-crystallin | 661 | 73.5 | 4.4 | 459 | 2 | I48854 | gene murine tumour |
| 589 | 74.5 | 4.5 | 3828 | 2 | T13857 | trithorax protein | 662 | 73.5 | 4.4 | 476 | 2 | B44997 | merozoite surface |
| 590 | 74.5 | 4.5 | 3944 | 2 | T19997 | hypothetical prote | 663 | 73.5 | 4.4 | 484 | 1 | A24994 | cellulose 1,4-beta |
| 591 | 74 | 4.5 | 147 | 2 | S09762 | hypothetical prote | 664 | 73.5 | 4.4 | 511 | 1 | VBGE1K | glycoprotein C - h |
| 592 | 74 | 4.5 | 223 | 2 | T21930 | hypothetical prote | 665 | 73.5 | 4.4 | 540 | 2 | H98086 | chaperonin GroEL [|
| 593 | 74 | 4.5 | 257 | 1 | MGNZBR | major surface glyco | 666 | 73.5 | 4.4 | 540 | 2 | G95222 | chaperonin, 60 kDa |
| 594 | 74 | 4.5 | 264 | 2 | A49149 | mesoderm developme | 667 | 73.5 | 4.4 | 542 | 2 | T19952 | hypothetical prote |
| 595 | 74 | 4.5 | 286 | 2 | S44835 | F54H12.3 protein - | 668 | 73.5 | 4.4 | 550 | 1 | VG1HD6 | E2 glycoprotein pr |
| 596 | 74 | 4.5 | 305 | 2 | AB2149 | hypothetical prote | 669 | 73.5 | 4.4 | 555 | 2 | T26413 | hypothetical prote |
| 597 | 74 | 4.5 | 317 | 2 | C85432 | hypothetical prote | 670 | 73.5 | 4.4 | 556 | 2 | C87609 | sensor histidine k |
| 598 | 74 | 4.5 | 332 | 2 | T31928 | hypothetical prote | 671 | 73.5 | 4.4 | 569 | 2 | A46462 | T cell activation |
| 599 | 74 | 4.5 | 339 | 1 | JT0756 | group-V allergen 1 | 672 | 73.5 | 4.4 | 601 | 2 | H90270 | hypothetical prote |
| 600 | 74 | 4.5 | 339 | 2 | A56274 | sulfur-regulated 3 | 673 | 73.5 | 4.4 | 606 | 2 | T39866 | hypothetical prote |
| 601 | 74 | 4.5 | 344 | 2 | T13975 | NADH2 dehydrogenas | 674 | 73.5 | 4.4 | 626 | 2 | AB1328 | probable peptidogl |
| 602 | 74 | 4.5 | 346 | 2 | H84512 | hypothetical prote | 675 | 73.5 | 4.4 | 654 | 2 | T33044 | hypothetical prote |
| 603 | 74 | 4.5 | 390 | 2 | C97889 | UDPglucose 6-dehyd | 676 | 73.5 | 4.4 | 696 | 2 | G81262 | probable integral |
| 604 | 74 | 4.5 | 397 | 2 | E97176 | N-terminal domain | 677 | 73.5 | 4.4 | 708 | 2 | F87245 | penicillin-binding |
| 605 | 74 | 4.5 | 412 | 1 | AJBORS | argininosuccinate | 678 | 73.5 | 4.4 | 713 | 2 | T44447 | neuregulin-3 (limp |
| 606 | 74 | 4.5 | 413 | 2 | S28066 | sexual differentia | 679 | 73.5 | 4.4 | 756 | 2 | JCS886 | signaling mediator |
| 607 | 74 | 4.5 | 435 | 2 | T20327 | hypothetical prote | 680 | 73.5 | 4.4 | 799 | 2 | H71255 | probable cell divi |
| 608 | 74 | 4.5 | 437 | 2 | AG1028 | prepinin (imported | 681 | 73.5 | 4.4 | 819 | 2 | B95136 | conserved domain p |
| 609 | 74 | 4.5 | 454 | 2 | T02100 | hypothetical prote | 682 | 73.5 | 4.4 | 901 | 2 | A44825 | phosphoprotein, sy |
| 610 | 74 | 4.5 | 540 | 1 | FOWVHL | gag polyprotein - | 683 | 73.5 | 4.4 | 905 | 2 | T02205 | Lu-ECAM-1 protein |
| 611 | 74 | 4.5 | 575 | 2 | S39484 | DNA-binding protei | 684 | 73.5 | 4.4 | 990 | 2 | H88733 | protein F32E10.3 [|
| 612 | 74 | 4.5 | 586 | 2 | S66697 | probable membrane | 685 | 73.5 | 4.4 | 1004 | 2 | T38074 | hypothetical prote |
| 613 | 74 | 4.5 | 600 | 2 | T06292 | hypothetical prote | 686 | 73.5 | 4.4 | 1139 | 1 | E64234 | cytadherence-acces |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|--------------------|-----|------|-----|------|---|--------|--------------------|
| 687 | 73.5 | 4.4 | 1291 | 2 | T22382 | hypothetical prote | 760 | 72.5 | 4.4 | 642 | 2 | T39607 | fork head protein |
| 688 | 73.5 | 4.4 | 2332 | 2 | T34434 | hypothetical prote | 761 | 72.5 | 4.4 | 648 | 2 | PC4395 | mucin 3 - human [f |
| 689 | 73.5 | 4.4 | 4385 | 2 | T25042 | hypothetical prote | 762 | 72.5 | 4.4 | 657 | 2 | AB2415 | conserved hypothet |
| 690 | 73 | 4.4 | 188 | 2 | C96593 | unknown protein, 9 | 763 | 72.5 | 4.4 | 663 | 2 | T18631 | hypothetical prote |
| 691 | 73 | 4.4 | 198 | 2 | E71837 | protein-export mem | 764 | 72.5 | 4.4 | 710 | 2 | A99486 | ABC transporter, b |
| 692 | 73 | 4.4 | 213 | 2 | S43949 | histone H1 - mouse | 765 | 72.5 | 4.4 | 728 | 2 | F72693 | probable phosphoes |
| 693 | 73 | 4.4 | 260 | 2 | I50109 | gastrulation prote | 766 | 72.5 | 4.4 | 729 | 2 | G96559 | hypothetical prote |
| 694 | 73 | 4.4 | 288 | 2 | JQ2365 | polyprotein - Bean | 767 | 72.5 | 4.4 | 743 | 2 | D86888 | penicillin-binding |
| 695 | 73 | 4.4 | 315 | 1 | HN2VZV | hemagglutinin prec | 768 | 72.5 | 4.4 | 749 | 2 | T44946 | transducer protein |
| 696 | 73 | 4.4 | 326 | 2 | G86333 | hypothetical prote | 769 | 72.5 | 4.4 | 896 | 2 | S36326 | membrane antigen g |
| 697 | 73 | 4.4 | 327 | 2 | S20074 | promastigote surfa | 770 | 72.5 | 4.4 | 907 | 1 | QQBE21 | clathrin assembly |
| 698 | 73 | 4.4 | 359 | 2 | S42787 | serine/threonine-r | 771 | 72.5 | 4.4 | 915 | 2 | S36327 | clathrin assembly |
| 699 | 73 | 4.4 | 369 | 2 | E84291 | iron (III) ABC tra | 772 | 72.5 | 4.4 | 944 | 2 | C70839 | probable mmp13 pro |
| 700 | 73 | 4.4 | 422 | 2 | A55417 | synaptotagmin II - | 773 | 72.5 | 4.4 | 982 | 2 | AS3253 | microtubule-associ |
| 701 | 73 | 4.4 | 428 | 1 | Q4ECAD | damX protein (aroS | 774 | 72.5 | 4.4 | 1016 | 1 | JS0428 | NAD ADP-ribosyltra |
| 702 | 73 | 4.4 | 441 | 2 | A43555 | GAP-43-related pro | 775 | 72.5 | 4.4 | 1036 | 2 | S73601 | protein P200 - Myc |
| 703 | 73 | 4.4 | 448 | 2 | G88639 | protein C34H4.2 [i | 776 | 72.5 | 4.4 | 1116 | 2 | S77213 | DNA-directed DNA p |
| 704 | 73 | 4.4 | 461 | 2 | T51044 | related to spore c | 777 | 72.5 | 4.4 | 1148 | 2 | T09073 | splicing factor Si |
| 705 | 73 | 4.4 | 469 | 2 | E64456 | hypothetical prote | 778 | 72.5 | 4.4 | 1152 | 2 | A33183 | microtubule-associ |
| 706 | 73 | 4.4 | 482 | 2 | A44997 | merozoite surface | 779 | 72.5 | 4.4 | 1180 | 2 | E86719 | hypothetical prote |
| 707 | 73 | 4.4 | 486 | 2 | S66097 | cell-cycle protein | 780 | 72.5 | 4.4 | 1199 | 2 | A40670 | nuclear envelope p |
| 708 | 73 | 4.4 | 486 | 2 | A89927 | elastin binding pr | 781 | 72.5 | 4.4 | 1219 | 2 | T14578 | nucleoporin Nup153 |
| 709 | 73 | 4.4 | 492 | 1 | CHBOA3 | gamma-aminobutyric | 782 | 72.5 | 4.4 | 1222 | 2 | T22490 | hypothetical prote |
| 710 | 73 | 4.4 | 496 | 2 | E90181 | hypothetical prote | 783 | 72.5 | 4.4 | 1309 | 1 | BVB9D9 | RAD9 protein - yea |
| 711 | 73 | 4.4 | 509 | 1 | A37259 | membrane glycoprot | 784 | 72.5 | 4.4 | 1312 | 2 | E95006 | beta-N-acetylhexos |
| 712 | 73 | 4.4 | 550 | 2 | C75557 | hypothetical prote | 785 | 72.5 | 4.4 | 1555 | 2 | T18688 | hypothetical prote |
| 713 | 73 | 4.4 | 558 | 2 | A98199 | translocated intim | 786 | 72.5 | 4.4 | 1635 | 2 | T14075 | chitinase (EC 3.2. |
| 714 | 73 | 4.4 | 558 | 2 | E86045 | probable transloca | 787 | 72.5 | 4.4 | 1847 | 2 | T18308 | probable vitelloge |
| 715 | 73 | 4.4 | 600 | 2 | E72027 | phosphoenolpyruvat | 788 | 72.5 | 4.4 | 1973 | 2 | G89608 | protein B0272.5 [i |
| 716 | 73 | 4.4 | 600 | 2 | A86597 | phosphoenolpyruvat | 789 | 72.5 | 4.4 | 1973 | 2 | T18686 | hypothetical prote |
| 717 | 73 | 4.4 | 669 | 2 | A46511 | envelope protein - | 790 | 72.5 | 4.4 | 2305 | 2 | B89608 | protein C23Fu2.1 [|
| 718 | 73 | 4.4 | 688 | 2 | A43491 | env polyprotein - | 791 | 72.5 | 4.4 | 2305 | 2 | T15571 | hypothetical prote |
| 719 | 73 | 4.4 | 720 | 2 | T51007 | hypothetical prote | 792 | 72.5 | 4.4 | 2314 | 1 | A46151 | protein-tyrosine-p |
| 720 | 73 | 4.4 | 728 | 2 | T20561 | hypothetical prote | 793 | 72.5 | 4.4 | 2897 | 2 | B48666 | cell proliferation |
| 721 | 73 | 4.4 | 781 | 2 | T49472 | hormone-sensitive | 794 | 72.5 | 4.4 | 3069 | 2 | H70656 | fatty-acid synthas |
| 722 | 73 | 4.4 | 814 | 2 | T33140 | hypothetical prote | 795 | 72.5 | 4.4 | 3256 | 2 | A48666 | cell proliferation |
| 723 | 73 | 4.4 | 880 | 2 | S44833 | F54H12.5 protein - | 796 | 72 | 4.3 | 139 | 2 | G98226 | hypothetical prote |
| 724 | 73 | 4.4 | 918 | 2 | A36337 | membrane glycoprot | 797 | 72 | 4.3 | 139 | 2 | AI3059 | hypothetical prote |
| 725 | 73 | 4.4 | 932 | 1 | VGEBEC | glycoprotein gi pr | 798 | 72 | 4.3 | 159 | 2 | F72758 | hypothetical prote |
| 726 | 73 | 4.4 | 958 | 2 | T10679 | hypothetical prote | 799 | 72 | 4.3 | 197 | 2 | T33525 | hypothetical prote |
| 727 | 73 | 4.4 | 1055 | 2 | H90023 | hypothetical prote | 800 | 72 | 4.3 | 199 | 2 | JE0351 | OX40 ligand protei |
| 728 | 73 | 4.4 | 1071 | 2 | T22327 | hypothetical prote | 801 | 72 | 4.3 | 236 | 2 | T03041 | hypothetical prote |
| 729 | 73 | 4.4 | 1256 | 1 | A43829 | muramidase-release | 802 | 72 | 4.3 | 246 | 2 | PC4397 | mucin 3 T10 - huma |
| 730 | 73 | 4.4 | 1320 | 2 | JC5630 | TCOF1 protein - mo | 803 | 72 | 4.3 | 282 | 2 | B37994 | RF2 protein - saim |
| 731 | 73 | 4.4 | 1345 | 2 | S46817 | hypothetical prote | 804 | 72 | 4.3 | 317 | 1 | GEHUS | bone sialoprotein |
| 732 | 73 | 4.4 | 1702 | 2 | AF1450 | IgA-specific metal | 805 | 72 | 4.3 | 322 | 2 | G69946 | phage-related prot |
| 733 | 73 | 4.4 | 1993 | 2 | GNNYH4 | probable peptidogl | 806 | 72 | 4.3 | 324 | 2 | S36646 | integrin-associate |
| 734 | 73 | 4.4 | 2179 | 1 | GNNYH4 | genome polyprotein | 807 | 72 | 4.3 | 330 | 2 | T49644 | hypothetical prote |
| 735 | 73 | 4.4 | 2285 | 2 | T12796 | probable transglyc | 808 | 72 | 4.3 | 334 | 2 | T19637 | hypothetical prote |
| 736 | 73 | 4.4 | 2416 | 2 | T13825 | adenomatous polypo | 809 | 72 | 4.3 | 425 | 1 | FOVGGC | gag polyprotein - |
| 737 | 73 | 4.4 | 2468 | 2 | A83412 | hypothetical prote | 810 | 72 | 4.3 | 428 | 2 | D86003 | hypothetical prote |
| 738 | 73 | 4.4 | 2722 | 2 | T20532 | hypothetical prote | 811 | 72 | 4.3 | 428 | 2 | F91157 | probable membrane |
| 739 | 72.5 | 4.4 | 263 | 2 | I51225 | snail1 protein - z | 812 | 72 | 4.3 | 460 | 2 | A84154 | amino acid transpo |
| 740 | 72.5 | 4.4 | 303 | 2 | S40973 | hypothetical prote | 813 | 72 | 4.3 | 508 | 2 | A33378 | fasciclin III prec |
| 741 | 72.5 | 4.4 | 314 | 2 | B95034 | dihydropterate sy | 814 | 72 | 4.3 | 509 | 2 | A96563 | probable protein k |
| 742 | 72.5 | 4.4 | 321 | 2 | T26153 | hypothetical prote | 815 | 72 | 4.3 | 544 | 2 | S07144 | neurofilament trip |
| 743 | 72.5 | 4.4 | 328 | 2 | S35336 | transcription fact | 816 | 72 | 4.3 | 548 | 1 | QRFGL | neurofilament trip |
| 744 | 72.5 | 4.4 | 340 | 2 | C90894 | probable LAC1-type | 817 | 72 | 4.3 | 576 | 2 | T38293 | hypothetical serin |
| 745 | 72.5 | 4.4 | 340 | 2 | F85723 | probable LAC1-type | 818 | 72 | 4.3 | 587 | 2 | S38634 | chaperonin, mitoch |
| 746 | 72.5 | 4.4 | 340 | 2 | G64905 | sugar-binding prot | 819 | 72 | 4.3 | 592 | 2 | D70863 | hypothetical prote |
| 747 | 72.5 | 4.4 | 382 | 2 | T27058 | hypothetical prote | 820 | 72 | 4.3 | 622 | 2 | A90570 | lipoprotein (impor |
| 748 | 72.5 | 4.4 | 391 | 2 | T35470 | probable integral | 821 | 72 | 4.3 | 674 | 2 | S74506 | ribonuclease E - S |
| 749 | 72.5 | 4.4 | 406 | 2 | T23934 | hypothetical prote | 822 | 72 | 4.3 | 677 | 2 | T00369 | hypothetical prote |
| 750 | 72.5 | 4.4 | 415 | 2 | T32490 | hypothetical prote | 823 | 72 | 4.3 | 736 | 2 | T41259 | hypothetical prote |
| 751 | 72.5 | 4.4 | 463 | 1 | A36479 | milk fat globule m | 824 | 72 | 4.3 | 770 | 1 | S30293 | transcription fact |
| 752 | 72.5 | 4.4 | 487 | 2 | S40820 | probable permease | 825 | 72 | 4.3 | 817 | 2 | T21336 | hypothetical prote |
| 753 | 72.5 | 4.4 | 498 | 1 | VGXPLM | surface glycoprote | 826 | 72 | 4.3 | 855 | 2 | D98004 | histidine Motif-Co |
| 754 | 72.5 | 4.4 | 499 | 2 | A12449 | hypothetical prote | 827 | 72 | 4.3 | 876 | 2 | T49801 | hypothetical prote |
| 755 | 72.5 | 4.4 | 507 | 2 | S05542 | hypothetical prote | 828 | 72 | 4.3 | 884 | 2 | T20405 | hypothetical prote |
| 756 | 72.5 | 4.4 | 511 | 2 | T35194 | transcription init | 829 | 72 | 4.3 | 958 | 2 | T26258 | hypothetical prote |
| 757 | 72.5 | 4.4 | 560 | 2 | T32661 | hypothetical prote | 830 | 72 | 4.3 | 1034 | 2 | S49947 | SM74 protein - yea |
| 758 | 72.5 | 4.4 | 580 | 2 | B38418 | jockey protein 1 - | 831 | 72 | 4.3 | 1038 | 2 | AG2187 | hypothetical prote |
| 759 | 72.5 | 4.4 | 610 | 2 | S35049 | mucin JER57 - huma | 832 | 72 | 4.3 | 1146 | 2 | S46837 | hypothetical prote |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|--------|--------------------|-----|------|-----|------|---|--------|--------------------|
| 833 | 72 | 4.3 | 1176 | 2 | T49482 | hypothetical prote | 906 | 71 | 4.3 | 370 | 2 | S49008 | fork head protein |
| 834 | 72 | 4.3 | 1196 | 2 | H85061 | hypothetical prote | 907 | 71 | 4.3 | 378 | 2 | S00842 | leukostatin precu |
| 835 | 72 | 4.3 | 1203 | 2 | T17415 | mycelial surface a | 908 | 71 | 4.3 | 379 | 1 | S71571 | alcohol dehydroge |
| 836 | 72 | 4.3 | 1388 | 2 | A57655 | tim (timeless) pro | 909 | 71 | 4.3 | 394 | 2 | T21752 | hypothetical prote |
| 837 | 72 | 4.3 | 1489 | 2 | T31108 | cyst germination s | 910 | 71 | 4.3 | 410 | 1 | S68153 | cellulase (EC 3.2. |
| 838 | 72 | 4.3 | 1547 | 2 | T28657 | blackjack protein, | 911 | 71 | 4.3 | 415 | 2 | A35560 | lysosomal membrane |
| 839 | 72 | 4.3 | 1570 | 2 | T18272 | 1-phosphatidylos | 912 | 71 | 4.3 | 433 | 2 | S19996 | hypothetical prote |
| 840 | 72 | 4.3 | 1778 | 2 | T50074 | probable nucleopor | 913 | 71 | 4.3 | 455 | 2 | A87913 | protein B0205.10 [|
| 841 | 72 | 4.3 | 1829 | 2 | T24583 | hypothetical prote | 914 | 71 | 4.3 | 462 | 2 | T32751 | hypothetical prote |
| 842 | 72 | 4.3 | 2441 | 2 | S39161 | CREB-binding prote | 915 | 71 | 4.3 | 474 | 1 | TVPTCA | Ca2+/calmodulin-de |
| 843 | 72 | 4.3 | 2578 | 2 | A56922 | transcription fact | 916 | 71 | 4.3 | 496 | 2 | T30976 | hypothetical prote |
| 844 | 72 | 4.3 | 2971 | 2 | T08026 | hypothetical prote | 917 | 71 | 4.3 | 500 | 1 | S60929 | probable aldehyde |
| 845 | 71.5 | 4.3 | 141 | 2 | A38196 | non-structural hyp | 918 | 71 | 4.3 | 502 | 2 | I52637 | Ca2+/calmodulin-de |
| 846 | 71.5 | 4.3 | 146 | 2 | S52800 | hypothetical prote | 919 | 71 | 4.3 | 530 | 2 | S62439 | hypothetical serin |
| 847 | 71.5 | 4.3 | 162 | 2 | C84948 | NADH2 dehydrogenas | 920 | 71 | 4.3 | 534 | 2 | G97703 | hypothetical prote |
| 848 | 71.5 | 4.3 | 164 | 2 | A26490 | histone H1. macron | 921 | 71 | 4.3 | 622 | 2 | T15467 | hypothetical prote |
| 849 | 71.5 | 4.3 | 178 | 2 | QJ1547 | stripe disease-spe | 922 | 71 | 4.3 | 626 | 2 | NEHUIA | platelet glycoprot |
| 850 | 71.5 | 4.3 | 231 | 2 | F84311 | hypothetical prote | 923 | 71 | 4.3 | 665 | 1 | VCMVVR | env polyprotein pr |
| 851 | 71.5 | 4.3 | 263 | 2 | S01360 | salivary glue prot | 924 | 71 | 4.3 | 669 | 2 | T08827 | hypothetical prote |
| 852 | 71.5 | 4.3 | 313 | 2 | QJ1862 | 31R protein - vari | 925 | 71 | 4.3 | 670 | 2 | T13739 | probable hormone r |
| 853 | 71.5 | 4.3 | 313 | 2 | T28598 | hypothetical prote | 926 | 71 | 4.3 | 711 | 2 | T48335 | receptor like prot |
| 854 | 71.5 | 4.3 | 313 | 2 | A34677 | secretory pathway | 927 | 71 | 4.3 | 719 | 2 | T27977 | lin-15A protein - |
| 855 | 71.5 | 4.3 | 363 | 2 | T25278 | hypothetical prote | 928 | 71 | 4.3 | 738 | 2 | I40719 | isocitrate dehydro |
| 856 | 71.5 | 4.3 | 372 | 2 | F43674 | US7 protein - huma | 929 | 71 | 4.3 | 751 | 2 | T21967 | hypothetical prote |
| 857 | 71.5 | 4.3 | 373 | 2 | S43455 | hypothetical prote | 930 | 71 | 4.3 | 767 | 1 | JU0474 | glucan 1,4-alpha-g |
| 858 | 71.5 | 4.3 | 381 | 2 | S65212 | hypothetical prote | 931 | 71 | 4.3 | 778 | 1 | ALBYG | glucan 1,4-alpha-g |
| 859 | 71.5 | 4.3 | 385 | 2 | T38113 | hypothetical serin | 932 | 71 | 4.3 | 784 | 2 | AH2560 | hypothetical prote |
| 860 | 71.5 | 4.3 | 392 | 2 | T49471 | mucin (muc3) relat | 933 | 71 | 4.3 | 785 | 2 | S54016 | SOK2 protein - yea |
| 861 | 71.5 | 4.3 | 393 | 2 | T49578 | hypothetical prote | 934 | 71 | 4.3 | 791 | 2 | T39924 | hypothetical prote |
| 862 | 71.5 | 4.3 | 395 | 2 | I52842 | CD43 Lp-3 antigen | 935 | 71 | 4.3 | 814 | 1 | KXBY | protein T23E7.2b [|
| 863 | 71.5 | 4.3 | 395 | 2 | A43545 | leukostatin CD43 p | 936 | 71 | 4.3 | 880 | 2 | D89756 | hypothetical prote |
| 864 | 71.5 | 4.3 | 408 | 2 | A46712 | glycoprotein Iia - | 937 | 71 | 4.3 | 968 | 2 | T00353 | hypothetical prote |
| 865 | 71.5 | 4.3 | 414 | 2 | B84600 | hypothetical prote | 938 | 71 | 4.3 | 977 | 2 | H84469 | hypothetical prote |
| 866 | 71.5 | 4.3 | 423 | 2 | T22865 | hypothetical prote | 939 | 71 | 4.3 | 982 | 2 | T19171 | hypothetical prote |
| 867 | 71.5 | 4.3 | 442 | 1 | S11712 | transcription init | 940 | 71 | 4.3 | 1032 | 2 | T18293 | guanylate kinase-1 |
| 868 | 71.5 | 4.3 | 443 | 1 | D64584 | heat shock protein | 941 | 71 | 4.3 | 1200 | 1 | SNPSO | ice nucleation pro |
| 869 | 71.5 | 4.3 | 466 | 2 | A10957 | chromosomal replic | 942 | 71 | 4.3 | 1204 | 2 | C75015 | probable pyrolysin |
| 870 | 71.5 | 4.3 | 482 | 2 | T48397 | S-receptor kinase- | 943 | 71 | 4.3 | 1244 | 2 | T19615 | hypothetical prote |
| 871 | 71.5 | 4.3 | 503 | 2 | G75262 | hypothetical prote | 944 | 71 | 4.3 | 1256 | 2 | G97902 | alpha-amylase (EC |
| 872 | 71.5 | 4.3 | 507 | 2 | T50398 | hypothetical serin | 945 | 71 | 4.3 | 1302 | 2 | T23236 | hypothetical prote |
| 873 | 71.5 | 4.3 | 540 | 1 | A55145 | thiamine-phosphate | 946 | 71 | 4.3 | 1326 | 2 | H89134 | protein F25G6.9 [1 |
| 874 | 71.5 | 4.3 | 584 | 2 | T19565 | hypothetical prote | 947 | 71 | 4.3 | 1367 | 2 | T33819 | hypothetical prote |
| 875 | 71.5 | 4.3 | 631 | 2 | I52257 | episialin - mouse | 948 | 71 | 4.3 | 1533 | 2 | T00344 | sister chromatid c |
| 876 | 71.5 | 4.3 | 661 | 1 | VCMVCB | env polyprotein - | 949 | 71 | 4.3 | 1583 | 2 | S59644 | major blood-stage |
| 877 | 71.5 | 4.3 | 665 | 2 | E81444 | probable methyl-ac | 950 | 71 | 4.3 | 1751 | 2 | A45604 | hypothetical prote |
| 878 | 71.5 | 4.3 | 675 | 2 | T47378 | probable transposa | 951 | 71 | 4.3 | 1819 | 2 | T32008 | probable fatty-aci |
| 879 | 71.5 | 4.3 | 755 | 2 | T20950 | hypothetical prote | 952 | 71 | 4.3 | 1842 | 2 | T43409 | fatty acid synthas |
| 880 | 71.5 | 4.3 | 760 | 1 | S07896 | transcription fact | 953 | 71 | 4.3 | 1842 | 2 | T38781 | host cell factor C |
| 881 | 71.5 | 4.3 | 882 | 2 | T01168 | hypothetical prote | 954 | 71 | 4.3 | 2035 | 2 | A40718 | probable transform |
| 882 | 71.5 | 4.3 | 1043 | 2 | T23875 | hypothetical prote | 955 | 71 | 4.3 | 2090 | 2 | S26058 | hypothetical prote |
| 883 | 71.5 | 4.3 | 1121 | 2 | T03764 | myosin-I binding p | 956 | 71 | 4.3 | 2848 | 2 | T32550 | hypothetical prote |
| 884 | 71.5 | 4.3 | 1156 | 2 | T43326 | germline RNA helic | 957 | 71 | 4.3 | 2957 | 2 | T33152 | hypothetical prote |
| 885 | 71.5 | 4.3 | 1172 | 2 | T32759 | hypothetical prote | 958 | 71 | 4.3 | 3035 | 1 | I46646 | ryanodine receptor |
| 886 | 71.5 | 4.3 | 1234 | 2 | T31623 | hypothetical prote | 959 | 70.5 | 4.3 | 118 | 2 | S49913 | cryptogein - Phyto |
| 887 | 71.5 | 4.3 | 1260 | 2 | A87046 | hypothetical prote | 960 | 70.5 | 4.3 | 128 | 2 | A35690 | mucin 3 (clone S1B |
| 888 | 71.5 | 4.3 | 1297 | 2 | T30274 | proteoliasin - se | 961 | 70.5 | 4.3 | 146 | 1 | ERAD32 | early E3 16k glyco |
| 889 | 71.5 | 4.3 | 1459 | 2 | T32271 | hypothetical prote | 962 | 70.5 | 4.3 | 172 | 2 | F49247 | merozoite surface |
| 890 | 71.5 | 4.3 | 1557 | 2 | D41214 | protein-tyrosine-p | 963 | 70.5 | 4.3 | 174 | 2 | E49247 | merozoite surface |
| 891 | 71.5 | 4.3 | 1566 | 2 | T20058 | hypothetical prote | 964 | 70.5 | 4.3 | 193 | 2 | G90125 | hypothetical prote |
| 892 | 71.5 | 4.3 | 1630 | 2 | C41214 | protein-tyrosine-p | 965 | 70.5 | 4.3 | 204 | 2 | S67295 | probable membrane |
| 893 | 71 | 4.3 | 98 | 2 | S53367 | mucin SAC (clone M | 966 | 70.5 | 4.3 | 209 | 2 | C89850 | conserved hypothet |
| 894 | 71 | 4.3 | 135 | 2 | T49996 | AtAGP4 - Arabidops | 967 | 70.5 | 4.3 | 211 | 2 | C71482 | probable endonucle |
| 895 | 71 | 4.3 | 168 | 2 | JN0073 | glycophorin A - mo | 968 | 70.5 | 4.3 | 212 | 2 | F86545 | hypothetical prote |
| 896 | 71 | 4.3 | 177 | 2 | G75285 | hypothetical prote | 969 | 70.5 | 4.3 | 212 | 2 | F27077 | hypothetical prote |
| 897 | 71 | 4.3 | 213 | 2 | A86228 | hypothetical prote | 970 | 70.5 | 4.3 | 236 | 2 | PC4396 | mucin 3 T9 - human |
| 898 | 71 | 4.3 | 240 | 2 | T33698 | hypothetical prote | 971 | 70.5 | 4.3 | 255 | 2 | I46606 | MHC SLA-DQ alpha c |
| 899 | 71 | 4.3 | 242 | 2 | T27226 | hypothetical prote | 972 | 70.5 | 4.3 | 264 | 2 | T09377 | hypothetical prote |
| 900 | 71 | 4.3 | 304 | 2 | T15922 | hypothetical prote | 973 | 70.5 | 4.3 | 284 | 2 | T28018 | hypothetical prote |
| 901 | 71 | 4.3 | 310 | 2 | T20535 | hypothetical prote | 974 | 70.5 | 4.3 | 288 | 2 | T41112 | hypothetical prote |
| 902 | 71 | 4.3 | 329 | 2 | T43012 | conserved hypothet | 975 | 70.5 | 4.3 | 308 | 2 | T29756 | hypothetical prote |
| 903 | 71 | 4.3 | 343 | 2 | S75435 | hypothetical prote | 976 | 70.5 | 4.3 | 312 | 2 | T25994 | hypothetical prote |
| 904 | 71 | 4.3 | 349 | 2 | T05857 | hypothetical prote | 977 | 70.5 | 4.3 | 314 | 2 | B97905 | dihydropteroate sy |
| 905 | 71 | 4.3 | 360 | 2 | T33835 | hypothetical prote | 978 | 70.5 | 4.3 | 316 | 1 | A43661 | dihydropteroate sy |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|--------|--------------------|------|------|-----|------|---|--------|--------------------|
| 979 | 70.5 | 4.3 | 321 | 2 | T19259 | hypothetical prote | 1052 | 70 | 4.2 | 350 | 2 | S22456 | hydroxyproline-ric |
| 980 | 70.5 | 4.3 | 330 | 2 | S28102 | rlx protein - Stap | 1053 | 70 | 4.2 | 350 | 2 | AH3043 | dehydrogenase Atu3 |
| 981 | 70.5 | 4.3 | 350 | 2 | A10139 | UTP-hexose-1-phosp | 1054 | 70 | 4.2 | 350 | 2 | D98242 | lipopolysaccharide |
| 982 | 70.5 | 4.3 | 380 | 1 | D34285 | ubiquinol-cytochro | 1055 | 70 | 4.2 | 355 | 2 | B26883 | neural cell adhesi |
| 983 | 70.5 | 4.3 | 382 | 2 | A28067 | lysosomal membra | 1056 | 70 | 4.2 | 357 | 2 | E72245 | hydrolase, ana/hip |
| 984 | 70.5 | 4.3 | 385 | 2 | F70591 | probable KefB prot | 1057 | 70 | 4.2 | 358 | 2 | A88082 | protein T05A8.7 li |
| 985 | 70.5 | 4.3 | 393 | 2 | S62335 | I71-7 protein - fr | 1058 | 70 | 4.2 | 360 | 2 | T08673 | hypothetical prote |
| 986 | 70.5 | 4.3 | 402 | 2 | E86185 | hypothetical prote | 1059 | 70 | 4.2 | 409 | 2 | T18726 | hypothetical prote |
| 987 | 70.5 | 4.3 | 403 | 1 | S35541 | transcription fact | 1060 | 70 | 4.2 | 424 | 2 | I51210 | synaptotagmin p65 |
| 988 | 70.5 | 4.3 | 427 | 2 | C88883 | protein JC8.10 lim | 1061 | 70 | 4.2 | 425 | 2 | T18723 | hypothetical prote |
| 989 | 70.5 | 4.3 | 431 | 1 | JC2002 | transcription fact | 1062 | 70 | 4.2 | 426 | 2 | T04985 | probable transamin |
| 990 | 70.5 | 4.3 | 433 | 2 | T11911 | NADH2 dehydrogenas | 1063 | 70 | 4.2 | 445 | 2 | S45713 | potassium channel |
| 991 | 70.5 | 4.3 | 433 | 2 | S37790 | probable serine/th | 1064 | 70 | 4.2 | 446 | 2 | S66268 | inward rectifier p |
| 992 | 70.5 | 4.3 | 445 | 2 | T23199 | hypothetical prote | 1065 | 70 | 4.2 | 455 | 2 | A80181 | hypothetical prote |
| 993 | 70.5 | 4.3 | 462 | 2 | A48933 | gamma-aminobutyric | 1066 | 70 | 4.2 | 456 | 2 | T38221 | hypothetical serin |
| 994 | 70.5 | 4.3 | 465 | 2 | H82345 | mannose-1-phosphat | 1067 | 70 | 4.2 | 458 | 2 | T26630 | hypothetical prote |
| 995 | 70.5 | 4.3 | 491 | 2 | T52398 | hypothetical prote | 1068 | 70 | 4.2 | 461 | 2 | T38698 | noc1 protein - fis |
| 996 | 70.5 | 4.3 | 522 | 2 | S41819 | nucleoporin p62 - | 1069 | 70 | 4.2 | 462 | 2 | T19830 | hypothetical prote |
| 997 | 70.5 | 4.3 | 526 | 2 | A34896 | adenylate cyclase- | 1070 | 70 | 4.2 | 487 | 2 | A11505 | hypothetical cell |
| 998 | 70.5 | 4.3 | 526 | 2 | C84552 | hypothetical prote | 1071 | 70 | 4.2 | 497 | 2 | T51195 | hypothetical prote |
| 999 | 70.5 | 4.3 | 562 | 2 | A85042 | hypothetical prote | 1072 | 70 | 4.2 | 529 | 2 | S18453 | variant surface gl |
| 1000 | 70.5 | 4.3 | 608 | 2 | A46312 | gag polyprotein - | 1073 | 70 | 4.2 | 542 | 2 | B47022 | chitinase (EC 3.2. |
| 1001 | 70.5 | 4.3 | 616 | 2 | T29234 | hypothetical prote | 1074 | 70 | 4.2 | 584 | 2 | JC7809 | sulfakinin recepto |
| 1002 | 70.5 | 4.3 | 629 | 2 | AE1525 | probable peptidogl | 1075 | 70 | 4.2 | 589 | 2 | A10684 | hypothetical prote |
| 1003 | 70.5 | 4.3 | 649 | 2 | T24505 | hypothetical prote | 1076 | 70 | 4.2 | 599 | 2 | G71481 | probable phosphoen |
| 1004 | 70.5 | 4.3 | 675 | 2 | D85065 | receptor protein k | 1077 | 70 | 4.2 | 609 | 2 | S62518 | hypothetical prote |
| 1005 | 70.5 | 4.3 | 716 | 2 | T28998 | hypothetical prote | 1078 | 70 | 4.2 | 611 | 2 | T22456 | hypothetical prote |
| 1006 | 70.5 | 4.3 | 809 | 2 | T18970 | hypothetical prote | 1079 | 70 | 4.2 | 613 | 2 | B90294 | hypothetical prote |
| 1007 | 70.5 | 4.3 | 814 | 2 | F59430 | GTPase regulator a | 1080 | 70 | 4.2 | 617 | 2 | T15408 | hypothetical prote |
| 1008 | 70.5 | 4.3 | 839 | 2 | I50590 | class I INCENP pr | 1081 | 70 | 4.2 | 625 | 2 | S34035 | hypothetical prote |
| 1009 | 70.5 | 4.3 | 846 | 2 | T38840 | hypothetical trp-a | 1082 | 70 | 4.2 | 651 | 2 | S18874 | nucleolin - Africa |
| 1010 | 70.5 | 4.3 | 874 | 2 | B86322 | F6A14.8 protein - | 1083 | 70 | 4.2 | 653 | 2 | E86787 | hypothetical prote |
| 1011 | 70.5 | 4.3 | 877 | 2 | I50591 | class II INCENP pr | 1084 | 70 | 4.2 | 662 | 2 | T50464 | glucose-regulated |
| 1012 | 70.5 | 4.3 | 893 | 2 | T18271 | hypothetical prote | 1085 | 70 | 4.2 | 697 | 2 | E96752 | hypothetical prote |
| 1013 | 70.5 | 4.3 | 899 | 2 | C84765 | hypothetical prote | 1086 | 70 | 4.2 | 706 | 2 | S33761 | transferrin precu |
| 1014 | 70.5 | 4.3 | 910 | 1 | S73361 | dnaJ homolog prote | 1087 | 70 | 4.2 | 714 | 2 | T22454 | hypothetical prote |
| 1015 | 70.5 | 4.3 | 942 | 2 | S53963 | MCS1 protein - yea | 1088 | 70 | 4.2 | 753 | 2 | T24869 | hypothetical prote |
| 1016 | 70.5 | 4.3 | 979 | 1 | A35913 | regulatory factor | 1089 | 70 | 4.2 | 768 | 2 | E86417 | unknown protein, 5 |
| 1017 | 70.5 | 4.3 | 999 | 1 | IUHUG3 | desmoglein 3 precu | 1090 | 70 | 4.2 | 770 | 2 | T51024 | related to CH22 zi |
| 1018 | 70.5 | 4.3 | 1015 | 2 | JC6552 | DNA topoisomerase | 1091 | 70 | 4.2 | 822 | 2 | T51049 | related to nucleol |
| 1019 | 70.5 | 4.3 | 1028 | 2 | E85089 | probable transposo | 1092 | 70 | 4.2 | 823 | 2 | F90914 | hypothetical prote |
| 1020 | 70.5 | 4.3 | 1032 | 2 | G89427 | protein T08D2.3 li | 1093 | 70 | 4.2 | 835 | 2 | JC6140 | cell surface-assoc |
| 1021 | 70.5 | 4.3 | 1052 | 2 | C64221 | hypothetical 114K | 1094 | 70 | 4.2 | 937 | 2 | A56517 | nucleoporin Nup98 |
| 1022 | 70.5 | 4.3 | 1106 | 2 | T31742 | hypothetical prote | 1095 | 70 | 4.2 | 971 | 2 | T19431 | hypothetical prote |
| 1023 | 70.5 | 4.3 | 1115 | 2 | A47541 | protein kinase IRE | 1096 | 70 | 4.2 | 971 | 2 | F88448 | protein C45G9.10 l |
| 1024 | 70.5 | 4.3 | 1123 | 2 | T18270 | hypothetical prote | 1097 | 70 | 4.2 | 1004 | 2 | A55142 | myosin-light-chain |
| 1025 | 70.5 | 4.3 | 1131 | 2 | T15787 | hypothetical prote | 1098 | 70 | 4.2 | 1186 | 2 | T19050 | hypothetical prote |
| 1026 | 70.5 | 4.3 | 1221 | 2 | A10193 | ribonuclease E (EC | 1099 | 70 | 4.2 | 1213 | 2 | A41724 | limb deformity (ld |
| 1027 | 70.5 | 4.3 | 1520 | 2 | T44231 | hypothetical prote | 1100 | 70 | 4.2 | 1274 | 2 | JN0015 | trp protein - frui |
| 1028 | 70.5 | 4.3 | 1603 | 2 | S17983 | gene posterior sex | 1101 | 70 | 4.2 | 1275 | 2 | JU0092 | trp protein - frui |
| 1029 | 70.5 | 4.3 | 1742 | 2 | T17120 | cellulase (EC 3.2. | 1102 | 70 | 4.2 | 1415 | 2 | T08945 | hypothetical prote |
| 1030 | 70.5 | 4.3 | 1872 | 2 | T00339 | hypothetical prote | 1103 | 70 | 4.2 | 1420 | 1 | A44361 | amiloride-sensitiv |
| 1031 | 70.5 | 4.3 | 2271 | 2 | F90073 | hypothetical prote | 1104 | 70 | 4.2 | 1589 | 2 | C44766 | defective chorion- |
| 1032 | 70.5 | 4.3 | 2717 | 2 | A34203 | DNA-binding protei | 1105 | 70 | 4.2 | 1784 | 2 | T10532 | gag-pol polyprotei |
| 1033 | 70.5 | 4.3 | 3054 | 1 | GNBVEV | genome polyprotein | 1106 | 70 | 4.2 | 1868 | 2 | S48938 | hypothetical prote |
| 1034 | 70 | 4.2 | 147 | 2 | JC7938 | type II antifreeze | 1107 | 70 | 4.2 | 2440 | 2 | S39162 | transcription coac |
| 1035 | 70 | 4.2 | 148 | 2 | T32622 | hypothetical prote | 1108 | 70 | 4.2 | 3163 | 1 | JQ1895 | genome polyprotein |
| 1036 | 70 | 4.2 | 150 | 2 | T52587 | probable arabinoga | 1109 | 69.5 | 4.2 | 120 | 1 | W4WL42 | E4 protein - human |
| 1037 | 70 | 4.2 | 150 | 2 | T48611 | agp6 protein - Ara | 1110 | 69.5 | 4.2 | 124 | 2 | E84613 | hypothetical prote |
| 1038 | 70 | 4.2 | 209 | 2 | AB2218 | hypothetical prote | 1111 | 69.5 | 4.2 | 146 | 2 | S52810 | hypothetical prote |
| 1039 | 70 | 4.2 | 210 | 2 | JC7830 | cytokine-inducible | 1112 | 69.5 | 4.2 | 171 | 2 | H86413 | hypothetical prote |
| 1040 | 70 | 4.2 | 214 | 2 | A46629 | mucin 6, gastric (| 1113 | 69.5 | 4.2 | 202 | 2 | A82378 | hypothetical prote |
| 1041 | 70 | 4.2 | 221 | 2 | T47592 | hypothetical prote | 1114 | 69.5 | 4.2 | 217 | 2 | S01358 | salivary glue prot |
| 1042 | 70 | 4.2 | 234 | 2 | G64858 | probable membrane | 1115 | 69.5 | 4.2 | 219 | 2 | B72291 | hypothetical prote |
| 1043 | 70 | 4.2 | 239 | 2 | B83709 | hypothetical prote | 1116 | 69.5 | 4.2 | 266 | 2 | H55590 | hypothetical prote |
| 1044 | 70 | 4.2 | 256 | 2 | AC2283 | hypothetical prote | 1117 | 69.5 | 4.2 | 271 | 2 | B96773 | hypothetical prote |
| 1045 | 70 | 4.2 | 298 | 2 | C55223 | minor tail protein | 1118 | 69.5 | 4.2 | 299 | 2 | G70784 | probable mmpS3 pro |
| 1046 | 70 | 4.2 | 310 | 2 | T26267 | hypothetical prote | 1119 | 69.5 | 4.2 | 313 | 2 | H36854 | hemagglutinin - va |
| 1047 | 70 | 4.2 | 311 | 2 | H96002 | probable sugar kin | 1120 | 69.5 | 4.2 | 316 | 2 | S58719 | probable membrane |
| 1048 | 70 | 4.2 | 321 | 2 | T42750 | hypothetical prote | 1121 | 69.5 | 4.2 | 326 | 2 | I48351 | fos-related antige |
| 1049 | 70 | 4.2 | 329 | 2 | S38082 | pathogenesis-relat | 1122 | 69.5 | 4.2 | 332 | 2 | F69437 | hypothetical prote |
| 1050 | 70 | 4.2 | 333 | 2 | G98297 | ribose ABC transpo | 1123 | 69.5 | 4.2 | 338 | 2 | S28004 | probable cell surf |
| 1051 | 70 | 4.2 | 333 | 2 | AH2985 | ABC transporter, m | 1124 | 69.5 | 4.2 | 364 | 2 | T32589 | hypothetical prote |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|--------|--------------------|------|------|-----|------|---|--------|--------------------|
| 1125 | 69.5 | 4.2 | 372 | 1 | Q0B588 | glycoprotein I pre | 1198 | 69 | 4.2 | 416 | 2 | T34279 | hypothetical prote |
| 1126 | 69.5 | 4.2 | 372 | 2 | T06745 | hypothetical prote | 1199 | 69 | 4.2 | 423 | 2 | T44258 | transducer protein |
| 1127 | 69.5 | 4.2 | 400 | 2 | T32705 | hypothetical prote | 1200 | 69 | 4.2 | 424 | 1 | VGBEE9 | glycoprotein gp63 |
| 1128 | 69.5 | 4.2 | 417 | 2 | AD0200 | isocitrate dehydro | 1201 | 69 | 4.2 | 427 | 2 | E83711 | hypothetical prote |
| 1129 | 69.5 | 4.2 | 423 | 2 | T24383 | hypothetical prote | 1202 | 69 | 4.2 | 431 | 2 | G86277 | Fl41l7.11 protein |
| 1130 | 69.5 | 4.2 | 425 | 2 | T24111 | hypothetical prote | 1203 | 69 | 4.2 | 443 | 2 | T14916 | mitosis-specific c |
| 1131 | 69.5 | 4.2 | 427 | 2 | T38526 | ubiquitin regulato | 1204 | 69 | 4.2 | 467 | 2 | T26195 | hypothetical prote |
| 1132 | 69.5 | 4.2 | 441 | 2 | C75076 | heme biosynthesis | 1205 | 69 | 4.2 | 483 | 2 | G86902 | dextranucrase (EC |
| 1133 | 69.5 | 4.2 | 450 | 2 | C90608 | hypothetical prote | 1206 | 69 | 4.2 | 486 | 2 | D64474 | hypothetical prote |
| 1134 | 69.5 | 4.2 | 458 | 2 | F86433 | protein T17H7.5 (i | 1207 | 69 | 4.2 | 490 | 1 | C57150 | NADP-reducing hydr |
| 1135 | 69.5 | 4.2 | 503 | 1 | VMUT1B | variant surface gl | 1208 | 69 | 4.2 | 495 | 2 | T38959 | hypothetical prote |
| 1136 | 69.5 | 4.2 | 514 | 2 | A44100 | cell adhesion mole | 1209 | 69 | 4.2 | 511 | 2 | I50114 | early growth respo |
| 1137 | 69.5 | 4.2 | 514 | 2 | A31643 | cell adhesion 80K | 1210 | 69 | 4.2 | 513 | 2 | S50915 | SiN3 protein-bindi |
| 1138 | 69.5 | 4.2 | 519 | 2 | S69989 | unspecific monooxy | 1211 | 69 | 4.2 | 525 | 2 | A35596 | nuclear pore glyco |
| 1139 | 69.5 | 4.2 | 520 | 2 | S14600 | E2 glycoprotein pr | 1212 | 69 | 4.2 | 538 | 2 | S60645 | NADH2 dehydrogenas |
| 1140 | 69.5 | 4.2 | 532 | 2 | G70986 | probable coA ligas | 1213 | 69 | 4.2 | 555 | 2 | B41492 | 58K antigen - Rick |
| 1141 | 69.5 | 4.2 | 537 | 2 | B97013 | and cellulose-bind | 1214 | 69 | 4.2 | 556 | 2 | S06838 | gamma-aminobutyric |
| 1142 | 69.5 | 4.2 | 538 | 2 | AG2902 | conserved hypothet | 1215 | 69 | 4.2 | 556 | 2 | S51892 | probable membrane |
| 1143 | 69.5 | 4.2 | 550 | 2 | H97677 | hypothetical prote | 1216 | 69 | 4.2 | 583 | 2 | T18999 | hypothetical prote |
| 1144 | 69.5 | 4.2 | 551 | 2 | G95176 | conserved hypothet | 1217 | 69 | 4.2 | 610 | 1 | I46001 | C4b-binding protei |
| 1145 | 69.5 | 4.2 | 552 | 2 | T25593 | hypothetical prote | 1218 | 69 | 4.2 | 611 | 2 | A53418 | calmegin precursor |
| 1146 | 69.5 | 4.2 | 568 | 2 | A34891 | Ig heavy chain pre | 1219 | 69 | 4.2 | 647 | 2 | B34457 | 204 protein - mous |
| 1147 | 69.5 | 4.2 | 574 | 2 | A86365 | probable auxin tra | 1220 | 69 | 4.2 | 650 | 2 | S22835 | alpha-egglutinin - |
| 1148 | 69.5 | 4.2 | 593 | 2 | S55189 | hypothetical prote | 1221 | 69 | 4.2 | 651 | 2 | T21175 | hypothetical prote |
| 1149 | 69.5 | 4.2 | 593 | 2 | T28865 | hypothetical prote | 1222 | 69 | 4.2 | 652 | 2 | S50210 | surface layer prot |
| 1150 | 69.5 | 4.2 | 610 | 2 | S59394 | protein kinase RCK | 1223 | 69 | 4.2 | 658 | 2 | T41309 | hypothetical threo |
| 1151 | 69.5 | 4.2 | 611 | 2 | A54086 | calnexin-t - mouse | 1224 | 69 | 4.2 | 670 | 2 | F84540 | hypothetical prote |
| 1152 | 69.5 | 4.2 | 629 | 2 | S20516 | dnak-type molecula | 1225 | 69 | 4.2 | 677 | 2 | S54561 | RNA14 protein - ye |
| 1153 | 69.5 | 4.2 | 640 | 2 | T25367 | hypothetical prote | 1226 | 69 | 4.2 | 725 | 2 | E96592 | hypothetical prote |
| 1154 | 69.5 | 4.2 | 645 | 2 | S41372 | dnak-type molecula | 1227 | 69 | 4.2 | 739 | 2 | H72364 | aspartokinase II - |
| 1155 | 69.5 | 4.2 | 646 | 2 | T19206 | hypothetical prote | 1228 | 69 | 4.2 | 790 | 2 | T34293 | hypothetical prote |
| 1156 | 69.5 | 4.2 | 658 | 2 | JC8011 | G protein-coupled | 1229 | 69 | 4.2 | 793 | 1 | KXRTF | furin (EC 3.4.21.7 |
| 1157 | 69.5 | 4.2 | 675 | 2 | T03744 | myoD protein inhib | 1230 | 69 | 4.2 | 814 | 2 | T49207 | receptor kinase-li |
| 1158 | 69.5 | 4.2 | 719 | 2 | T47727 | hypothetical prote | 1231 | 69 | 4.2 | 825 | 2 | S26706 | transcription fact |
| 1159 | 69.5 | 4.2 | 736 | 2 | T19366 | hypothetical prote | 1232 | 69 | 4.2 | 836 | 2 | T21631 | hypothetical prote |
| 1160 | 69.5 | 4.2 | 782 | 2 | A82940 | hypothetical prote | 1233 | 69 | 4.2 | 854 | 1 | QRHYLD | LDL receptor precu |
| 1161 | 69.5 | 4.2 | 816 | 2 | A9151 | fibroblast growth | 1234 | 69 | 4.2 | 871 | 2 | T28706 | hypothetical prote |
| 1162 | 69.5 | 4.2 | 833 | 2 | AF2089 | hypothetical prote | 1235 | 69 | 4.2 | 879 | 1 | QRRTLD | LDL receptor precu |
| 1163 | 69.5 | 4.2 | 844 | 2 | B64678 | NADH2 dehydrogenas | 1236 | 69 | 4.2 | 903 | 1 | VGBEK1 | glycoprotein B pre |
| 1164 | 69.5 | 4.2 | 850 | 1 | MMHUE4 | erythrocyte membra | 1237 | 69 | 4.2 | 988 | 2 | A40628 | probable transposa |
| 1165 | 69.5 | 4.2 | 852 | 2 | T46091 | hypothetical prote | 1238 | 69 | 4.2 | 995 | 2 | T27327 | hypothetical prote |
| 1166 | 69.5 | 4.2 | 862 | 2 | T48289 | hypothetical prote | 1239 | 69 | 4.2 | 1007 | 2 | JC8066 | hypothetical prote |
| 1167 | 69.5 | 4.2 | 871 | 2 | S47518 | cadherin - African | 1240 | 69 | 4.2 | 1157 | 2 | A55152 | mannose receptor p |
| 1168 | 69.5 | 4.2 | 942 | 2 | T19553 | hypothetical prote | 1241 | 69 | 4.2 | 1203 | 2 | T41294 | hypothetical prote |
| 1169 | 69.5 | 4.2 | 993 | 2 | AE1905 | outer membrane sec | 1242 | 69 | 4.2 | 1204 | 2 | F81158 | exodeoxyribonuclea |
| 1170 | 69.5 | 4.2 | 1051 | 2 | JC4091 | glycoprotein A - p | 1243 | 69 | 4.2 | 1215 | 2 | S60904 | hypothetical prote |
| 1171 | 69.5 | 4.2 | 1087 | 1 | QPNWSH | neurofilament trip | 1244 | 69 | 4.2 | 1360 | 2 | T34302 | cell polarity prot |
| 1172 | 69.5 | 4.2 | 1132 | 2 | T43483 | translation initia | 1245 | 69 | 4.2 | 1385 | 2 | T13415 | hypothetical prote |
| 1173 | 69.5 | 4.2 | 1460 | 2 | S48457 | nucleoporin RAT7 - | 1246 | 69 | 4.2 | 1455 | 1 | A48925 | hypothetical prote |
| 1174 | 69.5 | 4.2 | 1502 | 2 | S45429 | probable membrane | 1247 | 69 | 4.2 | 1624 | 2 | T25592 | hypothetical prote |
| 1175 | 69.5 | 4.2 | 1522 | 2 | S48904 | probable purine nu | 1248 | 69 | 4.2 | 1633 | 2 | T01879 | hypothetical prote |
| 1176 | 69.5 | 4.2 | 1870 | 2 | D88486 | protein F20H11.2 (| 1249 | 69 | 4.2 | 1680 | 2 | T41628 | probable transcrip |
| 1177 | 69.5 | 4.2 | 1875 | 2 | S38173 | myosin-like protei | 1250 | 69 | 4.2 | 1758 | 2 | S57015 | probable purine nu |
| 1178 | 69.5 | 4.2 | 1857 | 2 | A45627 | myosin heavy chain | 1251 | 69 | 4.2 | 1804 | 2 | H96597 | hypothetical prote |
| 1179 | 69.5 | 4.2 | 2894 | 2 | C64474 | hypothetical prote | 1252 | 69 | 4.2 | 1819 | 2 | D97033 | uncharacterized pr |
| 1180 | 69.5 | 4.2 | 4199 | 2 | S76412 | hypothetical prote | 1253 | 69 | 4.2 | 1963 | 1 | MMKW | myosin heavy chain |
| 1181 | 69 | 4.2 | 171 | 2 | T31478 | hypothetical prote | 1254 | 69 | 4.2 | 2067 | 2 | A42854 | probable spindle p |
| 1182 | 69 | 4.2 | 234 | 2 | T35448 | hypothetical prote | 1255 | 69 | 4.2 | 2329 | 2 | S44625 | C50C3.6 protein - |
| 1183 | 69 | 4.2 | 255 | 2 | T22429 | hypothetical prote | 1256 | 69 | 4.2 | 2361 | 2 | T25752 | hypothetical prote |
| 1184 | 69 | 4.2 | 258 | 2 | S23106 | p1A protein - shi | 1257 | 69 | 4.2 | 2464 | 1 | QRMSP1 | microtubule-associ |
| 1185 | 69 | 4.2 | 284 | 2 | T06241 | histone H1 (clone | 1258 | 68.5 | 4.1 | 168 | 2 | S52994 | arabinogalactan-li |
| 1186 | 69 | 4.2 | 299 | 2 | S44554 | citrate transport | 1259 | 68.5 | 4.1 | 189 | 1 | ERAD75 | early B3 20.6K gly |
| 1187 | 69 | 4.2 | 303 | 2 | S29185 | sodium channel pro | 1260 | 68.5 | 4.1 | 189 | 2 | JX0235 | core protein MGC-2 |
| 1188 | 69 | 4.2 | 339 | 2 | S08981 | malate dehydrogena | 1261 | 68.5 | 4.1 | 204 | 2 | S51232 | gibberellin-respon |
| 1189 | 69 | 4.2 | 339 | 2 | F97121 | probable membrans- | 1262 | 68.5 | 4.1 | 218 | 2 | AH1837 | hypothetical prote |
| 1190 | 69 | 4.2 | 343 | 2 | G86709 | hypothetical prote | 1263 | 68.5 | 4.1 | 246 | 2 | S47805 | hypothetical 27.4K |
| 1191 | 69 | 4.2 | 344 | 1 | RWRTC2 | T-cell surface gly | 1264 | 68.5 | 4.1 | 246 | 2 | D91186 | probable outer mem |
| 1192 | 69 | 4.2 | 356 | 2 | S73315 | protoporphyryn IX | 1265 | 68.5 | 4.1 | 246 | 2 | C86033 | probable outer mem |
| 1193 | 69 | 4.2 | 371 | 1 | F0MVCS | gag polyprotein - | 1266 | 68.5 | 4.1 | 257 | 2 | C84890 | hypothetical prote |
| 1194 | 69 | 4.2 | 382 | 2 | S71669 | finger protein MIG | 1267 | 68.5 | 4.1 | 261 | 2 | D84262 | hypothetical prote |
| 1195 | 69 | 4.2 | 387 | 2 | T15462 | hypothetical prote | 1268 | 68.5 | 4.1 | 280 | 2 | AE2031 | gamma-tocopherol m |
| 1196 | 69 | 4.2 | 396 | 2 | T26987 | hypothetical prote | 1269 | 68.5 | 4.1 | 287 | 2 | S45662 | histone H1 - tomat |
| 1197 | 69 | 4.2 | 400 | 1 | A39822 | leukosialin precur | 1270 | 68.5 | 4.1 | 287 | 2 | D95406 | hypothetical prote |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|--------|---------------------|------|----|-----|-----|---|--------|----------------------|
| 1271 | 68.5 | 4.1 | 288 | 2 | T22846 | hypothetical prote | 1344 | 68 | 4.1 | 208 | 1 | HSRT1T | histone H1t - rat |
| 1272 | 68.5 | 4.1 | 318 | 2 | T20063 | hypothetical prote | 1345 | 68 | 4.1 | 211 | 2 | H72608 | hypothetical prote |
| 1273 | 68.5 | 4.1 | 345 | 2 | T12344 | NADH2 dehydrogenas | 1346 | 68 | 4.1 | 228 | 2 | T33579 | hypothetical prote |
| 1274 | 68.5 | 4.1 | 349 | 2 | T42965 | glycoprotein - ate | 1347 | 68 | 4.1 | 245 | 2 | D81977 | hypothetical prote |
| 1275 | 68.5 | 4.1 | 358 | 2 | G70814 | probable far protey | 1348 | 68 | 4.1 | 246 | 2 | H90833 | major tail protein |
| 1276 | 68.5 | 4.1 | 379 | 2 | T35403 | probable polyprote | 1349 | 68 | 4.1 | 256 | 2 | B85691 | probable tail comp |
| 1277 | 68.5 | 4.1 | 385 | 2 | H97239 | polyferredoxin [im | 1350 | 68 | 4.1 | 268 | 2 | T32740 | hypothetical prote |
| 1278 | 68.5 | 4.1 | 385 | 2 | JC7783 | RAD 23B protein - | 1351 | 68 | 4.1 | 288 | 2 | T21790 | hypothetical prote |
| 1279 | 68.5 | 4.1 | 394 | 2 | G84206 | hypothetical prote | 1352 | 68 | 4.1 | 295 | 2 | S50316 | CIN5 protein - yea |
| 1280 | 68.5 | 4.1 | 408 | 1 | QRHUBE | beta-3-adrenergic | 1353 | 68 | 4.1 | 301 | 2 | H70644 | hypothetical prote |
| 1281 | 68.5 | 4.1 | 412 | 1 | AJMSRS | argininosuccinate | 1354 | 68 | 4.1 | 304 | 2 | G89790 | hypothetical prote |
| 1282 | 68.5 | 4.1 | 412 | 1 | AJRTRS | argininosuccinate | 1355 | 68 | 4.1 | 333 | 2 | T15367 | hypothetical prote |
| 1283 | 68.5 | 4.1 | 413 | 2 | T04520 | hypothetical prote | 1356 | 68 | 4.1 | 339 | 2 | AHQ050 | probable periplasm |
| 1284 | 68.5 | 4.1 | 414 | 1 | QRHUB3 | beta-3-adrenergic | 1357 | 68 | 4.1 | 360 | 2 | S69063 | probable membrane |
| 1285 | 68.5 | 4.1 | 414 | 2 | G64091 | cell division prot | 1358 | 68 | 4.1 | 372 | 2 | T45628 | glycerophosphodis |
| 1286 | 68.5 | 4.1 | 420 | 2 | A89962 | protein F59A7.1 li | 1359 | 68 | 4.1 | 378 | 2 | S61992 | SLG1 protein - yea |
| 1287 | 68.5 | 4.1 | 421 | 2 | S09595 | synaptotagmin P65 | 1360 | 68 | 4.1 | 380 | 1 | S51826 | alcohol dehydrogen |
| 1288 | 68.5 | 4.1 | 426 | 2 | A35641 | 5-aminoimidazole r | 1361 | 68 | 4.1 | 384 | 2 | H64161 | hypothetical prote |
| 1289 | 68.5 | 4.1 | 435 | 2 | C86340 | protein F2D10.28 (| 1362 | 68 | 4.1 | 387 | 2 | A56275 | 1,3-propanediol de |
| 1290 | 68.5 | 4.1 | 435 | 2 | T25350 | hypothetical prote | 1363 | 68 | 4.1 | 388 | 2 | T43019 | probable DNA-bindi |
| 1291 | 68.5 | 4.1 | 443 | 2 | F71929 | heat shock protein | 1364 | 68 | 4.1 | 402 | 2 | T20595 | hypothetical prote |
| 1292 | 68.5 | 4.1 | 458 | 2 | AC0121 | probable exported | 1365 | 68 | 4.1 | 416 | 2 | T19149 | hypothetical prote |
| 1293 | 68.5 | 4.1 | 498 | 1 | VGXPLA | surface glycoprote | 1366 | 68 | 4.1 | 420 | 2 | T42616 | hypothetical prote - |
| 1294 | 68.5 | 4.1 | 502 | 2 | T21935 | hypothetical prote | 1367 | 68 | 4.1 | 422 | 1 | BMHUIY | synaptotagmin I - |
| 1295 | 68.5 | 4.1 | 509 | 2 | T48459 | cytochrome P450-li | 1368 | 68 | 4.1 | 423 | 2 | T14531 | S-locus-specific g |
| 1296 | 68.5 | 4.1 | 514 | 1 | A47692 | fumarate hydratase | 1369 | 68 | 4.1 | 423 | 2 | H84257 | Htr13 transducer [|
| 1297 | 68.5 | 4.1 | 527 | 2 | T26732 | hypothetical prote | 1370 | 68 | 4.1 | 426 | 2 | I48379 | gene hb protein - |
| 1298 | 68.5 | 4.1 | 535 | 2 | B84443 | hypothetical prote | 1371 | 68 | 4.1 | 427 | 2 | JH0413 | synaptotagmin o-p6 |
| 1299 | 68.5 | 4.1 | 536 | 2 | AG1482 | hypothetical prote | 1372 | 68 | 4.1 | 452 | 2 | T46147 | zinc finger protei |
| 1300 | 68.5 | 4.1 | 553 | 2 | A49364 | 59 protein, brain | 1373 | 68 | 4.1 | 461 | 2 | D96647 | hypothetical prote |
| 1301 | 68.5 | 4.1 | 573 | 2 | H96744 | probable cytosolic | 1374 | 68 | 4.1 | 461 | 2 | T39862 | hypothetical prote |
| 1302 | 68.5 | 4.1 | 588 | 2 | JC8021 | chitinase (EC 3.2. | 1375 | 68 | 4.1 | 479 | 2 | A84588 | probable tyrosine |
| 1303 | 68.5 | 4.1 | 592 | 2 | T32402 | hypothetical prote | 1376 | 68 | 4.1 | 487 | 1 | S07061 | glutamate receptor |
| 1304 | 68.5 | 4.1 | 594 | 2 | S51412 | hypothetical prote | 1377 | 68 | 4.1 | 493 | 2 | D86652 | IMP dehydrogenase |
| 1305 | 68.5 | 4.1 | 630 | 2 | A39344 | tumor-associated m | 1378 | 68 | 4.1 | 500 | 2 | A11913 | apolipoprotein N-a |
| 1306 | 68.5 | 4.1 | 637 | 2 | T20981 | hypothetical prote | 1379 | 68 | 4.1 | 503 | 2 | T51782 | hypothetical prote |
| 1307 | 68.5 | 4.1 | 647 | 2 | S26386 | transcription fact | 1380 | 68 | 4.1 | 514 | 2 | S18449 | variant surface gl |
| 1308 | 68.5 | 4.1 | 659 | 2 | T40383 | hypothetical prote | 1381 | 68 | 4.1 | 515 | 2 | B84406 | TRK potassium upa |
| 1309 | 68.5 | 4.1 | 668 | 1 | F64370 | ferrous iron trans | 1382 | 68 | 4.1 | 516 | 2 | A31270 | radial spoke prote |
| 1310 | 68.5 | 4.1 | 670 | 2 | S22293 | zinc finger protei | 1383 | 68 | 4.1 | 537 | 1 | F0MVM7 | gag polyprotein - |
| 1311 | 68.5 | 4.1 | 696 | 2 | G71829 | probable outer mem | 1384 | 68 | 4.1 | 543 | 2 | A38093 | transformation-sen |
| 1312 | 68.5 | 4.1 | 697 | 2 | A86402 | protein T22C5.17 (| 1385 | 68 | 4.1 | 550 | 2 | T06379 | SAR DNA-binding pr |
| 1313 | 68.5 | 4.1 | 699 | 2 | T09483 | Cys-rich protein R | 1386 | 68 | 4.1 | 562 | 2 | B41035 | chitinase (EC 3.2. |
| 1314 | 68.5 | 4.1 | 721 | 2 | E70766 | hypothetical prote | 1387 | 68 | 4.1 | 562 | 2 | S50371 | chitinase (EC 3.2. |
| 1315 | 68.5 | 4.1 | 725 | 2 | T01268 | leucine-rich repea | 1388 | 68 | 4.1 | 573 | 2 | S50661 | hypothetical prote |
| 1316 | 68.5 | 4.1 | 737 | 2 | AG2156 | hypothetical prote | 1389 | 68 | 4.1 | 576 | 2 | S75958 | hypothetical prote |
| 1317 | 68.5 | 4.1 | 751 | 2 | AC2098 | hypothetical prote | 1390 | 68 | 4.1 | 581 | 2 | T22455 | hypothetical prote |
| 1318 | 68.5 | 4.1 | 763 | 2 | S55616 | glycoprotein H - e | 1391 | 68 | 4.1 | 590 | 2 | S66956 | hypothetical prote |
| 1319 | 68.5 | 4.1 | 770 | 2 | G88445 | protein C26E6.2 [i | 1392 | 68 | 4.1 | 599 | 1 | A54906 | afamin precursor - |
| 1320 | 68.5 | 4.1 | 795 | 2 | T20609 | hypothetical prote | 1393 | 68 | 4.1 | 600 | 2 | S56744 | mucin (clone pGM7- |
| 1321 | 68.5 | 4.1 | 798 | 2 | T50514 | hypothetical prote | 1394 | 68 | 4.1 | 610 | 2 | T22909 | hypothetical prote |
| 1322 | 68.5 | 4.1 | 825 | 1 | GLHQ | beta-glucosidase (| 1395 | 68 | 4.1 | 621 | 1 | YRNC | monophenol monooxy |
| 1323 | 68.5 | 4.1 | 846 | 2 | S52418 | GRP-binding regula | 1396 | 68 | 4.1 | 623 | 2 | T28051 | hypothetical prote |
| 1324 | 68.5 | 4.1 | 853 | 2 | H70939 | probable nirB prot | 1397 | 68 | 4.1 | 630 | 2 | S77346 | hypothetical prote |
| 1325 | 68.5 | 4.1 | 865 | 2 | AC1966 | hypothetical prote | 1398 | 68 | 4.1 | 632 | 2 | T48616 | hypothetical prote |
| 1326 | 68.5 | 4.1 | 914 | 2 | T25220 | hypothetical prote | 1399 | 68 | 4.1 | 638 | 2 | S36723 | FUN36 protein - ye |
| 1327 | 68.5 | 4.1 | 915 | 2 | T33030 | hypothetical prote | 1400 | 68 | 4.1 | 645 | 2 | T16078 | hypothetical prote |
| 1328 | 68.5 | 4.1 | 925 | 2 | T00781 | hypothetical prote | 1401 | 68 | 4.1 | 647 | 2 | T39141 | hypothetical prote |
| 1329 | 68.5 | 4.1 | 952 | 2 | T18837 | hypothetical prote | 1402 | 68 | 4.1 | 648 | 2 | T04837 | probable serine/th |
| 1330 | 68.5 | 4.1 | 1043 | 2 | T13172 | gag-like protein p | 1403 | 68 | 4.1 | 655 | 1 | A55726 | RNA-binding protei |
| 1331 | 68.5 | 4.1 | 1278 | 2 | A71609 | probable secreted | 1404 | 68 | 4.1 | 659 | 2 | H81431 | methyl-accepting c |
| 1332 | 68.5 | 4.1 | 1285 | 2 | H85041 | hypothetical prote | 1405 | 68 | 4.1 | 659 | 2 | A98085 | hypothetical prote |
| 1333 | 68.5 | 4.1 | 1311 | 2 | A56390 | mannosyl-glycoprot | 1406 | 68 | 4.1 | 662 | 2 | B81251 | probable methyl-ac |
| 1334 | 68.5 | 4.1 | 1435 | 2 | S69632 | regulatory protein | 1407 | 68 | 4.1 | 668 | 2 | B86831 | hypothetical prote |
| 1335 | 68.5 | 4.1 | 1438 | 2 | A48216 | neurexin III-alpha | 1408 | 68 | 4.1 | 669 | 2 | B70186 | translation elonga |
| 1336 | 68.5 | 4.1 | 1444 | 1 | A30588 | 140K adhesin precu | 1409 | 68 | 4.1 | 686 | 2 | S66693 | hypothetical prote |
| 1337 | 68.5 | 4.1 | 1541 | 2 | S46686 | hypothetical prote | 1410 | 68 | 4.1 | 695 | 2 | I51652 | dSRNA-binding prot |
| 1338 | 68.5 | 4.1 | 1791 | 2 | T24089 | hypothetical prote | 1411 | 68 | 4.1 | 698 | 1 | JX0202 | long-chain-fatty-a |
| 1339 | 68.5 | 4.1 | 2114 | 2 | E96505 | hypothetical prote | 1412 | 68 | 4.1 | 709 | 2 | S51793 | disbasic processing |
| 1340 | 68.5 | 4.1 | 2292 | 1 | GNNYEB | genome polyprotein | 1413 | 68 | 4.1 | 730 | 2 | A75486 | hypothetical prote |
| 1341 | 68.5 | 4.1 | 2292 | 1 | GNNYEB | genome polyprotein | 1414 | 68 | 4.1 | 733 | 2 | T01875 | probable long-chain |
| 1342 | 68.5 | 4.1 | 2292 | 2 | S55401 | capsid polyprotein | 1415 | 68 | 4.1 | 752 | 2 | T34355 | hypothetical prote |
| 1343 | 68 | 4.1 | 62 | 2 | S53366 | mucin 5AC (Clone M | 1416 | 68 | 4.1 | 761 | 2 | T03719 | probable thyroid r |


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A;Cross-references: GB:J05163; NID:G200334; PIDN:AAA39923.1; PID:g200335
C;Superfamily: human cell adhesion protein CD44
C;Keywords: cell adhesion; glycoprotein; membrane protein

Query Match      13.4%; Score 222.5; DB 2; Length 365;
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Matches 88; Conservative 56; Mismatches 150; Indels 65; Gaps 14;

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Db 6 WHTAWGLCLQLSLAHPHQIDLVNVCRYAGVFHVKEKGRYSISRTAEADLCQAFNSTLP 65
QY 70 GKQVETALKASFTCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCY 129
Db 66 TMDQMKLALSGFETCRYGFI-EGNVVPIRPHNAICAANHTGVYLLVTSNTSHDYTCF 124
QY 130 NSSDWTNNSCIPHIITTKDPIFNQTATQTTFEIVSDST--YSVASPYST----- 177
Db 125 NASAPPEEDC-----TSVTDLPNSFGPVTITTVNRDGTGRYSKKGEYRTHQEDIDASNI 179
QY 178 ----IPAPTTTPAPAS---TSIPRKKLICVTEVFMETSTWST--ETEPFVENKAAPK- 227
Db 180 DDVSSGSTIEKSTPSEYIILHYTPTEQPTGDDDSFFIRSTLATDRDSKDSRGSRT 239
QY 228 ----NEAAGFGG-----VPTALLVLALLFFGAAGLGFYVVKRYVKA 265
Db 240 VTHGSELAGHSSANQDSGVTTTSGPMRRPQIPWLLIILASL-LALALILAVC-----IAV 293
QY 266 FPTNNKQKQKEMI---ETKVVKEKANSDNPNEESKTKDKNPESKSPKTTVRCLEAE 321
Db 294 NSRRRCQKKLVINGNGTVEDRKPSELN-GEASKSQEMVHLVNKEPSETPDQCMTAD 351

RESULT 4
B38745
cell adhesion molecule CD44 precursor, long form (meta-1) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 09-Jul-2004
C;Accession: B38745; A38745
R;Guenther, U.; Hofmann, M.; Rudy, W.; Reber, S.; Zoeller, M.; Haubmann, I.; M
Cell 65, 13-24, 1991
A;Title: A new variant of glycoprotein CD44 confers metastatic potential to rat
A;Reference number: A38745; MUID:91191552; PMID:1707342
A;Accession: B38745
A;Status: preliminary
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A;Cross-references: UNIPROT:P26051; GB:M61874; NID:g576534; PIDN:AAA53534.1; PR
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A;Status: preliminary
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A;Cross-references: GB:M61875
C;Keywords: cell adhesion

Query Match      13.4%; Score 222; DB 2; Length 503;
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QY 75 ETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQFAAYCYNSDST 134
Db 70 ELALRKFGFETCRYGFI-EGHWVPIRPHNAICAANNTGVYILLASNTSHDYTCFNASAP 128
QY 135 WTNSCIPHIITTKDPIFNQTATQTTFEIVSDST--YSVASPYST-----IPAPT----- 182
Db 129 LEEDC-----TSVTDLPNSFGPVTITTVNRDGTGRYSKKGEYRTHQEDIDASNIIDEDVS 183
QY 183 -----TTPPA-PASTSIPRKKLICVTEVFMETSTWST--ETEPFVENKAAPKFAEAGF 233

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Db 184 SGTIEKSPGEGVILLHTDPTSOPTGDRDDAFFIGTLATATPWPWSAHTKQNBERTQW 243
QY 234 GGV---PTALLVLALLFFGAAGLGCYVVKVYK--AFPTNKNQOKEMETKVVKEKA 288
Db 244 NPIHSNPEVLQTTTWTMTIDRNSTGAHGNWTQEPQPFNNHVEYQDEE-ETPHATSTTW 302
QY 289 NDSNPNNEESKTKD-----NPBESKSP 310
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RESULT 5
A35616
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C:Species: Cricetinae gen. sp. (hamster)
C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C:Accession: A35616
R:Aruffo, A.; Stamenkovic, I.; Melnick, M.; Underhill, C.B.; Seed, B.
Cell 61, 1303-1313, 1990
A:Title: CD44 is the principal cell surface receptor for hyaluronate.
A:Reference number: A35616; MUID:90304889; PMID:1694723
A:Accession: A35616
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-362 <ARU>
A:Cross-references: UNIPROT:P20944
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; glycoprotein; transmembrane protein

Query Match 13.1%; Score 217.5; DB 2; Length 362;
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Matches 88; Conservative 46; Mismatches 149; Indels 63; Gaps 12;

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Db 18 SLAHEQIDNITCRVAGVFHVEKNGRYSISRTEADLCQAFNSTLPTMDQMYNALSKGFE 77

QY 84 TCSYGVGDGVFVVISRISPNPKCGKNGVGLWVKVPSRQFAAYCVNNSDVTWNSCIPEI 143
Db 78 TCRYGFI-EGHVVIPIQPNALCAANHGTGYILTSNTS-HYDYTCFNASAPLEEDC---- 131

QY 144 ITTKDPIFNQTATQTEFIVSDST-YSVASPYST-----IPAPTTTPPAPAS----- 190
Db 132 -TSVTDLPNSFEGPVTITVNRDGTYSKKGEYRTHQEDIDASNTTDDVSSGSSSEKST 190

QY 191 -----TSIPRKKLICVTEVFMETSTWSTE-----TTPFVEN 222
Db 191 SGGYVFHTYLTPIHSTADQDDPYFTGSTWATRDQSSMDPRGNSLTVTDGSKLTGHSSGN 250

QY 223 KAAFKNEAAGFG---GVPTALLVLALLFFGAAGLGCYVVKVYKAFPTNKNQOKEMIE 279
Db 251 QDSGANTTSRGRKQPOIPEWLIVLASL-LALALILAVC-----IAVNSRRCGQKKLVI 304

QY 280 TKVVKEEKANDSNPNNEESKTKDNPE-----ESKSPSKTTVRCLEAE 321
Db 305 NS--GNGKVEDRKPSLNGEASKSQBMVHLVNKEPSETPDQFWTAD 348

RESULT 6
A53286
cell-surface glycoprotein CD44 precursor - bovine
N:Alternate names: CD44 protein
C:Species: Bos primigenius taurus (cattle)
C>Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A53286; S21213
R:Bosworth, B.T.; St John, T.; Gallatin, W.M.; Harp, J.A.
Mol. Immunol. 28, 1131-1135, 1991
A:Title: Sequence of the bovine CD44 cDNA: comparison with human and mouse sequences.
A:Reference number: A53286; MUID:92017904; PMID:1922105
A:Accession: A53286
A:Molecule type: mRNA
A:Residues: 1-366 <BOS>

A:Cross-references: UNIPROT:Q29423; EMBL:X67881; NID:g186; PIDN:CAA44675.1; PID:g187
A>Note: sequence extracted from NCBI backbone (NCBIN:63418, NCBIP:63419)
C:Superfamily: human cell adhesion protein CD44
C:Keywords: cell adhesion; glycoprotein; transmembrane protein
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-366/Product: cell-surface glycoprotein CD44 #status predicted <MAT>
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F:25-57,100,110,120,222,260/Binding site: carbohydrate (Asn) (covalent) #status predicted:
Query Match 12.6%; Score 208.5; DB 2; Length 366;
Best Local Similarity 23.8%; Pred. No. 4.1e-09;
Matches 81; Conservative 44; Mismatches 142; Indels 73; Gaps 11;

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QY 80 ASFTCSYGVGDGVFVVISRISPNPKCGKNGVGLWVKVPSRQFAAYCVNNSDVTWNSC 139
Db 72 IGFETCRYGFI-EGHVVIPIHPNSICAANTGVILTSNTS-QYDTTCFNASAPPGEDC 129

QY 140 IPEIITTKDPIFNQTATQTEFIVSDST-YSVASPYSTIP-----APTTPPAPAS 190
Db 130 -----TSVTDLPNAEGPITITVNRDGTTRYTKGEYRTPNEDINPSVSPSPDDENS 184

QY 191 TSIPRKKLICVTEVF-----METSTMSTETEPFVENKAAFK 227
Db 185 SGSPSERSTSGYSIFHTHTLPTVHPSPRRPWSQRAENTSDTRDYGSSHDPSGRSVYTHA 244

QY 228 NEAAGFGG-----VPTALLVLALLFFGAAGLGCYVVKVYKAFKPP 269
Db 245 SESAGHSGSBEHGANTTSGPMRKQPOIPEWLIIILASL-LALALILAVC-----IAVNSRR 298

QY 270 NKNQOKEMIEYKVKVEEKANDSNPNNEESKTKDNPEESKS 309
Db 299 RCGQKKKLVIN-----NGNGTMEERKPSGLNGEASKS 330

RESULT 7
JH0417
cell adhesion molecule CD44 - human
C:Species: Homo sapiens (man)
C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 09-Jul-2004
C:Accession: JH0417; A32376; G02251; A32377
R:Harn, H.J.; Isola, N.; Cooper, D.L.
Biochem. Biophys. Res. Commun. 178, 1127-1134, 1991
A:Title: The multispecific cell adhesion molecule CD44 is represented in reticulocyte cDNA
A:Reference number: JH0417; MUID:91337049; PMID:1840487
A:Accession: JH0417
A:Molecule type: mRNA
A:Residues: 1-361 <HAR>
A:Cross-references: UNIPROT:Q29493; GB:M59040; NID:g180129; PIDN:AAA51950.1; PID:g180130
A:Experimental source: reticulocyte
A>Note: the authors translated the codon ATG for residues 63, 66 and 239 as Trp and GGA
R:Stamenkovic, I.; Amiot, M.; Pesando, J.M.; Seed, B.
Cell 56, 1057-1062, 1989
A:Title: A lymphocyte molecule implicated in lymph node homing is a member of the cartil
A:Reference number: A32376; MUID:89168434; PMID:2466575
A:Accession: A32376
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-238,'E',240-361 <STA>
A:Cross-references: GB:M24915; NID:g180196; PIDN:AAA35674.1; PID:g180197
R:Boesch, P.P.; Stevens, J.W.; Buckwalter, J.A.; Midura, R.J.
submitted to the EMBL Data Library, November 1995
A:Reference number: H00921
A:Accession: G02251
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-25,'M',27-108,'S',110-361 <BOS>
A:Cross-references: EMBL:U040373; NID:g1101785; PID:g1101786
R:Goldstein, L.A.; Zhou, D.F.H.; Picker, L.J.; Minty, C.N.; Bargatze, R.F.; Ding, J.F.;
Cell 56, 1063-1072, 1989

A:Experimental source: lymphocyte, cell line KG1a
R;Cooper, D.L.; Dougherty, G.; Harn, H.J.; Jackson, S.; Baptist, E.W.; Byers, J.; Datta, Biochem. Biophys. Res. Commun. 182, 569-578, 1992
A:Title: The complex CD44 transcriptional unit: alternative splicing of three internal exons
A:Reference number: PH0859; MUID:92134271; PMID:1734871
A:Accession: PH0859
A:Molecule type: DNA
A:Residues: 223-357 <COO>
R;Brown, T.A.; Bouchard, T.; St. John, T.; Wayner, E.; Carter, W.G. J. Cell Biol. 113, 207-221, 1991
A:Title: Human keratinocytes express a new CD44 core protein (CD44E) as a heparan-sulfate proteoglycan
A:Reference number: A39209; MUID:91177958; PMID:2007624
A:Accession: A39209
A:Molecule type: mRNA
A:Residues: 184-376 <BRO>
A:Cross-references: GB:X55938; NID:929802; PIDN:CAA39404.1; PID:9330047
R;Jackson, D.G.; Buckley, J.; Bell, J.I. J. Biol. Chem. 267, 4732-4739, 1992
A:Title: Multiple variants of the human lymphocyte homing receptor CD44 generated by independent alternative splicing of three internal exons
A:Reference number: A42402; MUID:92165834; PMID:1537855
A:Accession: A42402
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 217-223 288-359 <JAC>
A:Note: sequence extracted from NCBI backbone (NCBIN:83964, NCBIIP:83965)
A:Note: variant B
A:Accession: C42402
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 217-320 <J2>
A:Note: sequence extracted from NCBI backbone (NCBIN:83968, NCBIIP:83969)
A:Note: variant D
R;Shepley, M.P.; Racanelli, V.R. J. Virol. 68, 1301-1308, 1994
A:Title: A monoclonal antibody that blocks poliovirus attachment recognizes the lymphocyte homing receptor CD44
A:Reference number: A53029; MUID:94149816; PMID:7508992
A:Accession: A53029
A:Status: preliminary
A:Molecule type: protein
A:Residues: 67-76, 'X', '78-89 <SHE>
C:Genetics:
A:Gene: GDB:CD44; MDU2; MDU3; MI
A:Cross-references: GDB:120739; OMIM:107269
A:Map position: lipter-11p13
A:Introns: 35/1; 65/1; 133/1
C:Superfamily: human cell adhesion protein CD44
C:Keywords: alternative splicing; cell adhesion; chondroitin sulfate proteoglycan; glycosylation; lymphocyte homing receptor CD44, splice form CD44R1 #status predicted <F>
F;1-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status predicted <F>
F;1-223,288-426/Product: lymphocyte homing receptor CD44, splice form CD44R2 #status predicted <F>
F;299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;354/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
Query Match 12.0%; Score 199.5; DB 2; Length 426;
Best Local Similarity 22.2%; Pred. No. 2.6e-08;
Matches 83; Conservative 48; Mismatches 138; Indels 105; Gaps 12;
QY 25 LRAEELSIQVCRIMGITLVSKKANQQLNFTAKACRLGLSLACKQOVETALKASRET 84
DB 17 LSLAQIDLNITCRFAGVHVEKNRYSISRTEADLCKAFNSTLPTMAOMEKALSIGFET 76
QY 85 CSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSROFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVIPIRHPNSICAAANTGVILTSNTS-QYDYTCFNASAPPEDCTSVTD 134
QY 141 -----PEIITKDPINFQTATQTE-----FI 163
DB 135 LPNADFPGPITITVNRDGRYVQKGEYRNPDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 164 -----VSDST-----YSVASPYSTIPAPTTTPAPASTSIPRRKKLIC 201
DB 195 FYTFSTVHIPEDSPWITDSDIRPTNMDSHSTTLQPTANPNGLVEDLDRGTGLSM 254
QY 202 VTEFVMTSTMSTETETEPFVENK-----AAFKNEAAG 232
DB 255 TTQO-SNSQSFSTSHGLEEDKHPTTTLTSSNRNDVTG 293
Query Match 12.0%; Score 199.5; DB 2; Length 426;
Best Local Similarity 22.2%; Pred. No. 2.6e-08;
Matches 83; Conservative 48; Mismatches 138; Indels 105; Gaps 12;
QY 25 LRAEELSIQVCRIMGITLVSKKANQQLNFTAKACRLGLSLACKQOVETALKASRET 84
DB 17 LSLAQIDLNITCRFAGVHVEKNRYSISRTEADLCKAFNSTLPTMAOMEKALSIGFET 76
QY 85 CSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSROFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVIPIRHPNSICAAANTGVILTSNTS-QYDYTCFNASAPPEDCTSVTD 134
QY 141 -----PEIITKDPINFQTATQTE-----FI 163
DB 135 LPNADFPGPITITVNRDGRYVQKGEYRNPDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 164 -----VSDST-----YSVASPYSTIPAPTTTPAPASTSIPRRKKLIC 201
DB 195 FYTFSTVHIPEDSPWITDSDIRPTNMDSHSTTLQPTANPNGLVEDLDRGTGLSM 254
QY 202 VTEFVMTSTMSTETETEPFVENK-----AAFKNEAAGFGGVP-----TALLVLALL 246

DB 255 TTQO-SNSQSFSTSHGLEEDKHPTTTLTSSNRNDVTGRRDPNHSSEGTLL----- 308
QY 247 FFGAAAGLFCYVKRVKAPFTNKQKQEMIEIKV-----VKEEKANDSNPN-EESKKT 300
DB 309 -----EGYTSYHPHTKESRTFIPVTSAKTSGFGVTAVTVGDSNSNVRSLSG 355
QY 301 DKNPEESKSPSKTT 314
DB 356 DQDTFHPSGSHTT 369
RESULT 11
SI3530
CD44E protein, epithelial - human
C:Species: Homo sapiens (man)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C:Accession: SI3530
R;Stamenkovic, I.; Aruffo, A.; Amiot, M.; Seed, B. EMBO J. 10, 343-348, 1991
A:Title: The hematopoietic and epithelial forms of CD44 are distinct polypeptides with different extracellular domains
A:Reference number: SI3530; MUID:91122041; PMID:1991450
A:Accession: SI3530
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-493 <STA>
A:Cross-references: EMBL:X55150; NID:929800; PIDN:CAA38951.1; PID:929801
C:Keywords: transmembrane protein
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 3.1e-08;
Matches 66; Conservative 39; Mismatches 100; Indels 75; Gaps 8;
QY 25 LRAEELSIQVCRIMGITLVSKKANQQLNFTAKACRLGLSLACKQOVETALKASRET 84
DB 17 LSLAQIDLNITCRFAGVHVEKNRYSISRTEADLCKAFNSTLPTMAOMEKALSIGFET 76
QY 85 CSYGWVGDFVVISRISPNPKCGKNGVGLIWKVPVSROFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVIPIRHPNSICAAANTGVILTSNTS-QYDYTCFNASAPPEDCTSVTD 134
QY 141 -----PEIITKDPINFQTATQTE-----FI 163
DB 135 LPNADFPGPITITVNRDGRYVQKGEYRNPDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 164 -----VSDST-----YSVASPYSTIPAPTTTPAPASTSIPRRKKLIC 201
DB 195 FYTFSTVHIPEDSPWITDSDIRPTNMDSHSTTLQPTANPNGLVEDLDRGTGLSM 254
QY 202 VTEFVMTSTMSTETETEPFVENK-----AAFKNEAAG 232
DB 255 TTQO-SNSQSFSTSHGLEEDKHPTTTLTSSNRNDVTG 293
RESULT 12
I77371
CD44R5 - human
C:Species: Homo sapiens (man)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jul-2000
C:Accession: I77371
R;Tanabe, K.K.; Nishi, T.; Sava, H. Mol. Carcinog. 7, 212-220, 1993
A:Title: Novel variants of CD44 arising from alternative splicing: changes in the CD44 extracellular domain
A:Reference number: I57483; MUID:93356912; PMID:8352881
A:Accession: I77371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-395 <RES>
A:Cross-references: GB:S66400; NID:9435697; PIDN:AAB27919.1; PID:9435700
C:Genetics:
A:Gene: GDB:CD44
A:Cross-references: GDB:120739; OMIM:107269
A:Map position: 11pter-11p13

A;Introns: 257/1
C;Superfamily: human cell adhesion protein CD44

Query Match 11.9%; Score 198; DB 2; Length 395;
Best Local Similarity 23.0%; Pred. No. 3.1e-08;
Matches 85; Conservative 49; Mismatches 145; Indels 90; Gaps 14;

QY 25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTFAKEACRLGLSLAGKQOVETALKASPET 84
DB 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGPET 76
QY 85 CSYGMVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVVIPIHPNSICAANNVTGYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134
QY 141 -----PEIITKDPINFNTQATOTTEFIVSDSYVASPYST 177
DB 135 LPNAFDGPITITIVNRDGTTRYVQKGEYRTNPEDIYPSNPTDDVSSGSSRSSTSGGYI 194
QY 168 --TYSVASPY-----STIPATPTTPPAPASTSI-PRRKKLICVTEFVEMETSTWST 214
DB 195 FYTFSTVHPIDPDESPWITDSTRIPATNMDSHSTTLQPTANPNTGLVEDLDRGTPLSM 254
QY 215 ET-----EPFVENKAAAFNEAAGF-----GG-----VPTALLVLALLFFGA 250
DB 255 TTRDQDTHPSPGSGSTHSGESDGHSGSQEGGANTTSGPIPTPQIPPEWLIIILASL-LAL 313
QY 251 AAGLFCYVYKRVKAPFPFNKNQOKEMIETK---VVKBEKANDSNPNESKTKDK----N 303
DB 314 ALILAVC-----IAVNSRRRCQKKLVINSNGAVEDRKPSGLN-GEASKSQEMVHLVN 367
QY 304 PRESKSPSK 312
DB 368 KESSETPDQ 376

RESULT 13
I37369
epican - human
C;Species: Homo sapiens (man)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 03-Aug-2001
C;Accession: I37369; S24631
R;Kugelman, L.C.; Ganguly, S.; Haggerty, J.G.; Weisman, S.M.; Milstone, L.M.
J. Invest. Dermatol. 99, 866-891, 1992
A;Title: The core protein of epican, a heparan sulfate proteoglycan on keratinocytes, is
A;Note: corrected and republished from J. Invest. Dermatol. 99, 381-385, 1992
A;Reference number: I37369; PMID:1281868
A;Accession: I37369
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-699 <RES>
A;Cross-references: EMBL:X66733; NID:g31190; PID:g31191

Query Match 11.9%; Score 196.5; DB 2; Length 699;
Best Local Similarity 25.4%; Pred. No. 8.3e-08;
Matches 60; Conservative 34; Mismatches 93; Indels 49; Gaps 7;

QY 25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTFAKEACRLGLSLAGKQOVETALKASPET 84
DB 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALSIGPET 76
QY 85 CSYGMVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVVIPIHPNSICAANNVTGYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134
QY 141 -----PEIITKDPINFNTQATOTTEFIVSDSYVASPYST 177
DB 135 LPNAFDGPITITIVNRDGTTRYVQKGEYRTNPEDIYPSNPTDDVSSGSSRSSTSGGY- 193
QY 171 VASPYSTI-PAPTTTPP--APASTSIPIRRKKLICVTEFVEMETSTWSTETEPFVENK 223
DB 194 IFYTFSTVHPIDPDESPWITDSTRIPATSI-----TSSNTISAGWEPNEENE 240

RESULT 14
S24240
lymphocyte surface antigen CD44 precursor - horse
C;Species: Equus caballus (domestic horse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: I46245; S24240
R;Tavernor, A.S.; Deverson, E.V.; Coadwell, W.J.; Lunn, D.P.; Zhang, C.; Davis, W.; Butc
immunogenetics 37, 474-477, 1993
A;Title: Molecular cloning of equine CD44 cDNA by a COS cell expression system.
A;Reference number: I46245; MUID:93170897; PMID:8436424
A;Accession: I46245
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-359 <TA>
A;Cross-references: UNIPROT:Q05078; EMBL:X68662; NID:g1059; PIDN:CAA47331.1; PID:g1060
C;Superfamily: human cell adhesion protein CD44
C;Keywords: surface antigen; transmembrane protein

Query Match 11.2%; Score 186; DB 2; Length 359;
Best Local Similarity 24.6%; Pred. No. 2.5e-07;
Matches 84; Conservative 42; Mismatches 159; Indels 56; Gaps 11;

QY 25 LRAEELSIQVSCRIMGITLVSKKANQQLNFTFAKEACRLGLSLAGKQOVETALKASPET 84
DB 17 LSLAQIDLNITCRFAGVFHVEKNGRYSISRTEAADLCKAFNSTLPTMAQMEKALNIGPET 76
QY 85 CSYGMVGDFVVISRISPNKCGKNGVGLIWKVPVSRQFAAYCYNSSDTWTNSCI---- 140
DB 77 CRYGFI-EGHVVIPIHPNSICAANNVTGYILTSNTS-QYDTYCFNASAPPEEDCTSVTD 134
QY 141 -----PEIIT-----TKDPIFNTQATOTTEFIVSDSYVASPYST 177
DB 135 LPNAFDGPITITIVNRDGTTRYVQKGEYRTNPEDIYPSNPTDDVSSGSSRSSTSGGYSI 194
QY 178 IPA--PTTTP-----PAPASTSIPIRRKKLICVTEFVEMETSTWSTETEPFVENK 223
DB 195 FHTHLPTTRPTQDQSSPMWSDSPEKPTTKDRASGRAQTTHGSETSGHSGSQ---EGG 251
QY 224 AAFKNEAAGFGVPTALLVLALLFFGAAGLGFCYVYKRVKAFPTNKNQOKEMIETK-- 281
DB 252 ASTTSGPIRRRQIPPEWLIIILASL-LALALILAVC-----IAVNSRRRCQKKLVINNGN 305
QY 282 -VVKEEKANDSNPNESKTKDKNPEESKSPKTTVRCLEAE 321
DB 306 GAVDDRKASGLN-GEASKSQEMVHLVNKESSETQDQFWTAD 345

RESULT 15
I50421
aggrecan precursor - chicken
N;Alternate names: cartilage chondroitin sulfate proteoglycan core protein
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I50421; S39796; S27356; A25442; A32002; I50216; A37072; B37072
R;Li, H.; Schwartz, N.B.; Vertel, B.M.
J. Biol. Chem. 268, 23504-23511, 1993
A;Title: cDNA cloning of chick cartilage chondroitin sulfate (aggrecan) core protein and
A;Reference number: I50421; MUID:94043149; PMID:8226878
A;Accession: I50421
A;Status: preliminary;
A;Molecule type: mRNA
A;Residues: 1-2109 <LIX>
A;Cross-references: UNIPROT:P07898; GB:L21913; NID:g416133; PIDN:AAB19128.1; PID:g4161334
R;Chandrasekaran, L.; Tanzer, M.L.
Biochem. J. 296, 885-887, 1993
A;Reference number: S39796; MUID:94107258; PMID:8280087
A;Contents: annotation; erratum
A;Accession: S39796
A;Molecule type: mRNA
A;Residues: 1-361, 'DL', 364-600, 'R', 602-999, 'R', 1001-1028, 'P', 1030-1250, 'D', 1252-1602, 'A',
A;Cross-references: GB:M88101
R;Chandrasekaran, L.; Tanzer, M.L.

| | Query Match | 9.0%; | Score 148.5; | DB 1; | Length 2109; |
|----|-----------------------|---|-------------------|-------|--------------------|
| | Best Local Similarity | 27.0%; | Pred. No. 0.0023; | | |
| | Matches | 74; | Conservative | 27; | Mismatches 104; |
| | | | | | Indels 69; Gaps 13 |
| Qy | 50 | QQLNFTAKEACRLGLSLACKQVETALKASFETCSYGWVDGFV--VISRI SPNPKG | 107 | | |
| Db | 258 | EKFTQEAFDKCHSLGARLATTGELYLAWKQDMCSAGWLADRSVRYPI SRAPN--CG | 315 | | |
| Qy | 108 | KNGYGVV-LIWKVPV-----SRQFAAYCYNSSDTWTNSCIP-----EITTKDPIFWT | 153 | | |
| Db | 316 | GNLVGVRTVYLNPNQOTGYPHPSRYDAICYSGDD--FEALVPGLFTDEVGTGSAFTI | 373 | | |
| Qy | 154 | QTATQT-----TEFIVSDSTYSVASPYSTIPATPTTPTPAPASTSI PRKKLICV | 203 | | |
| Db | 374 | QTVTQTEVELPLPNRVTE--EEARGSIATLEPMBITATATELVEAFVLPD-----LPAT | 426 | | |

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 5, 2005, 17:27:34 ; Search time 137.148 Seconds
(without alignments)
974.620 Million cell updates/sec

Perfect score: 1657

Sequence: 1 MARCFSLVLLTSIWTRLL.....NPESKSPSKTVRCLEAEV 322

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1846076 seqs, 415116000 residues

Total number of hits satisfying chosen parameters: 1846076

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCUT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 3 | 1657 | 100.0 | 322 | 9 | US-09-905-291A-201 |
| 93 | 1657 | 100.0 | 322 | 14 | US-10-223-085-32 |
| 94 | 1657 | 100.0 | 322 | 14 | US-10-223-084-32 |
| 95 | 1657 | 100.0 | 322 | 14 | US-10-223-088-32 |
| 96 | 1657 | 100.0 | 322 | 14 | US-10-223-090-32 |
| 98 | 1657 | 100.0 | 322 | 14 | US-10-223-087-32 |
| 101 | 1657 | 100.0 | 322 | 14 | US-10-223-083-32 |
| 102 | 1657 | 100.0 | 322 | 14 | US-10-079-111-1 |
| 103 | 1657 | 100.0 | 322 | 14 | US-10-223-089-32 |
| 108 | 1657 | 100.0 | 322 | 14 | US-10-299-976-201 |
| 136 | 1657 | 100.0 | 322 | 14 | US-10-063-742-6 |
| 211 | 1657 | 100.0 | 322 | 14 | US-10-299-937-201 |
| 3 | 1657 | 100.0 | 322 | 9 | US-09-905-291A-201 |
| 93 | 1657 | 100.0 | 322 | 14 | US-10-223-085-32 |
| 94 | 1657 | 100.0 | 322 | 14 | US-10-223-084-32 |
| 95 | 1657 | 100.0 | 322 | 14 | US-10-223-088-32 |
| 96 | 1657 | 100.0 | 322 | 14 | US-10-223-090-32 |
| 98 | 1657 | 100.0 | 322 | 14 | US-10-223-087-32 |
| 101 | 1657 | 100.0 | 322 | 14 | US-10-223-083-32 |
| 102 | 1657 | 100.0 | 322 | 14 | US-10-079-111-1 |
| 103 | 1657 | 100.0 | 322 | 14 | US-10-223-089-32 |
| 108 | 1657 | 100.0 | 322 | 14 | US-10-299-976-201 |
| 136 | 1657 | 100.0 | 322 | 14 | US-10-063-742-6 |
| 211 | 1657 | 100.0 | 322 | 14 | US-10-299-937-201 |

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|--------------------|-------|-----|----|---------------------|--------------------|
| Sequence 32, Appl | 100.0 | 322 | 14 | US-10-223-081-32 | Sequence 32, Appl |
| Sequence 32, Appl | 100.0 | 322 | 14 | US-10-223-082-32 | Sequence 32, Appl |
| Sequence 201, Appl | 100.0 | 322 | 15 | US-10-298-993-201 | Sequence 201, Appl |
| Sequence 32, Appl | 100.0 | 322 | 15 | US-10-305-654-32 | Sequence 32, Appl |
| Sequence 201, Appl | 100.0 | 322 | 15 | US-10-448-923-201 | Sequence 201, Appl |
| Sequence 201, Appl | 100.0 | 322 | 15 | US-10-449-656-201 | Sequence 201, Appl |
| Sequence 201, Appl | 100.0 | 322 | 15 | US-10-448-713-201 | Sequence 201, Appl |
| Sequence 201, Appl | 100.0 | 322 | 15 | US-10-425-447-201 | Sequence 201, Appl |
| Sequence 32, Appl | 100.0 | 322 | 15 | US-10-081-056-32 | Sequence 32, Appl |
| Sequence 201, Appl | 100.0 | 322 | 16 | US-10-215-371-201 | Sequence 201, Appl |
| Sequence 201, Appl | 100.0 | 322 | 16 | US-10-771-187-201 | Sequence 201, Appl |
| Sequence 6, Appl | 100.0 | 322 | 17 | US-10-972-317-6 | Sequence 6, Appl |
| Sequence 201, Appl | 100.0 | 322 | 17 | US-10-963-467-201 | Sequence 201, Appl |
| Sequence 201, Appl | 100.0 | 322 | 17 | US-10-978-255-201 | Sequence 201, Appl |
| Sequence 201, Appl | 100.0 | 322 | 18 | US-10-797-366-201 | Sequence 201, Appl |
| Sequence 64, Appl | 100.0 | 322 | 18 | US-10-820-474A-64 | Sequence 64, Appl |
| Sequence 5685, Ap | 100.0 | 322 | 18 | US-10-756-149-5685 | Sequence 5685, Ap |
| Sequence 2349, Ap | 99.8 | 344 | 15 | US-10-276-774-2349 | Sequence 2349, Ap |
| Sequence 2, Appl | 99.6 | 322 | 14 | US-10-291-634-2 | Sequence 2, Appl |
| Sequence 2665, Ap | 99.6 | 322 | 15 | US-10-264-237-2665 | Sequence 2665, Ap |
| Sequence 3909, Ap | 98.9 | 322 | 16 | US-10-723-860-3909 | Sequence 3909, Ap |
| Sequence 2, Appl | 91.2 | 297 | 15 | US-10-138-588-2 | Sequence 2, Appl |
| Sequence 700, App | 49.5 | 255 | 10 | US-09-866-050A-700 | Sequence 700, App |
| Sequence 8, Appl | 13.8 | 364 | 18 | US-10-024-607-8 | Sequence 8, Appl |
| Sequence 3, Appl | 13.5 | 339 | 14 | US-10-291-634-3 | Sequence 3, Appl |
| Sequence 73, Appl | 13.4 | 365 | 9 | US-09-870-759-73 | Sequence 73, Appl |
| Sequence 69, Appl | 13.4 | 365 | 10 | US-09-751-708A-73 | Sequence 69, Appl |
| Sequence 50, Appl | 13.4 | 365 | 16 | US-10-428-817A-50 | Sequence 50, Appl |
| Sequence 341, App | 12.6 | 368 | 16 | US-10-937-758A-50 | Sequence 341, App |
| Sequence 1285, Ap | 12.6 | 668 | 16 | US-10-473-127-1285 | Sequence 1285, Ap |
| Sequence 1047, Ap | 12.6 | 668 | 17 | US-10-741-600-1047 | Sequence 1047, Ap |
| Sequence 253, App | 12.6 | 668 | 17 | US-10-482-029-253 | Sequence 253, App |
| Sequence 32, Appl | 12.5 | 361 | 11 | US-09-836-544-32 | Sequence 32, Appl |
| Sequence 1276, Ap | 12.5 | 361 | 16 | US-10-473-127-1276 | Sequence 1276, Ap |
| Sequence 1292, Ap | 12.5 | 361 | 16 | US-10-473-127-1292 | Sequence 1292, Ap |
| Sequence 1296, Ap | 12.5 | 361 | 16 | US-10-473-127-1296 | Sequence 1296, Ap |
| Sequence 1298, Ap | 12.5 | 361 | 16 | US-10-473-127-1298 | Sequence 1298, Ap |
| Sequence 1300, Ap | 12.5 | 361 | 16 | US-10-473-127-1300 | Sequence 1300, Ap |
| Sequence 1302, Ap | 12.5 | 361 | 16 | US-10-473-127-1302 | Sequence 1302, Ap |
| Sequence 1304, Ap | 12.5 | 361 | 16 | US-10-473-127-1304 | Sequence 1304, Ap |
| Sequence 1275, Ap | 12.4 | 361 | 16 | US-10-473-127-1275 | Sequence 1275, Ap |
| Sequence 1309, Ap | 12.4 | 361 | 16 | US-10-473-127-1309 | Sequence 1309, Ap |
| Sequence 1310, Ap | 12.4 | 361 | 16 | US-10-473-127-1310 | Sequence 1310, Ap |
| Sequence 255, App | 12.4 | 361 | 17 | US-10-482-029-255 | Sequence 255, App |
| Sequence 131, App | 12.4 | 361 | 17 | US-10-852-335A-131 | Sequence 131, App |
| Sequence 340, App | 12.3 | 361 | 16 | US-10-741-601-340 | Sequence 340, App |
| Sequence 1288, Ap | 12.3 | 361 | 16 | US-10-473-127-1288 | Sequence 1288, Ap |
| Sequence 1048, Ap | 12.3 | 361 | 17 | US-10-741-600-1048 | Sequence 1048, Ap |
| Sequence 2, Appl | 12.3 | 700 | 17 | US-10-486-226-2 | Sequence 2, Appl |
| Sequence 1306, Ap | 12.3 | 700 | 16 | US-10-473-127-1306 | Sequence 1306, Ap |
| Sequence 1308, Ap | 12.3 | 436 | 16 | US-10-473-127-1308 | Sequence 1308, Ap |
| Sequence 176, App | 12.3 | 742 | 16 | US-10-648-593-176 | Sequence 176, App |
| Sequence 1282, Ap | 12.3 | 742 | 16 | US-10-473-127-1282 | Sequence 1282, Ap |
| Sequence 1319, Ap | 12.3 | 742 | 16 | US-10-473-127-1319 | Sequence 1319, Ap |
| Sequence 1054, Ap | 12.3 | 742 | 17 | US-10-741-600-1054 | Sequence 1054, Ap |
| Sequence 545, App | 12.3 | 742 | 18 | US-10-287-436A-545 | Sequence 545, App |
| Sequence 1236, Ap | 12.3 | 742 | 18 | US-10-287-436A-1236 | Sequence 1236, Ap |
| Sequence 1307, Ap | 12.2 | 431 | 16 | US-10-473-127-1307 | Sequence 1307, Ap |
| Sequence 3, Appl | 12.2 | 361 | 16 | US-10-663-244-3 | Sequence 3, Appl |
| Sequence 1273, Ap | 12.2 | 361 | 16 | US-10-473-127-1273 | Sequence 1273, Ap |
| Sequence 1284, Ap | 12.2 | 675 | 16 | US-10-473-127-1284 | Sequence 1284, Ap |
| Sequence 344, App | 12.2 | 691 | 16 | US-10-741-601-344 | Sequence 344, App |
| Sequence 1287, Ap | 12.2 | 691 | 16 | US-10-473-127-1287 | Sequence 1287, Ap |
| Sequence 1053, Ap | 12.2 | 691 | 17 | US-10-741-600-1053 | Sequence 1053, Ap |
| Sequence 16, Appl | 12.2 | 742 | 10 | US-09-983-000A-16 | Sequence 16, Appl |
| Sequence 206, App | 12.2 | 742 | 15 | US-10-116-275-206 | Sequence 206, App |
| Sequence 1, Appl | 12.2 | 742 | 16 | US-10-663-244-1 | Sequence 1, Appl |
| Sequence 338, App | 12.2 | 742 | 16 | US-10-741-601-338 | Sequence 338, App |
| Sequence 339, App | 12.2 | 742 | 16 | US-10-741-601-339 | Sequence 339, App |
| Sequence 1286, Ap | 12.2 | 742 | 16 | US-10-473-127-1286 | Sequence 1286, Ap |
| Sequence 1311, Ap | 12.2 | 742 | 16 | US-10-473-127-1311 | Sequence 1311, Ap |
| Sequence 40, Appl | 12.2 | 742 | 17 | US-10-690-880-40 | Sequence 40, Appl |

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|-----|-------|------|------|--------------------|----------------------|---------------------|------|-------|------|------|-------------------|--------------------|-------------------|
| 302 | 12.2 | 742 | 17 | US-10-741-600-1046 | Sequence 1046, Ap | 375 | 133 | 8.0 | 1394 | 9 | US-09-842-930A-25 | Sequence 25, Appl | |
| 303 | 12.2 | 742 | 17 | US-10-741-600-1049 | Sequence 1049, Ap | 376 | 133 | 8.0 | 1394 | 17 | US-10-990-844-25 | Sequence 25, Appl | |
| 304 | 12.2 | 742 | 17 | US-10-652-981-15 | Sequence 16, Appl | 377 | 133 | 8.0 | 1416 | 14 | US-10-133-172-4 | Sequence 4, Appl | |
| 305 | 12.1 | 425 | 16 | US-10-473-127-1283 | Sequence 1283, Ap | 378 | 133 | 8.0 | 1431 | 9 | US-09-842-930A-2 | Sequence 2, Appl | |
| 306 | 199.5 | 12.0 | 493 | 11 | US-09-836-544-34 | Sequence 34, Appl | 379 | 133 | 8.0 | 1431 | 14 | US-10-133-172-2 | Sequence 2, Appl |
| 307 | 199.5 | 12.0 | 493 | 16 | US-10-663-244-2 | Sequence 2, Appl | 380 | 133 | 8.0 | 1431 | 17 | US-10-990-844-2 | Sequence 2, Appl |
| 308 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1278 | Sequence 1278, Ap | 381 | 133 | 8.0 | 1653 | 14 | US-10-133-172-20 | Sequence 20, Appl |
| 309 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1279 | Sequence 1279, Ap | 382 | 131.5 | 7.9 | 883 | 14 | US-10-195-970-3 | Sequence 3, Appl |
| 310 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1289 | Sequence 1289, Ap | 383 | 131.5 | 7.9 | 883 | 15 | US-10-453-420-3 | Sequence 3, Appl |
| 311 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1293 | Sequence 1293, Ap | 384 | 131 | 7.9 | 649 | 10 | US-09-759-130B-333 | Sequence 333, App |
| 312 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1297 | Sequence 1297, Ap | 385 | 131 | 7.9 | 649 | 14 | US-10-189-123-63 | Sequence 63, Appl |
| 313 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1299 | Sequence 1299, Ap | 386 | 131 | 7.9 | 649 | 14 | US-10-188-495-63 | Sequence 63, Appl |
| 314 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1301 | Sequence 1301, Ap | 387 | 131 | 7.9 | 649 | 16 | US-10-741-790-333 | Sequence 333, App |
| 315 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1303 | Sequence 1303, Ap | 388 | 131 | 7.9 | 671 | 10 | US-09-759-130B-331 | Sequence 331, App |
| 316 | 199.5 | 12.0 | 493 | 16 | US-10-473-127-1305 | Sequence 1305, Ap | 389 | 131 | 7.9 | 671 | 14 | US-10-189-123-61 | Sequence 61, Appl |
| 317 | 199.5 | 12.0 | 700 | 14 | US-10-012-969C-2 | Sequence 2, Appl | 390 | 131 | 7.9 | 671 | 14 | US-10-188-495-61 | Sequence 61, Appl |
| 318 | 199 | 12.0 | 338 | 16 | US-10-473-127-1271 | Sequence 1271, Ap | 391 | 131 | 7.9 | 671 | 16 | US-10-741-790-331 | Sequence 331, App |
| 319 | 199 | 12.0 | 338 | 16 | US-10-473-127-1315 | Sequence 1315, Ap | 400 | 131 | 7.9 | 911 | 14 | US-10-237-535-52 | Sequence 52, Appl |
| 320 | 198 | 11.9 | 395 | 16 | US-10-473-127-1281 | Sequence 1281, Ap | 409 | 131 | 7.9 | 911 | 14 | US-10-239-196-52 | Sequence 52, Appl |
| 321 | 197 | 11.9 | 719 | 16 | US-10-473-127-1270 | Sequence 1270, Ap | 500 | 131 | 7.9 | 911 | 15 | US-10-312-352-24 | Sequence 24, Appl |
| 322 | 197 | 11.9 | 719 | 16 | US-10-473-127-1316 | Sequence 1316, Ap | 501 | 131 | 7.9 | 911 | 17 | US-10-936-626-89 | Sequence 89, Appl |
| 323 | 196.5 | 11.9 | 535 | 16 | US-10-473-127-1317 | Sequence 1317, Appl | 502 | 131 | 7.9 | 911 | 17 | US-10-938-061-89 | Sequence 89, Appl |
| 324 | 196.5 | 11.9 | 535 | 17 | US-10-741-600-1044 | Sequence 1044, Ap | 503 | 130.5 | 7.9 | 883 | 10 | US-09-759-130B-342 | Sequence 342, App |
| 325 | 196.5 | 11.9 | 699 | 16 | US-10-473-127-1274 | Sequence 1274, Ap | 504 | 130.5 | 7.9 | 883 | 14 | US-10-195-970-6 | Sequence 6, Appl |
| 326 | 196.5 | 11.9 | 699 | 16 | US-10-473-127-1280 | Sequence 1280, Ap | 505 | 130.5 | 7.9 | 883 | 14 | US-10-189-123-72 | Sequence 72, Appl |
| 327 | 196.5 | 11.9 | 699 | 16 | US-10-473-127-1313 | Sequence 1313, Ap | 506 | 130.5 | 7.9 | 883 | 14 | US-10-188-495-72 | Sequence 72, Appl |
| 328 | 196.5 | 11.9 | 699 | 17 | US-10-696-639-71 | Sequence 71, Appl | 507 | 130.5 | 7.9 | 883 | 15 | US-10-453-420-6 | Sequence 6, Appl |
| 329 | 196 | 11.8 | 293 | 16 | US-10-473-127-1277 | Sequence 1277, Ap | 508 | 130.5 | 7.9 | 883 | 16 | US-10-741-790-342 | Sequence 342, App |
| 330 | 196 | 11.8 | 294 | 16 | US-10-473-127-1290 | Sequence 1290, Ap | 509 | 130.5 | 7.9 | 1082 | 15 | US-10-264-237-275 | Sequence 275, Ap |
| 331 | 196 | 11.8 | 294 | 16 | US-10-473-127-1312 | Sequence 1312, Ap | 510 | 130.5 | 7.9 | 2316 | 18 | US-10-287-436A-566 | Sequence 566, App |
| 332 | 196 | 11.8 | 395 | 16 | US-10-741-601-345 | Sequence 345, App | 511 | 129.5 | 7.8 | 2570 | 15 | US-10-028-248A-42 | Sequence 42, Appl |
| 333 | 196 | 11.8 | 395 | 16 | US-10-741-600-1052 | Sequence 1052, Ap | 512 | 129.5 | 7.8 | 2570 | 15 | US-10-107-782-42 | Sequence 42, Appl |
| 334 | 196 | 11.8 | 425 | 16 | US-10-741-601-337 | Sequence 337, App | 513 | 128.5 | 7.8 | 95 | 16 | US-10-473-127-1291 | Sequence 1291, Ap |
| 335 | 196 | 11.8 | 425 | 16 | US-10-741-600-1045 | Sequence 1045, Ap | 514 | 128 | 7.7 | 2212 | 15 | US-10-028-248A-43 | Sequence 43, Appl |
| 336 | 196 | 11.8 | 493 | 16 | US-10-741-601-343 | Sequence 343, App | 515 | 128 | 7.7 | 2212 | 15 | US-10-107-782-43 | Sequence 43, Appl |
| 337 | 196 | 11.8 | 493 | 17 | US-10-741-600-1051 | Sequence 1051, Ap | 516 | 127.5 | 7.7 | 671 | 10 | US-09-983-000A-14 | Sequence 14, Appl |
| 338 | 194.5 | 11.7 | 742 | 18 | US-10-450-763-47430 | Sequence 47430, A | 517 | 127.5 | 7.7 | 671 | 17 | US-10-652-981-14 | Sequence 14, Appl |
| 339 | 191.5 | 11.6 | 676 | 16 | US-10-473-127-1268 | Sequence 1268, Ap | 518 | 127.5 | 7.7 | 671 | 17 | US-10-936-626-90 | Sequence 90, Appl |
| 340 | 191.5 | 11.6 | 676 | 16 | US-10-473-127-1318 | Sequence 1318, Ap | 519 | 127.5 | 7.7 | 671 | 17 | US-10-938-061-90 | Sequence 90, Appl |
| 341 | 191 | 11.5 | 271 | 16 | US-10-473-127-1272 | Sequence 1272, Ap | 520 | 127.5 | 7.7 | 671 | 17 | US-10-852-335A-97 | Sequence 97, Appl |
| 342 | 191 | 11.5 | 271 | 16 | US-10-473-127-1314 | Sequence 1314, Ap | 521 | 127.5 | 7.7 | 911 | 15 | US-10-453-420-8 | Sequence 8, Appl |
| 343 | 191 | 11.5 | 470 | 16 | US-10-473-127-1269 | Sequence 1269, Ap | 522 | 127.5 | 7.7 | 911 | 15 | US-10-295-027-260 | Sequence 260, App |
| 344 | 191 | 11.5 | 470 | 16 | US-10-473-127-1317 | Sequence 1317, Ap | 523 | 127 | 7.7 | 277 | 15 | US-10-295-027-294 | Sequence 294, App |
| 345 | 187 | 11.3 | 112 | 17 | US-10-487-620-2 | Sequence 2, Appl | 524 | 127 | 7.7 | 277 | 16 | US-10-755-889-118 | Sequence 118, App |
| 346 | 186.5 | 11.3 | 113 | 17 | US-10-487-620-6 | Sequence 6, Appl | 525 | 126.5 | 7.6 | 457 | 10 | US-09-774-638-108 | Sequence 108, App |
| 347 | 185 | 11.2 | 112 | 17 | US-10-487-620-8 | Sequence 8, Appl | 526 | 126.5 | 7.6 | 457 | 10 | US-09-969-730-110 | Sequence 110, App |
| 348 | 183 | 11.0 | 112 | 17 | US-10-487-620-10 | Sequence 10, Appl | 527 | 126.5 | 7.6 | 457 | 15 | US-10-621-363-110 | Sequence 110, App |
| 349 | 182 | 11.0 | 112 | 17 | US-10-487-620-4 | Sequence 4, Appl | 528 | 124.5 | 7.5 | 482 | 15 | US-10-104-047-3794 | Sequence 3794, Ap |
| 350 | 181 | 10.9 | 112 | 17 | US-10-487-620-12 | Sequence 12, Appl | 531 | 121.5 | 7.3 | 360 | 9 | US-09-905-291A-213 | Sequence 213, App |
| 351 | 180 | 10.9 | 920 | 18 | US-10-450-763-47426 | Sequence 47426, A | 1062 | 121.5 | 7.3 | 360 | 14 | US-10-174-587-28 | Sequence 28, Appl |
| 352 | 170 | 10.3 | 34 | 9 | US-09-864-761-47905 | Sequence 47905, A | 1097 | 121.5 | 7.3 | 360 | 14 | US-10-299-976-213 | Sequence 213, App |
| 353 | 161 | 9.7 | 90 | 9 | US-09-799-118-3 | Sequence 3, Appl | 1099 | 121.5 | 7.3 | 360 | 14 | US-10-299-937-213 | Sequence 213, App |
| 354 | 153.5 | 9.3 | 90 | 10 | US-09-927-463-8 | Sequence 8, Appl | 1109 | 121.5 | 7.3 | 360 | 15 | US-10-298-993-213 | Sequence 213, App |
| 355 | 153.5 | 9.3 | 90 | 16 | US-10-837-671-8 | Sequence 8, Appl | 1114 | 121.5 | 7.3 | 360 | 15 | US-10-448-923-213 | Sequence 213, App |
| 356 | 150 | 9.1 | 510 | 15 | US-10-104-047-2580 | Sequence 2580, Ap | 1115 | 121.5 | 7.3 | 360 | 15 | US-10-449-656-213 | Sequence 213, App |
| 357 | 148.5 | 9.0 | 80 | 17 | US-10-487-620-23 | Sequence 23, Appl | 1116 | 121.5 | 7.3 | 360 | 15 | US-10-448-713-213 | Sequence 213, App |
| 358 | 145 | 8.8 | 277 | 9 | US-09-799-118-2 | Sequence 2, Appl | 1118 | 121.5 | 7.3 | 360 | 15 | US-10-425-447-213 | Sequence 213, App |
| 359 | 145 | 8.8 | 277 | 14 | US-10-247-671-185 | Sequence 185, App | 1126 | 121.5 | 7.3 | 360 | 16 | US-10-215-371-213 | Sequence 213, App |
| 360 | 145 | 8.8 | 277 | 15 | US-10-295-027-292 | Sequence 292, App | 1127 | 121.5 | 7.3 | 360 | 16 | US-10-771-187-213 | Sequence 213, App |
| 361 | 145 | 8.8 | 277 | 15 | US-10-295-027-1237 | Sequence 1237, Ap | 1128 | 121.5 | 7.3 | 360 | 17 | US-10-963-467-213 | Sequence 213, App |
| 362 | 145 | 8.8 | 277 | 16 | US-10-723-860-4326 | Sequence 4326, Ap | 1129 | 121.5 | 7.3 | 360 | 17 | US-10-978-255-213 | Sequence 213, App |
| 363 | 145 | 8.8 | 1069 | 15 | US-10-028-248A-39 | Sequence 39, Appl | 1130 | 121.5 | 7.3 | 360 | 18 | US-10-797-366-213 | Sequence 213, App |
| 364 | 145 | 8.8 | 1069 | 15 | US-10-107-782-39 | Sequence 39, Appl | 1134 | 121 | 7.3 | 528 | 10 | US-09-759-130B-341 | Sequence 341, App |
| 365 | 145 | 8.8 | 2626 | 15 | US-10-634-574-4 | Sequence 4, Appl | 1135 | 121 | 7.3 | 528 | 14 | US-10-189-123-71 | Sequence 71, Appl |
| 366 | 143.5 | 8.7 | 95 | 15 | US-10-424-599-248857 | Sequence 248857, A | 1136 | 121 | 7.3 | 528 | 14 | US-10-188-495-71 | Sequence 71, Appl |
| 367 | 134 | 8.1 | 897 | 15 | US-10-028-248A-41 | Sequence 41, Appl | 1137 | 121 | 7.3 | 528 | 16 | US-10-741-790-341 | Sequence 341, App |
| 368 | 134 | 8.1 | 897 | 15 | US-10-028-248A-211 | Sequence 211, App | 1138 | 121 | 7.3 | 528 | 17 | US-10-314-942-20 | Sequence 20, Appl |
| 369 | 134 | 8.1 | 897 | 15 | US-10-107-782-41 | Sequence 41, Appl | 1139 | 118.5 | 7.2 | 1642 | 17 | US-10-741-600-1176 | Sequence 1176, Ap |
| 370 | 134 | 8.1 | 897 | 15 | US-10-107-782-211 | Sequence 211, App | 1140 | 118.5 | 7.2 | 1642 | 17 | US-10-741-600-1178 | Sequence 1178, Ap |
| 371 | 134 | 8.1 | 2675 | 15 | US-10-028-248A-2 | Sequence 2, Appl | 1141 | 118.5 | 7.2 | 3396 | 16 | US-10-788-792-170 | Sequence 170, App |
| 372 | 134 | 8.1 | 2675 | 15 | US-10-107-782-2 | Sequence 2, Appl | 1142 | 118.5 | 7.2 | 3396 | 17 | US-10-741-600-1172 | Sequence 1172, Ap |
| 373 | 133 | 8.0 | 1192 | 15 | US-10-028-248A-40 | Sequence 40, Appl | 1143 | 118.5 | 7.2 | 3396 | 17 | US-10-741-600-1173 | Sequence 1173, Ap |
| 374 | 133 | 8.0 | 1192 | 15 | US-10-107-782-40 | Sequence 40, Appl | 1144 | 118.5 | 7.2 | 3396 | 18 | US-10-631-467-773 | Sequence 773, App |

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|------|-------|-----|------|----|----------------------|-------------------|------|-------|-----|------|----|----------------------|--------------------|
| 1145 | 117 | 7.1 | 340 | 15 | US-10-112-944-397 | Sequence 397, App | 1218 | 101.5 | 6.1 | 590 | 20 | US-11-058-709-12 | Sequence 12, Appl |
| 1146 | 116 | 7.0 | 2397 | 18 | US-10-631-467-1518 | Sequence 1518, Ap | 1219 | 100.5 | 6.1 | 402 | 15 | US-10-343-953-2 | Sequence 2, Appl |
| 1147 | 114.5 | 6.9 | 1257 | 18 | US-10-698-190-22 | Sequence 22, Appl | 1220 | 100.5 | 6.1 | 402 | 15 | US-10-257-174-47 | Sequence 47, Appl |
| 1148 | 113.5 | 6.8 | 97 | 9 | US-09-799-118-5 | Sequence 5, Appl | 1221 | 100.5 | 6.1 | 1379 | 20 | US-11-097-143-33612 | Sequence 33612, A |
| 1149 | 112.5 | 6.8 | 287 | 9 | US-09-764-853-576 | Sequence 576, App | 1222 | 99.5 | 6.0 | 402 | 16 | US-10-481-698-17 | Sequence 17, Appl |
| 1150 | 111.5 | 6.7 | 402 | 15 | US-10-282-122A-64209 | Sequence 64209, A | 1223 | 99 | 6.0 | 201 | 15 | US-10-120-907A-40 | Sequence 40, Appl |
| 1151 | 111 | 6.7 | 104 | 15 | US-10-028-248A-46 | Sequence 46, Appl | 1224 | 99 | 6.0 | 201 | 15 | US-10-120-907A-41 | Sequence 41, Appl |
| 1152 | 111 | 6.7 | 104 | 15 | US-10-107-782-46 | Sequence 46, Appl | 1225 | 99 | 6.0 | 260 | 15 | US-10-460-512-3 | Sequence 3, Appl |
| 1153 | 111 | 6.7 | 655 | 16 | US-10-270-253-2 | Sequence 2, Appl | 1226 | 99 | 6.0 | 260 | 16 | US-10-897-911-3 | Sequence 3, Appl |
| 1154 | 111 | 6.7 | 655 | 17 | US-10-741-600-1174 | Sequence 1174, Ap | 1227 | 99 | 6.0 | 260 | 17 | US-10-898-615-3 | Sequence 3, Appl |
| 1155 | 111 | 6.7 | 2409 | 14 | US-10-177-293-90 | Sequence 90, Appl | 1228 | 99 | 6.0 | 1428 | 20 | US-11-097-143-37923 | Sequence 37923, A |
| 1156 | 111 | 6.7 | 2409 | 17 | US-10-741-600-1175 | Sequence 1175, Ap | 1229 | 99 | 6.0 | 5376 | 15 | US-10-028-248A-74 | Sequence 74, Appl |
| 1157 | 111 | 6.7 | 2409 | 17 | US-10-741-600-1177 | Sequence 1177, Ap | 1230 | 99 | 6.0 | 5376 | 15 | US-10-107-782-74 | Sequence 74, Appl |
| 1158 | 111 | 6.7 | 2409 | 17 | US-10-482-029-134 | Sequence 194, App | 1231 | 98.5 | 5.9 | 1126 | 20 | US-11-097-143-35952 | Sequence 35952, A |
| 1159 | 111 | 6.7 | 2409 | 17 | US-10-852-335A-184 | Sequence 184, App | 1232 | 98 | 5.9 | 2112 | 20 | US-11-097-143-8001 | Sequence 8001, Ap |
| 1160 | 110 | 6.6 | 341 | 10 | US-09-948-820-48 | Sequence 48, Appl | 1233 | 95.5 | 5.8 | 376 | 9 | US-09-801-368-206 | Sequence 206, App |
| 1161 | 110 | 6.6 | 341 | 16 | US-10-613-076-48 | Sequence 48, Appl | 1234 | 95.5 | 5.8 | 585 | 17 | US-10-868-381-58 | Sequence 58, Appl |
| 1162 | 109 | 6.6 | 1321 | 14 | US-10-241-220-82 | Sequence 82, Appl | 1235 | 95.5 | 5.8 | 1217 | 16 | US-10-437-963-183891 | Sequence 183891, A |
| 1163 | 109 | 6.6 | 1321 | 15 | US-10-293-027-282 | Sequence 282, App | 1236 | 95.5 | 5.8 | 5374 | 15 | US-10-028-248A-75 | Sequence 75, Appl |
| 1164 | 109 | 6.6 | 1321 | 16 | US-10-408-765A-1421 | Sequence 1421, Ap | 1237 | 95.5 | 5.8 | 5374 | 15 | US-10-107-782-75 | Sequence 75, Appl |
| 1165 | 109 | 6.6 | 1321 | 16 | US-10-872-972-82 | Sequence 82, Appl | 1238 | 93.5 | 5.6 | 258 | 9 | US-09-764-853-840 | Sequence 840, App |
| 1166 | 109 | 6.6 | 1321 | 16 | US-10-872-991-82 | Sequence 82, Appl | 1239 | 93.5 | 5.6 | 258 | 14 | US-10-091-438-205 | Sequence 205, App |
| 1167 | 109 | 6.6 | 1321 | 18 | US-10-698-190-18 | Sequence 18, Appl | 1240 | 93.5 | 5.6 | 261 | 9 | US-09-764-853-669 | Sequence 669, App |
| 1168 | 108 | 6.5 | 322 | 15 | US-10-120-907A-32 | Sequence 32, Appl | 1241 | 93.5 | 5.6 | 261 | 14 | US-10-091-438-144 | Sequence 144, App |
| 1169 | 108 | 6.5 | 322 | 15 | US-10-120-907A-33 | Sequence 33, Appl | 1242 | 93.5 | 5.6 | 320 | 18 | US-10-450-763-31869 | Sequence 31869, A |
| 1170 | 108 | 6.5 | 354 | 15 | US-10-120-907A-3 | Sequence 3, Appl | 1243 | 93.5 | 5.6 | 339 | 17 | US-10-391-939A-2 | Sequence 2, Appl |
| 1171 | 108 | 6.5 | 354 | 15 | US-10-120-907A-7 | Sequence 7, Appl | 1244 | 93.5 | 5.6 | 339 | 17 | US-10-391-939A-28 | Sequence 28, Appl |
| 1172 | 108 | 6.5 | 354 | 15 | US-10-120-907A-9 | Sequence 9, Appl | 1245 | 93.5 | 5.6 | 359 | 14 | US-10-188-012-17 | Sequence 17, Appl |
| 1173 | 108 | 6.5 | 354 | 15 | US-10-120-907A-11 | Sequence 11, Appl | 1246 | 93.5 | 5.6 | 359 | 14 | US-10-188-012-19 | Sequence 19, Appl |
| 1174 | 108 | 6.5 | 354 | 15 | US-10-120-907A-13 | Sequence 13, Appl | 1247 | 93.5 | 5.6 | 359 | 14 | US-10-188-012-23 | Sequence 23, Appl |
| 1175 | 108 | 6.5 | 354 | 15 | US-10-120-907A-15 | Sequence 15, Appl | 1248 | 93.5 | 5.6 | 359 | 15 | US-10-295-027-302 | Sequence 302, App |
| 1176 | 108 | 6.5 | 354 | 15 | US-10-120-907A-17 | Sequence 17, Appl | 1249 | 93.5 | 5.6 | 359 | 15 | US-10-188-832-64 | Sequence 64, Appl |
| 1177 | 108 | 6.5 | 354 | 15 | US-10-120-907A-19 | Sequence 19, Appl | 1250 | 93.5 | 5.6 | 359 | 17 | US-10-391-939A-4 | Sequence 4, Appl |
| 1178 | 108 | 6.5 | 354 | 15 | US-10-120-907A-21 | Sequence 21, Appl | 1251 | 93.5 | 5.6 | 359 | 17 | US-10-663-497-17 | Sequence 17, Appl |
| 1179 | 108 | 6.5 | 354 | 15 | US-10-120-907A-23 | Sequence 23, Appl | 1252 | 93.5 | 5.6 | 359 | 17 | US-10-663-497-19 | Sequence 19, Appl |
| 1180 | 108 | 6.5 | 354 | 15 | US-10-120-907A-24 | Sequence 24, Appl | 1253 | 93.5 | 5.6 | 359 | 17 | US-10-663-497-23 | Sequence 23, Appl |
| 1181 | 108 | 6.5 | 354 | 15 | US-10-120-907A-28 | Sequence 28, Appl | 1254 | 93.5 | 5.6 | 359 | 17 | US-10-718-321-8 | Sequence 8, Appl |
| 1182 | 108 | 6.5 | 354 | 15 | US-10-120-907A-29 | Sequence 29, Appl | 1255 | 93.5 | 5.6 | 359 | 17 | US-10-847-918-25 | Sequence 25, Appl |
| 1183 | 108 | 6.5 | 354 | 15 | US-10-120-907A-30 | Sequence 30, Appl | 1256 | 93.5 | 5.6 | 366 | 18 | US-10-450-763-38282 | Sequence 38282, A |
| 1184 | 108 | 6.5 | 354 | 15 | US-10-120-907A-36 | Sequence 36, Appl | 1257 | 93.5 | 5.6 | 1595 | 17 | US-10-484-218-20 | Sequence 20, Appl |
| 1185 | 108 | 6.5 | 354 | 15 | US-10-120-907A-38 | Sequence 38, Appl | 1258 | 92.5 | 5.6 | 40 | 17 | US-10-487-620-26 | Sequence 26, Appl |
| 1186 | 108 | 6.5 | 354 | 15 | US-10-120-907A-42 | Sequence 42, Appl | 1259 | 92.5 | 5.6 | 300 | 9 | US-09-953-499-10 | Sequence 10, Appl |
| 1187 | 108 | 6.5 | 354 | 15 | US-10-120-907A-64 | Sequence 64, Appl | 1260 | 92.5 | 5.6 | 300 | 14 | US-10-265-542-10 | Sequence 10, Appl |
| 1188 | 108 | 6.5 | 354 | 15 | US-10-120-907A-66 | Sequence 66, Appl | 1261 | 92.5 | 5.6 | 300 | 16 | US-10-633-008-10 | Sequence 10, Appl |
| 1189 | 108 | 6.5 | 354 | 18 | US-10-754-473-19 | Sequence 19, Appl | 1262 | 92.5 | 5.6 | 300 | 16 | US-10-785-220-10 | Sequence 10, Appl |
| 1190 | 108 | 6.5 | 354 | 18 | US-10-754-473-22 | Sequence 22, Appl | 1263 | 92.5 | 5.6 | 300 | 16 | US-10-785-221-10 | Sequence 10, Appl |
| 1191 | 108 | 6.5 | 721 | 15 | US-10-120-907A-5 | Sequence 5, Appl | 1264 | 92.5 | 5.6 | 300 | 16 | US-10-785-433-10 | Sequence 10, Appl |
| 1192 | 108 | 6.5 | 721 | 15 | US-10-120-907A-25 | Sequence 25, Appl | 1265 | 92.5 | 5.6 | 300 | 16 | US-10-767-374-10 | Sequence 10, Appl |
| 1193 | 108 | 6.5 | 721 | 15 | US-10-120-907A-43 | Sequence 43, Appl | 1266 | 92.5 | 5.6 | 300 | 16 | US-10-785-607-10 | Sequence 10, Appl |
| 1194 | 108 | 6.5 | 721 | 15 | US-10-120-907A-65 | Sequence 65, Appl | 1267 | 92.5 | 5.6 | 300 | 16 | US-10-785-351-12 | Sequence 12, Appl |
| 1195 | 108 | 6.5 | 721 | 15 | US-10-120-907A-67 | Sequence 67, Appl | 1268 | 92.5 | 5.6 | 300 | 18 | US-10-767-904-10 | Sequence 10, Appl |
| 1196 | 107 | 6.5 | 93 | 14 | US-10-133-172-5 | Sequence 5, Appl | 1269 | 92.5 | 5.6 | 365 | 14 | US-10-188-012-21 | Sequence 21, Appl |
| 1197 | 107 | 6.5 | 315 | 15 | US-10-667-723-4 | Sequence 4, Appl | 1270 | 92.5 | 5.6 | 365 | 17 | US-10-663-497-21 | Sequence 21, Appl |
| 1198 | 107 | 6.5 | 339 | 18 | US-10-754-473-21 | Sequence 21, Appl | 1271 | 92.5 | 5.6 | 569 | 15 | US-10-282-122A-60442 | Sequence 60442, A |
| 1199 | 107 | 6.5 | 354 | 15 | US-10-120-907A-39 | Sequence 39, Appl | 1272 | 92.5 | 5.6 | 994 | 15 | US-10-369-493-1516 | Sequence 1516, Ap |
| 1200 | 107 | 6.5 | 355 | 15 | US-10-120-907A-31 | Sequence 31, Appl | 1273 | 92.5 | 5.6 | 364 | 14 | US-10-188-012-25 | Sequence 25, Appl |
| 1201 | 107 | 6.5 | 355 | 18 | US-10-754-473-20 | Sequence 20, Appl | 1274 | 92 | 5.6 | 364 | 17 | US-10-663-497-25 | Sequence 372, Appl |
| 1202 | 107 | 6.5 | 1268 | 18 | US-10-698-190-24 | Sequence 24, Appl | 1275 | 92 | 5.6 | 966 | 9 | US-09-801-368-372 | Sequence 372, Appl |
| 1203 | 107 | 6.5 | 1795 | 20 | US-11-097-143-36210 | Sequence 36210, A | 1276 | 92 | 5.6 | 966 | 16 | US-10-451-467A-52 | Sequence 52, Appl |
| 1204 | 107 | 6.5 | 2420 | 15 | US-10-028-248A-4 | Sequence 4, Appl | 1277 | 91.5 | 5.5 | 166 | 9 | US-09-764-853-777 | Sequence 777, App |
| 1205 | 107 | 6.5 | 2420 | 15 | US-10-107-782-4 | Sequence 4, Appl | 1278 | 91.5 | 5.5 | 166 | 14 | US-10-091-438-181 | Sequence 181, App |
| 1206 | 105 | 6.3 | 354 | 15 | US-10-120-907A-37 | Sequence 37, Appl | 1279 | 91.5 | 5.5 | 350 | 14 | US-10-239-431A-6 | Sequence 6, Appl |
| 1207 | 105 | 6.3 | 354 | 18 | US-10-754-473-18 | Sequence 18, Appl | 1280 | 91.5 | 5.5 | 376 | 14 | US-10-239-431A-4 | Sequence 4, Appl |
| 1208 | 104 | 6.3 | 98 | 9 | US-09-799-118-4 | Sequence 4, Appl | 1281 | 91.5 | 5.5 | 610 | 14 | US-10-239-431A-2 | Sequence 2, Appl |
| 1209 | 104 | 6.3 | 139 | 16 | US-10-741-601-342 | Sequence 342, App | 1282 | 91.5 | 5.5 | 639 | 9 | US-09-825-144-9 | Sequence 9, Appl |
| 1210 | 104 | 6.3 | 139 | 16 | US-10-473-127-2037 | Sequence 2037, Ap | 1283 | 91.5 | 5.5 | 639 | 9 | US-09-823-240-5 | Sequence 5, Appl |
| 1211 | 104 | 6.3 | 139 | 17 | US-10-473-127-2040 | Sequence 2040, Ap | 1284 | 91.5 | 5.5 | 681 | 15 | US-10-353-856-33 | Sequence 23, Appl |
| 1212 | 104 | 6.3 | 139 | 17 | US-10-741-600-1050 | Sequence 1050, Ap | 1285 | 91.5 | 5.5 | 1103 | 15 | US-10-369-493-3228 | Sequence 3228, Ap |
| 1213 | 104 | 6.3 | 1712 | 20 | US-11-097-143-8400 | Sequence 8400, Ap | 1286 | 91 | 5.5 | 246 | 14 | US-10-032-201B-188 | Sequence 188, App |
| 1214 | 102.5 | 6.2 | 309 | 15 | US-10-120-907A-24753 | Sequence 24753, A | 1287 | 91 | 5.5 | 2207 | 16 | US-10-437-963-189767 | Sequence 189767, A |
| 1215 | 102 | 6.2 | 309 | 15 | US-10-425-114-41494 | Sequence 41494, A | 1288 | 91 | 5.5 | 4262 | 17 | US-10-704-781-4 | Sequence 4, Appl |
| 1216 | 101.5 | 6.1 | 380 | 15 | US-10-369-493-6206 | Sequence 6206, Ap | 1289 | 91 | 5.5 | 4493 | 17 | US-10-704-781-3 | Sequence 3, Appl |
| 1217 | 101.5 | 6.1 | 590 | 10 | US-09-957-187-12 | Sequence 12, Appl | 1290 | 90.5 | 5.5 | 463 | 15 | US-10-425-114-66913 | Sequence 66913, A |

| | | | | | | | | | | | | | |
|------|------|-----|------|----|----------------------|-------------------|------|------|-----|-------|----|----------------------|-------------------|
| 1291 | 90.5 | 5.5 | 463 | 16 | US-10-425-115-322413 | Sequence 322413, | 1364 | 86.5 | 5.2 | 503 | 15 | US-10-369-493-1943 | Sequence 1943, Ap |
| 1292 | 90.5 | 5.5 | 1705 | 15 | US-10-442-017-17 | Sequence 17, Appl | 1365 | 86.5 | 5.2 | 687 | 15 | US-10-282-122A-53666 | Sequence 53666, A |
| 1293 | 90.5 | 5.5 | 514 | 20 | US-11-097-143-7350 | Sequence 7350, Ap | 1366 | 86.5 | 5.2 | 714 | 18 | US-10-450-763-45506 | Sequence 45506, A |
| 1294 | 90.5 | 5.5 | 1976 | 20 | US-11-097-143-35049 | Sequence 35049, A | 1367 | 86.5 | 5.2 | 714 | 18 | US-10-450-763-46006 | Sequence 46006, A |
| 1295 | 90 | 5.4 | 364 | 14 | US-10-188-012-27 | Sequence 27, Appl | 1368 | 86.5 | 5.2 | 1579 | 18 | US-10-504-582-158 | Sequence 158, App |
| 1296 | 90 | 5.4 | 364 | 17 | US-10-663-497-27 | Sequence 27, Appl | 1369 | 86.5 | 5.2 | 1579 | 18 | US-10-263-929-122 | Sequence 122, App |
| 1297 | 90 | 5.4 | 629 | 20 | US-11-097-143-5313 | Sequence 5313, Ap | 1370 | 86.5 | 5.2 | 2781 | 16 | US-10-723-860-1472 | Sequence 1472, Ap |
| 1298 | 90 | 5.4 | 957 | 10 | US-09-840-746-19 | Sequence 19, Appl | 1371 | 86.5 | 5.2 | 2781 | 18 | US-10-754-342-10 | Sequence 10, Appl |
| 1299 | 90 | 5.4 | 1130 | 16 | US-10-425-115-339478 | Sequence 339478, | 1372 | 86.5 | 5.2 | 2907 | 18 | US-10-754-342-1 | Sequence 1, Appl |
| 1300 | 90 | 5.4 | 1217 | 16 | US-10-734-564-122 | Sequence 122, App | 1373 | 86 | 5.2 | 390 | 17 | US-10-732-923-20210 | Sequence 20210, A |
| 1301 | 90 | 5.4 | 1367 | 9 | US-09-801-368-108 | Sequence 108, App | 1374 | 86 | 5.2 | 857 | 15 | US-10-425-114-45539 | Sequence 45539, A |
| 1302 | 89.5 | 5.4 | 195 | 15 | US-10-074-978A-350 | Sequence 350, App | 1375 | 86 | 5.2 | 1080 | 14 | US-10-205-219-62 | Sequence 62, Appl |
| 1303 | 89.5 | 5.4 | 305 | 14 | US-10-188-012-5 | Sequence 5, Appl | 1376 | 86 | 5.2 | 1086 | 18 | US-10-450-763-58747 | Sequence 58747, A |
| 1304 | 89.5 | 5.4 | 305 | 14 | US-10-188-012-7 | Sequence 7, Appl | 1377 | 86 | 5.2 | 1190 | 18 | US-10-450-763-36034 | Sequence 36034, A |
| 1305 | 89.5 | 5.4 | 305 | 17 | US-10-663-497-5 | Sequence 5, Appl | 1378 | 85.5 | 5.2 | 346 | 15 | US-10-416-328-6 | Sequence 6, Appl |
| 1306 | 89.5 | 5.4 | 305 | 17 | US-10-663-497-7 | Sequence 7, Appl | 1379 | 85.5 | 5.2 | 346 | 15 | US-10-432-290-11 | Sequence 11, Appl |
| 1307 | 89.5 | 5.4 | 1368 | 17 | US-10-732-923-13518 | Sequence 13518, A | 1380 | 85.5 | 5.2 | 652 | 16 | US-10-467-490-5 | Sequence 5, Appl |
| 1308 | 89.5 | 5.4 | 1369 | 17 | US-10-732-923-13517 | Sequence 13517, A | 1381 | 85.5 | 5.2 | 652 | 16 | US-10-467-490-5 | Sequence 5, Appl |
| 1309 | 89 | 5.4 | 416 | 16 | US-10-684-432-68 | Sequence 24429, A | 1382 | 85.5 | 5.2 | 662 | 16 | US-10-425-115-230245 | Sequence 230245, |
| 1310 | 89 | 5.4 | 416 | 15 | US-10-371-525-26 | Sequence 26, Appl | 1383 | 85.5 | 5.2 | 686 | 15 | US-10-282-122A-43763 | Sequence 43763, A |
| 1311 | 89 | 5.4 | 416 | 15 | US-10-371-089-26 | Sequence 26, Appl | 1384 | 85.5 | 5.2 | 781 | 15 | US-10-074-978A-286 | Sequence 286, App |
| 1312 | 89 | 5.4 | 416 | 15 | US-10-371-089-26 | Sequence 26, Appl | 1385 | 85.5 | 5.2 | 781 | 15 | US-10-664-456-16 | Sequence 16, Appl |
| 1313 | 89 | 5.4 | 416 | 15 | US-10-371-260-26 | Sequence 26, Appl | 1386 | 85.5 | 5.2 | 792 | 9 | US-09-802-207-27 | Sequence 27, Appl |
| 1314 | 89 | 5.4 | 416 | 16 | US-10-684-432-68 | Sequence 24429, A | 1387 | 85.5 | 5.2 | 841 | 16 | US-10-467-490-2 | Sequence 2, Appl |
| 1315 | 89 | 5.4 | 416 | 18 | US-10-287-436A-533 | Sequence 533, App | 1388 | 85.5 | 5.2 | 841 | 20 | US-11-097-143-39828 | Sequence 39828, A |
| 1316 | 89 | 5.4 | 416 | 18 | US-10-287-436A-1224 | Sequence 1224, Ap | 1389 | 85.5 | 5.2 | 862 | 16 | US-10-437-963-115723 | Sequence 115723, |
| 1317 | 89 | 5.4 | 846 | 20 | US-11-097-143-35090 | Sequence 35090, A | 1390 | 85.5 | 5.2 | 862 | 16 | US-10-437-963-115723 | Sequence 3, Appl |
| 1318 | 89 | 5.4 | 882 | 20 | US-11-097-143-28098 | Sequence 28098, A | 1391 | 85.5 | 5.2 | 1794 | 10 | US-09-965-738-299 | Sequence 299, App |
| 1319 | 89 | 5.4 | 1441 | 16 | US-10-437-963-138354 | Sequence 138354, | 1392 | 85.5 | 5.2 | 1799 | 10 | US-09-965-738-149 | Sequence 149, App |
| 1320 | 89 | 5.4 | 2588 | 16 | US-10-437-963-138279 | Sequence 138279, | 1393 | 85.5 | 5.2 | 1821 | 10 | US-09-965-738-82 | Sequence 82, Appl |
| 1321 | 88.5 | 5.3 | 165 | 15 | US-10-424-599-216371 | Sequence 216371, | 1394 | 85.5 | 5.2 | 2055 | 14 | US-10-193-874-20 | Sequence 20, Appl |
| 1322 | 88.5 | 5.3 | 358 | 18 | US-10-450-763-45673 | Sequence 45673, A | 1395 | 85.5 | 5.2 | 2586 | 9 | US-09-729-485A-11 | Sequence 11, Appl |
| 1323 | 88.5 | 5.3 | 481 | 20 | US-11-097-143-17043 | Sequence 17043, A | 1396 | 85.5 | 5.2 | 2586 | 9 | US-09-729-485A-14 | Sequence 14, Appl |
| 1324 | 88.5 | 5.3 | 615 | 15 | US-10-238-818-14 | Sequence 14, Appl | 1397 | 85.5 | 5.2 | 2586 | 9 | US-09-802-318-11 | Sequence 11, Appl |
| 1325 | 88 | 5.3 | 125 | 15 | US-10-424-599-221671 | Sequence 221671, | 1398 | 85.5 | 5.2 | 2586 | 9 | US-09-802-318-14 | Sequence 14, Appl |
| 1326 | 88 | 5.3 | 995 | 10 | US-09-984-130-48 | Sequence 48, Appl | 1399 | 85.5 | 5.2 | 2586 | 9 | US-09-905-129-11 | Sequence 11, Appl |
| 1327 | 88 | 5.3 | 995 | 10 | US-09-836-353A-48 | Sequence 48, Appl | 1400 | 85.5 | 5.2 | 2586 | 9 | US-09-905-129-14 | Sequence 14, Appl |
| 1328 | 88 | 5.3 | 3507 | 15 | US-10-369-493-5784 | Sequence 5784, Ap | 1401 | 85.5 | 5.2 | 2586 | 9 | US-09-991-630-11 | Sequence 11, Appl |
| 1329 | 87.5 | 5.3 | 536 | 14 | US-10-218-743-21 | Sequence 21, Appl | 1402 | 85.5 | 5.2 | 2586 | 9 | US-09-991-630-14 | Sequence 14, Appl |
| 1330 | 87.5 | 5.3 | 555 | 14 | US-10-218-743-15 | Sequence 15, Appl | 1403 | 85.5 | 5.2 | 2586 | 15 | US-10-454-351-11 | Sequence 11, Appl |
| 1331 | 87.5 | 5.3 | 555 | 14 | US-10-218-743-18 | Sequence 18, Appl | 1404 | 85.5 | 5.2 | 2586 | 15 | US-10-454-351-14 | Sequence 14, Appl |
| 1332 | 87.5 | 5.3 | 649 | 16 | US-10-425-115-295178 | Sequence 295178, | 1405 | 85.5 | 5.2 | 2587 | 9 | US-09-729-485A-16 | Sequence 16, Appl |
| 1333 | 87.5 | 5.3 | 717 | 15 | US-10-104-047-3100 | Sequence 3100, Ap | 1406 | 85.5 | 5.2 | 2587 | 9 | US-09-802-318-16 | Sequence 16, Appl |
| 1334 | 87.5 | 5.3 | 1085 | 14 | US-10-159-339-10 | Sequence 10, Appl | 1407 | 85.5 | 5.2 | 2587 | 9 | US-09-905-129-16 | Sequence 16, Appl |
| 1335 | 87.5 | 5.3 | 1085 | 15 | US-10-041-615-108 | Sequence 108, App | 1408 | 85.5 | 5.2 | 2587 | 9 | US-09-991-630-15 | Sequence 15, Appl |
| 1336 | 87.5 | 5.3 | 1085 | 15 | US-10-436-715-21 | Sequence 21, Appl | 1409 | 85.5 | 5.2 | 2587 | 15 | US-10-454-351-16 | Sequence 16, Appl |
| 1337 | 87.5 | 5.3 | 1085 | 15 | US-10-436-715-75 | Sequence 75, Appl | 1410 | 85.5 | 5.2 | 2587 | 9 | US-09-991-630-24 | Sequence 24, Appl |
| 1338 | 87.5 | 5.3 | 1322 | 15 | US-10-369-493-13040 | Sequence 13040, A | 1411 | 85.5 | 5.2 | 2589 | 15 | US-10-454-351-24 | Sequence 24, Appl |
| 1339 | 87 | 5.3 | 288 | 9 | US-09-216-393-341 | Sequence 341, App | 1412 | 85.5 | 5.2 | 5877 | 14 | US-10-142-515-11 | Sequence 11, Appl |
| 1340 | 87 | 5.3 | 288 | 14 | US-09-216-393-344 | Sequence 344, App | 1413 | 85.5 | 5.2 | 5935 | 14 | US-10-243-243A-8 | Sequence 8, Appl |
| 1341 | 87 | 5.3 | 288 | 14 | US-10-321-856-341 | Sequence 341, App | 1414 | 85.5 | 5.2 | 11721 | 10 | US-09-965-738-162 | Sequence 162, App |
| 1342 | 87 | 5.3 | 288 | 14 | US-10-321-856-344 | Sequence 344, App | 1415 | 85.5 | 5.2 | 22152 | 16 | US-10-715-066-5 | Sequence 5, Appl |
| 1343 | 87 | 5.3 | 363 | 17 | US-10-926-543-87 | Sequence 87, Appl | 1416 | 85 | 5.1 | 326 | 20 | US-11-097-143-41430 | Sequence 41430, A |
| 1344 | 87 | 5.3 | 363 | 18 | US-10-631-467-1565 | Sequence 1565, Ap | 1417 | 85 | 5.1 | 472 | 16 | US-10-746-264-7 | Sequence 7, Appl |
| 1345 | 87 | 5.3 | 611 | 15 | US-10-425-114-54378 | Sequence 54378, A | 1418 | 85 | 5.1 | 472 | 17 | US-10-976-042-25 | Sequence 25, Appl |
| 1346 | 87 | 5.3 | 631 | 9 | US-09-841-132-325 | Sequence 325, App | 1419 | 85 | 5.1 | 472 | 18 | US-10-995-266-7 | Sequence 7, Appl |
| 1347 | 87 | 5.3 | 631 | 16 | US-10-872-155-325 | Sequence 325, App | 1420 | 85 | 5.1 | 573 | 16 | US-10-437-963-142231 | Sequence 142231, |
| 1348 | 87 | 5.3 | 650 | 16 | US-10-425-115-353793 | Sequence 353793, | 1421 | 85 | 5.1 | 627 | 15 | US-10-369-493-18499 | Sequence 18499, A |
| 1349 | 87 | 5.3 | 664 | 17 | US-10-197-220-168 | Sequence 168, App | 1422 | 85 | 5.1 | 635 | 15 | US-10-425-114-58558 | Sequence 58558, A |
| 1350 | 87 | 5.3 | 1016 | 10 | US-09-841-260-95 | Sequence 95, Appl | 1423 | 85 | 5.1 | 637 | 15 | US-10-949-749-2621 | Sequence 2621, Ap |
| 1351 | 87 | 5.3 | 1016 | 13 | US-10-007-693-95 | Sequence 95, Appl | 1424 | 85 | 5.1 | 782 | 16 | US-10-739-930-6279 | Sequence 6279, Ap |
| 1352 | 87 | 5.3 | 1016 | 16 | US-10-467-534-41 | Sequence 41, Appl | 1425 | 85 | 5.1 | 1049 | 20 | US-11-097-143-7953 | Sequence 7953, Ap |
| 1353 | 87 | 5.3 | 1016 | 16 | US-10-762-058-95 | Sequence 95, Appl | 1426 | 85 | 5.1 | 1061 | 15 | US-10-291-265-347 | Sequence 347, App |
| 1354 | 87 | 5.3 | 1016 | 17 | US-10-197-220-95 | Sequence 95, Appl | 1427 | 85 | 5.1 | 1091 | 15 | US-10-291-265-348 | Sequence 348, App |
| 1355 | 87 | 5.3 | 1016 | 17 | US-10-498-327-95 | Sequence 95, Appl | 1428 | 85 | 5.1 | 1205 | 18 | US-10-756-149-5715 | Sequence 5715, Ap |
| 1356 | 87 | 5.3 | 1537 | 9 | US-09-801-368-108 | Sequence 104, App | 1429 | 85 | 5.1 | 1354 | 20 | US-11-097-143-36711 | Sequence 36711, A |
| 1357 | 87 | 5.3 | 1537 | 15 | US-10-369-493-1398 | Sequence 1398, Ap | 1430 | 85 | 5.1 | 1438 | 15 | US-10-297-639-2 | Sequence 2, Appl |
| 1358 | 87 | 5.3 | 1537 | 17 | US-10-324-035-17 | Sequence 17, Appl | 1431 | 85 | 5.1 | 1671 | 15 | US-10-187-975-18 | Sequence 18, Appl |
| 1359 | 87 | 5.3 | 1575 | 20 | US-11-097-143-28878 | Sequence 28878, A | 1432 | 85 | 5.1 | 1765 | 17 | US-10-766-993-1 | Sequence 1, Appl |
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| 150 | 84 | 5.1 | 216 | 3 | US-08-928-361B-8 | Sequence 8, Appli | 223 | 81 | 4.9 | 531 | 4 | US-09-248-796A-15560 | Sequence 15560, A |
| 151 | 84 | 5.1 | 216 | 3 | US-08-928-361B-27 | Sequence 27, Appl | 224 | 81 | 4.9 | 855 | 2 | US-08-816-693A-2 | Sequence 2, Appli |
| 152 | 84 | 5.1 | 216 | 4 | US-09-588-995A-8 | Sequence 8, Appli | 225 | 81 | 4.9 | 855 | 3 | US-08-885-231-2 | Sequence 2, Appli |
| 153 | 84 | 5.1 | 920 | 1 | US-07-718-575-10 | Sequence 10, Appl | 226 | 81 | 4.9 | 855 | 3 | US-09-496-672-2 | Sequence 2, Appli |
| 154 | 84 | 5.1 | 920 | 1 | US-08-481-206-10 | Sequence 10, Appl | 227 | 81 | 4.9 | 855 | 4 | US-09-618-425-11 | Sequence 11, Appl |
| 155 | 84 | 5.1 | 920 | 2 | US-08-486-269A-10 | Sequence 10, Appl | 228 | 81 | 4.9 | 883 | 4 | US-09-248-796A-18931 | Sequence 18931, A |
| 156 | 84 | 5.1 | 1721 | 3 | US-08-700-651-5 | Sequence 5, Appli | 229 | 80.5 | 4.9 | 334 | 4 | US-09-197-970B-7 | Sequence 7, Appli |
| 157 | 84 | 5.1 | 1721 | 3 | US-08-928-361B-6 | Sequence 6, Appli | 230 | 80.5 | 4.9 | 478 | 4 | US-09-345-473E-51 | Sequence 51, Appl |
| 158 | 84 | 5.1 | 1721 | 4 | US-09-588-995A-6 | Sequence 6, Appli | 231 | 80.5 | 4.9 | 556 | 4 | US-08-233-087A-2 | Sequence 2, Appli |
| 159 | 84 | 5.1 | 1837 | 3 | US-08-928-361B-5 | Sequence 5, Appli | 232 | 80.5 | 4.9 | 595 | 2 | US-09-949-016-11052 | Sequence 11052, A |
| 160 | 84 | 5.1 | 1837 | 4 | US-09-588-995A-5 | Sequence 5, Appli | 233 | 80.5 | 4.9 | 595 | 3 | US-09-006-353A-9 | Sequence 9, Appli |
| 161 | 83.5 | 5.0 | 346 | 2 | US-08-687-702-36 | Sequence 36, Appl | 234 | 80.5 | 4.9 | 595 | 4 | US-09-573-986-9 | Sequence 9, Appli |
| 162 | 83.5 | 5.0 | 393 | 3 | US-09-377-557-14 | Sequence 14, Appl | 235 | 80.5 | 4.9 | 595 | 4 | US-09-949-016-6048 | Sequence 6048, Ap |
| 163 | 83.5 | 5.0 | 562 | 2 | US-08-687-702-1 | Sequence 1, Appli | 236 | 80.5 | 4.9 | 624 | 4 | US-09-877-730-24 | Sequence 24, Appl |
| 164 | 83.5 | 5.0 | 879 | 1 | US-08-220-151-2 | Sequence 2, Appli | 237 | 80.5 | 4.9 | 642 | 4 | US-09-949-016-8043 | Sequence 8043, Ap |
| 165 | 83.5 | 5.0 | 879 | 1 | US-08-220-151-3 | Sequence 3, Appli | 238 | 80.5 | 4.9 | 673 | 4 | US-09-949-016-7388 | Sequence 7388, Ap |
| 166 | 83.5 | 5.0 | 879 | 1 | US-08-413-118-2 | Sequence 2, Appli | 239 | 80.5 | 4.9 | 712 | 4 | US-09-877-730-22 | Sequence 22, Appl |
| 167 | 83.5 | 5.0 | 879 | 1 | US-08-413-118-3 | Sequence 3, Appli | 240 | 80.5 | 4.9 | 793 | 4 | US-09-877-730-28 | Sequence 28, Appl |
| 168 | 83.5 | 5.0 | 879 | 1 | US-08-413-118-106 | Sequence 106, App | 241 | 80.5 | 4.9 | 991 | 4 | US-09-877-730-12 | Sequence 12, Appl |
| 169 | 83.5 | 5.0 | 879 | 3 | US-08-473-446-2 | Sequence 2, Appli | 242 | 80.5 | 4.9 | 1069 | 4 | US-09-877-730-2 | Sequence 2, Appli |
| 170 | 83.5 | 5.0 | 879 | 3 | US-08-473-446-3 | Sequence 3, Appli | 243 | 80.5 | 4.9 | 1072 | 4 | US-09-877-730-18 | Sequence 18, Appl |
| 171 | 83.5 | 5.0 | 879 | 3 | US-08-473-446-106 | Sequence 106, App | 244 | 80.5 | 4.9 | 1150 | 4 | US-09-877-730-8 | Sequence 8, Appli |
| 172 | 83.5 | 5.0 | 5179 | 4 | US-09-538-092-1258 | Sequence 1258, Ap | 245 | 80 | 4.8 | 52 | 1 | US-08-225-477B-10 | Sequence 10, Appl |
| 173 | 83 | 5.0 | 147 | 3 | US-09-230-637-43 | Sequence 43, Appl | 246 | 80 | 4.8 | 52 | 5 | PCT-US95-04353-10 | Sequence 10, Appl |
| 174 | 83 | 5.0 | 175 | 4 | US-09-270-767-33553 | Sequence 33553, A | 247 | 80 | 4.8 | 95 | 4 | US-09-252-991A-28504 | Sequence 28504, A |
| 175 | 83 | 5.0 | 175 | 4 | US-09-270-767-48770 | Sequence 48770, A | 248 | 80 | 4.8 | 251 | 4 | US-09-248-796A-23216 | Sequence 23216, A |
| 176 | 83 | 5.0 | 205 | 4 | US-09-248-796A-21984 | Sequence 21984, A | 249 | 80 | 4.8 | 257 | 4 | US-09-902-540-15102 | Sequence 15102, A |
| 177 | 83 | 5.0 | 351 | 4 | US-09-248-796A-23675 | Sequence 23675, A | 250 | 80 | 4.8 | 372 | 4 | US-09-248-796A-19896 | Sequence 19896, A |
| 178 | 83 | 5.0 | 409 | 4 | US-09-538-092-1214 | Sequence 1214, Ap | 251 | 80 | 4.8 | 404 | 4 | US-09-270-767-41751 | Sequence 41751, A |
| 179 | 83 | 5.0 | 409 | 4 | US-09-949-016-6281 | Sequence 6281, Ap | 252 | 80 | 4.8 | 423 | 4 | US-09-270-767-44448 | Sequence 44448, A |
| 180 | 83 | 5.0 | 454 | 4 | US-09-949-016-11120 | Sequence 11120, A | 253 | 80 | 4.8 | 451 | 1 | US-08-287-001A-2 | Sequence 2, Appli |
| 181 | 83 | 5.0 | 736 | 3 | US-09-457-040B-26 | Sequence 26, Appl | 254 | 80 | 4.8 | 451 | 5 | PCT-US95-09941-2 | Sequence 2, Appli |
| 182 | 82.5 | 5.0 | 203 | 4 | US-09-270-767-35040 | Sequence 35040, A | 255 | 80 | 4.8 | 468 | 2 | US-08-959-011-3 | Sequence 3, Appli |
| 183 | 82.5 | 5.0 | 203 | 4 | US-09-270-767-50257 | Sequence 50257, A | 256 | 80 | 4.8 | 823 | 4 | US-09-248-796A-16699 | Sequence 16699, A |
| 184 | 82.5 | 5.0 | 219 | 3 | US-09-134-001C-5651 | Sequence 5651, Ap | 257 | 80 | 4.8 | 893 | 4 | US-08-189-738A-18 | Sequence 18, Appl |
| 185 | 82.5 | 5.0 | 447 | 4 | US-09-252-991A-28081 | Sequence 28081, A | 258 | 79.5 | 4.8 | 153 | 4 | US-09-252-991A-17880 | Sequence 17880, A |
| 186 | 82.5 | 5.0 | 591 | 4 | US-09-270-767-32687 | Sequence 32687, A | 259 | 79.5 | 4.8 | 154 | 4 | US-09-270-767-40476 | Sequence 40476, A |
| 187 | 82.5 | 5.0 | 591 | 4 | US-09-270-767-47904 | Sequence 47904, A | 260 | 79.5 | 4.8 | 154 | 4 | US-09-270-767-55692 | Sequence 55692, A |
| 188 | 82.5 | 5.0 | 790 | 4 | US-09-949-016-7017 | Sequence 7017, Ap | 261 | 79.5 | 4.8 | 324 | 4 | US-09-489-039A-8593 | Sequence 8593, Ap |
| 189 | 82.5 | 5.0 | 790 | 4 | US-09-949-016-8169 | Sequence 8169, Ap | 262 | 79.5 | 4.8 | 374 | 4 | US-09-248-796A-17283 | Sequence 2, Appli |
| 190 | 82.5 | 5.0 | 790 | 4 | US-09-949-016-8170 | Sequence 8170, Ap | 263 | 79.5 | 4.8 | 461 | 1 | US-08-385-229-2 | Sequence 2, Appli |
| 191 | 82.5 | 5.0 | 866 | 1 | US-08-405-392-17 | Sequence 17, Appl | 264 | 79.5 | 4.8 | 461 | 2 | US-08-650-000-2 | Sequence 2, Appli |
| 192 | 82.5 | 5.0 | 866 | 3 | US-08-487-691-17 | Sequence 17, Appl | 265 | 79.5 | 4.8 | 461 | 3 | US-09-042-785A-7 | Sequence 7, Appli |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|-------------------|
| 266 | 79.5 | 4.8 | 461 | 3 | US-08-477-347-3 | Sequence 3, Appli | 357 | 77 | 4.6 | 162 | 3 | US-09-068-140A-2 | Sequence 2, Appli |
| 267 | 79.5 | 4.8 | 461 | 3 | US-09-006-353A-4 | Sequence 4, Appli | 358 | 77 | 4.6 | 173 | 3 | US-09-068-140A-13 | Sequence 13, Appl |
| 268 | 79.5 | 4.8 | 461 | 3 | US-08-476-862-2 | Sequence 2, Appli | 359 | 77 | 4.6 | 249 | 3 | US-08-700-651-15 | Sequence 15, Appl |
| 269 | 79.5 | 4.8 | 461 | 4 | US-09-573-986-4 | Sequence 4, Appli | 360 | 77 | 4.6 | 249 | 3 | US-08-928-361B-20 | Sequence 20, Appl |
| 270 | 79.5 | 4.8 | 461 | 4 | US-08-406-824A-2 | Sequence 2, Appli | 361 | 77 | 4.6 | 249 | 4 | US-09-588-995A-20 | Sequence 20, Appl |
| 271 | 79.5 | 4.8 | 461 | 4 | US-09-800-909-2 | Sequence 2, Appli | 362 | 77 | 4.6 | 714 | 4 | US-09-949-016-7038 | Sequence 7038, Ap |
| 272 | 79.5 | 4.8 | 461 | 4 | US-09-758-124-2 | Sequence 3, Appli | 363 | 77 | 4.6 | 908 | 4 | US-09-949-016-7580 | Sequence 7580, Ap |
| 273 | 79.5 | 4.8 | 461 | 4 | US-09-800-908-3 | Sequence 3, Appli | 364 | 77 | 4.6 | 1140 | 4 | US-09-538-092-647 | Sequence 647, App |
| 274 | 79.5 | 4.8 | 461 | 4 | US-09-896-096A-17 | Sequence 17, Appl | 365 | 77 | 4.6 | 1401 | 3 | US-09-127-670-6 | Sequence 6, Appli |
| 275 | 79.5 | 4.8 | 461 | 4 | US-09-949-016-6019 | Sequence 6019, Ap | 366 | 77 | 4.6 | 2123 | 3 | US-08-968-685A-10 | Sequence 10, Appl |
| 276 | 79.5 | 4.8 | 461 | 6 | 5395760-2 | Patent No. 5395760 | 367 | 76.5 | 4.6 | 134 | 4 | US-09-248-796A-27317 | Sequence 27317, A |
| 277 | 79.5 | 4.8 | 461 | 6 | 5395760-2 | Patent No. 5395760 | 368 | 76.5 | 4.6 | 240 | 2 | US-08-114-555A-8 | Sequence 8, Appli |
| 278 | 79.5 | 4.8 | 461 | 4 | US-09-949-016-7840 | Sequence 7840, Ap | 369 | 76.5 | 4.6 | 240 | 2 | US-08-559-397A-14 | Sequence 14, Appl |
| 279 | 79.5 | 4.8 | 515 | 4 | US-09-198-452A-1094 | Sequence 1094, Ap | 370 | 76.5 | 4.6 | 303 | 4 | US-09-248-796A-14269 | Sequence 14269, A |
| 280 | 79.5 | 4.8 | 515 | 4 | US-09-438-185A-1021 | Sequence 1021, Ap | 371 | 76.5 | 4.6 | 348 | 3 | US-09-216-295-16 | Sequence 16, Appl |
| 281 | 79.5 | 4.8 | 559 | 4 | US-09-543-681A-7241 | Sequence 7241, Ap | 372 | 76.5 | 4.6 | 348 | 4 | US-09-632-570-16 | Sequence 16, Appl |
| 282 | 79.5 | 4.8 | 601 | 4 | US-09-270-767-45496 | Sequence 45496, A | 373 | 76.5 | 4.6 | 348 | 4 | US-09-632-573-46 | Sequence 46, Appl |
| 283 | 79.5 | 4.8 | 756 | 1 | US-08-434-730-16 | Sequence 16, Appl | 374 | 76.5 | 4.6 | 382 | 1 | US-08-415-818-7 | Sequence 7, Appli |
| 284 | 79.5 | 4.8 | 985 | 5 | PCT-US96-03916-6 | Sequence 6, Appli | 375 | 76.5 | 4.6 | 382 | 2 | US-08-894-236-7 | Sequence 7, Appli |
| 285 | 79.5 | 4.8 | 985 | 5 | PCT-US96-03916-6 | Sequence 6, Appli | 376 | 76.5 | 4.6 | 382 | 2 | US-08-894-236-7 | Sequence 7, Appli |
| 286 | 79.5 | 4.8 | 1114 | 4 | US-09-262-537-34 | Sequence 34, Appl | 377 | 76.5 | 4.6 | 382 | 5 | PCT-US96-01444-7 | Sequence 7, Appli |
| 287 | 79.5 | 4.8 | 1123 | 4 | US-09-262-537-34 | Sequence 34, Appl | 378 | 76.5 | 4.6 | 397 | 4 | US-09-198-452A-201 | Sequence 201, App |
| 288 | 79.5 | 4.8 | 1177 | 4 | US-09-262-537-2 | Sequence 2, Appli | 379 | 76.5 | 4.6 | 397 | 4 | US-09-438-185A-188 | Sequence 188, App |
| 289 | 79.5 | 4.8 | 1403 | 4 | US-09-262-537-6 | Sequence 6, Appli | 380 | 76.5 | 4.6 | 452 | 4 | US-09-248-796A-16219 | Sequence 16219, A |
| 290 | 79 | 4.8 | 175 | 3 | US-08-700-651-12 | Sequence 12, Appl | 381 | 76.5 | 4.6 | 484 | 1 | US-08-127-499A-26 | Sequence 26, Appl |
| 291 | 79 | 4.8 | 175 | 3 | US-08-928-361B-17 | Sequence 17, Appl | 382 | 76.5 | 4.6 | 484 | 1 | US-08-482-847-26 | Sequence 26, Appl |
| 292 | 79 | 4.8 | 175 | 4 | US-09-588-995A-17 | Sequence 17, Appl | 383 | 76.5 | 4.6 | 901 | 4 | US-09-248-796A-14747 | Sequence 14747, A |
| 293 | 79 | 4.8 | 217 | 4 | US-09-949-016-11174 | Sequence 11174, A | 384 | 76.5 | 4.6 | 1013 | 3 | US-08-860-886-2 | Sequence 2, Appli |
| 294 | 79 | 4.8 | 334 | 4 | US-09-107-532A-6336 | Sequence 6336, Ap | 385 | 76.5 | 4.6 | 5037 | 4 | US-09-424-783-4 | Sequence 4, Appli |
| 295 | 79 | 4.8 | 374 | 4 | US-09-489-847-166 | Sequence 166, App | 386 | 76 | 4.6 | 5037 | 4 | US-09-270-767-61124 | Sequence 4, Appli |
| 305 | 79 | 4.8 | 398 | 4 | US-09-248-796A-21599 | Sequence 21599, A | 387 | 76 | 4.6 | 299 | 4 | US-09-270-767-44350 | Sequence 44350, A |
| 306 | 79 | 4.8 | 638 | 4 | US-09-248-796A-18739 | Sequence 18739, A | 388 | 76 | 4.6 | 321 | 4 | US-09-248-796A-20146 | Sequence 20146, A |
| 307 | 79 | 4.8 | 1312 | 3 | US-09-345-882-29 | Sequence 29, Appl | 389 | 76 | 4.6 | 345 | 4 | US-09-543-681A-6150 | Sequence 6150, Ap |
| 308 | 79 | 4.8 | 1848 | 3 | US-08-296-791-6 | Sequence 6, Appli | 390 | 76 | 4.6 | 380 | 3 | US-09-134-001C-4558 | Sequence 4558, Ap |
| 309 | 79 | 4.8 | 1848 | 4 | US-09-839-996-6 | Sequence 6, Appli | 391 | 76 | 4.6 | 386 | 4 | US-09-328-352-4722 | Sequence 4722, Ap |
| 310 | 79 | 4.8 | 1848 | 4 | US-10-080-505-6 | Sequence 6, Appli | 392 | 76 | 4.6 | 402 | 4 | US-09-270-767-45612 | Sequence 45612, A |
| 311 | 79 | 4.8 | 1848 | 4 | US-10-080-505-6 | Sequence 6, Appli | 393 | 76 | 4.6 | 563 | 4 | US-09-949-016-10405 | Sequence 10405, A |
| 312 | 79 | 4.8 | 1848 | 5 | PCT-US95-10661A-6 | Sequence 6, Appli | 402 | 76 | 4.6 | 687 | 1 | US-08-232-538-6 | Sequence 6, Appli |
| 313 | 79 | 4.8 | 3969 | 3 | US-08-061-376-5 | Sequence 5, Appli | 403 | 76 | 4.6 | 687 | 1 | US-08-232-538-6 | Sequence 6, Appli |
| 314 | 78.5 | 4.7 | 130 | 3 | US-08-700-651-9 | Sequence 9, Appli | 404 | 76 | 4.6 | 687 | 3 | US-09-427-353-2 | Sequence 2, Appli |
| 315 | 78.5 | 4.7 | 130 | 3 | US-08-928-361B-14 | Sequence 14, Appl | 405 | 76 | 4.6 | 687 | 3 | US-08-874-678-1 | Sequence 1, Appli |
| 316 | 78.5 | 4.7 | 130 | 4 | US-09-588-995A-14 | Sequence 14, Appl | 406 | 76 | 4.6 | 758 | 2 | US-08-643-839-1 | Sequence 1, Appli |
| 317 | 78.5 | 4.7 | 324 | 4 | US-09-248-796A-23680 | Sequence 23680, A | 407 | 76 | 4.6 | 758 | 3 | US-09-051-363-24 | Sequence 24, Appl |
| 318 | 78.5 | 4.7 | 324 | 4 | US-09-489-039A-9383 | Sequence 9383, Ap | 408 | 76 | 4.6 | 758 | 3 | US-09-348-886-1 | Sequence 1, Appli |
| 319 | 78.5 | 4.7 | 431 | 4 | US-09-949-016-8402 | Sequence 8402, Ap | 409 | 76 | 4.6 | 758 | 3 | US-08-232-538-14 | Sequence 14, Appl |
| 320 | 78.5 | 4.7 | 542 | 4 | US-09-538-092-289 | Sequence 289, App | 410 | 76 | 4.6 | 780 | 2 | US-08-786-164-14 | Sequence 14, Appl |
| 321 | 78.5 | 4.7 | 595 | 1 | US-08-225-989-2 | Sequence 2, Appli | 411 | 76 | 4.6 | 780 | 4 | US-09-248-796A-16090 | Sequence 16090, A |
| 322 | 78.5 | 4.7 | 595 | 1 | US-08-570-923-2 | Sequence 2, Appli | 412 | 76 | 4.6 | 985 | 4 | US-09-078-347A-3 | Sequence 3, Appli |
| 323 | 78.5 | 4.7 | 595 | 1 | US-08-580-014-2 | Sequence 2, Appli | 413 | 76 | 4.6 | 1014 | 3 | US-09-596-248D-25 | Sequence 25, Appl |
| 324 | 78.5 | 4.7 | 595 | 3 | US-09-921-785-2 | Sequence 2, Appli | 414 | 76 | 4.6 | 1014 | 4 | US-09-596-248D-47 | Sequence 47, Appl |
| 325 | 78.5 | 4.7 | 595 | 4 | US-09-921-667-6 | Sequence 6, Appli | 415 | 76 | 4.6 | 1063 | 4 | US-08-750-141A-3 | Sequence 3, Appli |
| 326 | 78.5 | 4.7 | 595 | 4 | US-09-628-126-2 | Sequence 2, Appli | 416 | 76 | 4.6 | 1338 | 3 | US-09-119-014D-6 | Sequence 6, Appli |
| 327 | 78.5 | 4.7 | 653 | 4 | US-09-520-781-10 | Sequence 10, Appl | 417 | 76 | 4.6 | 1338 | 4 | US-08-961-083-90 | Sequence 90, Appl |
| 328 | 78.5 | 4.7 | 3224 | 2 | US-08-705-660-34 | Sequence 34, Appl | 418 | 76 | 4.6 | 1401 | 3 | US-08-781-891-206 | Sequence 206, App |
| 329 | 78.5 | 4.7 | 3224 | 3 | US-08-989-045-34 | Sequence 34, Appl | 419 | 76 | 4.6 | 1401 | 3 | US-09-618-166-206 | Sequence 206, App |
| 330 | 78.5 | 4.7 | 3224 | 4 | US-09-538-092-1161 | Sequence 1161, Ap | 420 | 76 | 4.6 | 1426 | 3 | US-09-136-574A-43 | Sequence 43, Appl |
| 331 | 78.5 | 4.7 | 3224 | 4 | US-09-315-355A-34 | Sequence 34, Appl | 421 | 76 | 4.6 | 1645 | 4 | US-09-976-594-769 | Sequence 769, App |
| 332 | 78.5 | 4.7 | 280 | 4 | US-09-806-536A-1 | Sequence 1, Appli | 422 | 75.5 | 4.6 | 258 | 3 | US-08-961-083-90 | Sequence 90, Appl |
| 333 | 78 | 4.7 | 300 | 4 | US-09-248-796A-16245 | Sequence 16245, A | 423 | 75.5 | 4.6 | 258 | 4 | US-09-536-784-90 | Sequence 90, Appl |
| 334 | 78 | 4.7 | 398 | 4 | US-09-248-796A-14978 | Sequence 14978, A | 424 | 75.5 | 4.6 | 348 | 1 | US-08-035-392-2 | Sequence 2, Appli |
| 335 | 78 | 4.7 | 494 | 4 | US-09-248-796A-16546 | Sequence 16546, A | 425 | 75.5 | 4.6 | 348 | 1 | US-08-504-511A-2 | Sequence 2, Appli |
| 336 | 78 | 4.7 | 564 | 4 | US-10-069-540A-2 | Sequence 2, Appli | 426 | 75.5 | 4.6 | 430 | 1 | US-08-035-392-4 | Sequence 4, Appli |
| 337 | 78 | 4.7 | 609 | 4 | US-09-198-452A-579 | Sequence 579, App | 427 | 75.5 | 4.6 | 430 | 1 | US-08-504-511A-4 | Sequence 4, Appli |
| 338 | 78 | 4.7 | 1006 | 4 | US-09-949-016-7897 | Sequence 7897, Ap | 428 | 75.5 | 4.6 | 451 | 3 | US-09-134-001C-4461 | Sequence 4, Appli |
| 339 | 78 | 4.7 | 1442 | 1 | US-08-015-986A-3 | Sequence 3, Appli | 429 | 75.5 | 4.6 | 453 | 4 | US-09-230-225B-4 | Sequence 4, Appli |
| 340 | 78 | 4.7 | 1442 | 2 | US-08-446-363-3 | Sequence 3, Appli | 430 | 75.5 | 4.6 | 510 | 4 | US-09-270-767-43633 | Sequence 43633, A |
| 341 | 78 | 4.7 | 1744 | 4 | US-09-438-185A-542 | Sequence 542, App | 431 | 75.5 | 4.6 | 511 | 1 | US-08-220-151-17 | Sequence 17, Appl |
| 342 | 78 | 4.7 | 2176 | 4 | US-09-949-016-9923 | Sequence 9923, Ap | 432 | 75.5 | 4.6 | 511 | 3 | US-08-413-118-17 | Sequence 17, Appl |
| 343 | 78 | 4.7 | 514 | 3 | US-09-377-557-10 | Sequence 10, Appl | 433 | 75.5 | 4.6 | 511 | 3 | US-08-473-446-17 | Sequence 17, Appl |
| 344 | 77.5 | 4.7 | 514 | 3 | US-08-738-168B-15 | Sequence 15, Appl | 434 | 75.5 | 4.6 | 565 | 3 | US-08-961-083-218 | Sequence 218, App |
| 345 | 77.5 | 4.7 | 1262 | 4 | US-09-107-433-5067 | Sequence 5067, Ap | 435 | 75.5 | 4.6 | 565 | 4 | US-09-536-784-218 | Sequence 218, App |
| 346 | 77.5 | 4.7 | 1475 | 4 | US-09-538-092-1160 | Sequence 1160, Ap | 436 | 75.5 | 4.6 | 639 | 4 | US-09-949-016-6812 | Sequence 6812, Ap |
| 347 | 77.5 | 4.7 | 3969 | 4 | US-09-538-092-1262 | Sequence 1262, Ap | 437 | 75.5 | 4.6 | 641 | 4 | US-10-164-595-46 | Sequence 46, Appl |
| 348 | 77.5 | 4.7 | | | | | 438 | 75.5 | 4.6 | 652 | 4 | US-09-949-016-7323 | Sequence 7323, Ap |

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|-----|------|-----|------|---|----------------------|---------------------|-----|------|-----|------|---|----------------------|--------------------|
| 439 | 75 | 4.5 | 210 | 4 | US-09-270-767-32951 | Sequence 32951, A | 512 | 74 | 4.5 | 323 | 4 | US-09-270-767-44688 | Sequence 44688, A |
| 440 | 75 | 4.5 | 420 | 4 | US-09-270-767-48168 | Sequence 48168, A | 513 | 74 | 4.5 | 339 | 1 | US-08-433-854-4 | Sequence 4, Appli |
| 441 | 75 | 4.5 | 424 | 1 | US-08-419-414-2 | Sequence 2, Appli | 514 | 74 | 4.5 | 339 | 1 | US-08-174-745A-4 | Sequence 4, Appli |
| 442 | 75 | 4.5 | 425 | 4 | US-09-748-537-14 | Sequence 14, Appli | 515 | 74 | 4.5 | 339 | 2 | US-08-195-947-4 | Sequence 4, Appli |
| 443 | 75 | 4.5 | 554 | 2 | US-08-524-051-2 | Sequence 2, Appli | 516 | 74 | 4.5 | 339 | 2 | US-08-433-885-4 | Sequence 4, Appli |
| 444 | 75 | 4.5 | 554 | 3 | US-09-052-778-16 | Sequence 16, Appli | 517 | 74 | 4.5 | 339 | 2 | US-08-433-908B-4 | Sequence 4, Appli |
| 445 | 75 | 4.5 | 557 | 4 | US-09-248-796A-26892 | Sequence 26892, A | 518 | 74 | 4.5 | 339 | 3 | US-08-410-614-4 | Sequence 4, Appli |
| 446 | 75 | 4.5 | 904 | 3 | US-09-198-484-2 | Sequence 2, Appli | 519 | 74 | 4.5 | 370 | 4 | US-09-270-767-37418 | Sequence 37418, A |
| 447 | 75 | 4.5 | 941 | 4 | US-07-757-022B-14 | Sequence 14, Appli | 520 | 74 | 4.5 | 370 | 4 | US-09-270-767-52635 | Sequence 52635, A |
| 448 | 75 | 4.5 | 1022 | 4 | US-07-757-022B-84 | Sequence 84, Appli | 521 | 74 | 4.5 | 395 | 4 | US-09-949-016-9564 | Sequence 9564, Ap |
| 449 | 75 | 4.5 | 1038 | 4 | US-07-757-022B-74 | Sequence 74, Appli | 522 | 74 | 4.5 | 422 | 4 | US-09-949-016-8251 | Sequence 8251, Ap |
| 450 | 75 | 4.5 | 1049 | 4 | US-07-757-022B-58 | Sequence 58, Appli | 523 | 74 | 4.5 | 428 | 4 | US-09-134-000C-6457 | Sequence 6457, Ap |
| 451 | 75 | 4.5 | 1140 | 4 | US-07-757-022B-104 | Sequence 104, Appli | 524 | 74 | 4.5 | 472 | 3 | US-09-625-188-6 | Sequence 6, Appli |
| 452 | 75 | 4.5 | 1151 | 1 | US-08-286-889-37 | Sequence 37, Appli | 525 | 74 | 4.5 | 493 | 4 | US-09-248-796A-17819 | Sequence 17819, A |
| 453 | 75 | 4.5 | 1151 | 1 | US-08-485-618-37 | Sequence 37, Appli | 526 | 74 | 4.5 | 681 | 3 | US-08-760-615-4 | Sequence 4, Appli |
| 454 | 75 | 4.5 | 1151 | 1 | US-08-362-652-37 | Sequence 37, Appli | 527 | 74 | 4.5 | 681 | 4 | US-09-336-910A-2 | Sequence 2, Appli |
| 455 | 75 | 4.5 | 1151 | 2 | US-08-605-672-37 | Sequence 37, Appli | 528 | 74 | 4.5 | 778 | 4 | US-09-248-796A-16358 | Sequence 16358, A |
| 456 | 75 | 4.5 | 1151 | 2 | US-08-482-293A-37 | Sequence 37, Appli | 529 | 74 | 4.5 | 910 | 4 | US-09-270-767-42083 | Sequence 42083, A |
| 457 | 75 | 4.5 | 1151 | 3 | US-08-943-363-37 | Sequence 37, Appli | 530 | 74 | 4.5 | 1021 | 4 | US-09-903-540-16773 | Sequence 16773, A |
| 458 | 75 | 4.5 | 1151 | 3 | US-09-193-043-37 | Sequence 37, Appli | 531 | 74 | 4.5 | 1693 | 3 | US-08-840-316-1 | Sequence 1, Appli |
| 459 | 75 | 4.5 | 1151 | 4 | US-09-688-307A-37 | Sequence 37, Appli | 532 | 74 | 4.5 | 1693 | 3 | US-08-803-523-1 | Sequence 1, Appli |
| 460 | 75 | 4.5 | 1151 | 4 | US-09-350-259-37 | Sequence 37, Appli | 533 | 74 | 4.5 | 1693 | 3 | US-08-471-971-1 | Sequence 1, Appli |
| 461 | 75 | 4.5 | 1161 | 3 | US-09-193-043-55 | Sequence 55, Appli | 534 | 74 | 4.5 | 1693 | 4 | US-09-402-776-1 | Sequence 1, Appli |
| 462 | 75 | 4.5 | 1161 | 4 | US-09-688-307A-55 | Sequence 55, Appli | 535 | 74 | 4.5 | 1693 | 4 | US-08-470-246-1 | Sequence 1, Appli |
| 463 | 75 | 4.5 | 1161 | 4 | US-09-350-259-55 | Sequence 55, Appli | 536 | 74 | 4.5 | 1693 | 4 | US-08-316-765-1 | Sequence 1, Appli |
| 464 | 75 | 4.5 | 1162 | 2 | US-08-728-323A-2 | Sequence 2, Appli | 537 | 74 | 4.5 | 1693 | 4 | US-09-724-475-1 | Sequence 1, Appli |
| 465 | 75 | 4.5 | 1162 | 3 | US-09-298-568-2 | Sequence 2, Appli | 538 | 74 | 4.5 | 1693 | 5 | PCT-US93-08849A-1 | Sequence 1, Appli |
| 466 | 75 | 4.5 | 1162 | 4 | US-09-410-399-2 | Sequence 2, Appli | 539 | 74 | 4.5 | 1693 | 5 | PCT-US93-08849-1 | Sequence 1, Appli |
| 467 | 75 | 4.5 | 1162 | 4 | US-09-894-273-2 | Sequence 2, Appli | 540 | 74 | 4.5 | 1729 | 4 | US-09-134-000C-5675 | Sequence 5675, Ap |
| 468 | 75 | 4.5 | 1270 | 4 | US-07-757-022B-44 | Sequence 44, Appli | 541 | 74 | 4.5 | 2414 | 1 | US-08-227-536-2 | Sequence 2, Appli |
| 469 | 75 | 4.5 | 1311 | 4 | US-07-757-022B-42 | Sequence 42, Appli | 542 | 74 | 4.5 | 2414 | 4 | US-09-538-092-1289 | Sequence 1289, Ap |
| 470 | 75 | 4.5 | 1313 | 4 | US-07-757-022B-142 | Sequence 142, Appli | 543 | 74 | 4.5 | 2414 | 5 | PCT-US95-04682-2 | Sequence 2, Appli |
| 471 | 75 | 4.5 | 1314 | 4 | US-07-757-022B-50 | Sequence 50, Appli | 544 | 73.5 | 4.4 | 124 | 3 | US-08-700-651-11 | Sequence 11, Appli |
| 472 | 75 | 4.5 | 1320 | 4 | US-07-757-022B-60 | Sequence 60, Appli | 545 | 73.5 | 4.4 | 124 | 3 | US-08-928-361B-16 | Sequence 16, Appli |
| 473 | 75 | 4.5 | 1320 | 4 | US-07-757-022B-46 | Sequence 46, Appli | 546 | 73.5 | 4.4 | 124 | 4 | US-09-588-995A-1 | Sequence 16, Appli |
| 474 | 75 | 4.5 | 1320 | 4 | US-10-164-595-58 | Sequence 58, Appli | 547 | 73.5 | 4.4 | 128 | 3 | US-08-700-651-7 | Sequence 7, Appli |
| 475 | 75 | 4.5 | 1354 | 4 | US-07-757-022B-48 | Sequence 48, Appli | 548 | 73.5 | 4.4 | 128 | 3 | US-08-928-361B-12 | Sequence 12, Appli |
| 476 | 75 | 4.5 | 1361 | 4 | US-07-757-022B-40 | Sequence 40, Appli | 549 | 73.5 | 4.4 | 128 | 4 | US-09-588-995A-12 | Sequence 12, Appli |
| 477 | 75 | 4.5 | 1363 | 4 | US-07-757-022B-52 | Sequence 52, Appli | 550 | 73.5 | 4.4 | 130 | 3 | US-08-700-651-8 | Sequence 8, Appli |
| 478 | 75 | 4.5 | 1404 | 4 | US-07-757-022B-2 | Sequence 2, Appli | 551 | 73.5 | 4.4 | 130 | 3 | US-08-928-361B-13 | Sequence 13, Appli |
| 479 | 75 | 4.5 | 1404 | 4 | US-07-757-022B-62 | Sequence 62, Appli | 552 | 73.5 | 4.4 | 130 | 4 | US-09-588-995A-13 | Sequence 13, Appli |
| 480 | 75 | 4.5 | 1404 | 4 | US-10-164-595-78 | Sequence 78, Appli | 553 | 73.5 | 4.4 | 138 | 3 | US-08-700-651-10 | Sequence 10, Appli |
| 481 | 75 | 4.5 | 1404 | 4 | US-09-298-970A-1 | Sequence 1, Appli | 554 | 73.5 | 4.4 | 138 | 3 | US-08-928-361B-15 | Sequence 15, Appli |
| 482 | 75 | 4.5 | 1411 | 4 | US-09-949-016-10827 | Sequence 10827, A | 555 | 73.5 | 4.4 | 138 | 4 | US-09-588-995A-15 | Sequence 15, Appli |
| 483 | 74.5 | 4.5 | 1409 | 4 | US-09-107-532A-4999 | Sequence 4999, Ap | 556 | 73.5 | 4.4 | 262 | 4 | US-09-248-796A-21451 | Sequence 21451, A |
| 484 | 74.5 | 4.5 | 145 | 3 | US-08-808-599A-41 | Sequence 41, Appli | 557 | 73.5 | 4.4 | 321 | 4 | US-09-107-433-4282 | Sequence 4282, Ap |
| 485 | 74.5 | 4.5 | 186 | 4 | US-09-252-991A-20433 | Sequence 20433, A | 558 | 73.5 | 4.4 | 382 | 4 | US-09-248-796A-17276 | Sequence 17276, A |
| 486 | 74.5 | 4.5 | 216 | 4 | US-09-248-796A-25076 | Sequence 25076, A | 559 | 73.5 | 4.4 | 397 | 3 | US-08-991-426-4 | Sequence 4, Appli |
| 487 | 74.5 | 4.5 | 270 | 4 | US-09-134-000C-3553 | Sequence 3553, Ap | 560 | 73.5 | 4.4 | 397 | 3 | US-09-143-470-4 | Sequence 4, Appli |
| 488 | 74.5 | 4.5 | 312 | 4 | US-09-248-796A-20143 | Sequence 20143, A | 561 | 73.5 | 4.4 | 397 | 4 | US-08-649-006A-4 | Sequence 4, Appli |
| 489 | 74.5 | 4.5 | 333 | 4 | US-09-107-532A-6475 | Sequence 6475, Ap | 562 | 73.5 | 4.4 | 397 | 4 | US-09-771-023-4 | Sequence 4, Appli |
| 490 | 74.5 | 4.5 | 386 | 4 | US-09-270-767-44120 | Sequence 44120, A | 563 | 73.5 | 4.4 | 427 | 2 | US-08-282-197C-53 | Sequence 53, Appli |
| 491 | 74.5 | 4.5 | 429 | 4 | US-09-949-016-8183 | Sequence 8183, Ap | 564 | 73.5 | 4.4 | 499 | 4 | US-09-561-763-2 | Sequence 2, Appli |
| 492 | 74.5 | 4.5 | 429 | 4 | US-09-949-016-8184 | Sequence 8184, Ap | 565 | 73.5 | 4.4 | 499 | 4 | US-09-431-367B-2 | Sequence 2, Appli |
| 493 | 74.5 | 4.5 | 478 | 2 | US-08-456-670B-40 | Sequence 40, Appli | 566 | 73.5 | 4.4 | 540 | 4 | US-09-583-110-3685 | Sequence 3685, Ap |
| 494 | 74.5 | 4.5 | 530 | 4 | US-09-912-935-38 | Sequence 38, Appli | 567 | 73.5 | 4.4 | 570 | 4 | US-09-565-501A-104 | Sequence 104, App |
| 495 | 74.5 | 4.5 | 564 | 4 | US-09-949-016-6898 | Sequence 6898, Ap | 568 | 73.5 | 4.4 | 570 | 4 | US-09-639-286A-104 | Sequence 104, App |
| 496 | 74.5 | 4.5 | 565 | 4 | US-09-949-016-6902 | Sequence 6902, Ap | 569 | 73.5 | 4.4 | 570 | 4 | US-09-874-923-104 | Sequence 104, App |
| 497 | 74.5 | 4.5 | 587 | 4 | US-09-815-923-4 | Sequence 4, Appli | 570 | 73.5 | 4.4 | 638 | 1 | US-08-463-262A-11 | Sequence 11, Appli |
| 498 | 74.5 | 4.5 | 639 | 4 | US-09-248-796A-20583 | Sequence 20583, A | 571 | 73.5 | 4.4 | 638 | 1 | US-08-463-989-11 | Sequence 11, Appli |
| 499 | 74.5 | 4.5 | 758 | 4 | US-09-949-016-8288 | Sequence 8288, Ap | 572 | 73.5 | 4.4 | 638 | 3 | US-09-003-574-11 | Sequence 11, Appli |
| 500 | 74.5 | 4.5 | 794 | 4 | US-09-252-991A-28569 | Sequence 28569, A | 573 | 73.5 | 4.4 | 638 | 3 | US-09-003-570-11 | Sequence 11, Appli |
| 501 | 74.5 | 4.5 | 998 | 2 | US-08-449-645A-20 | Sequence 20, Appli | 574 | 73.5 | 4.4 | 641 | 4 | US-09-864-541A-11 | Sequence 11, Appli |
| 502 | 74.5 | 4.5 | 998 | 2 | US-08-702-367A-20 | Sequence 20, Appli | 575 | 73.5 | 4.4 | 641 | 4 | US-09-613-303-51 | Sequence 51, Appli |
| 503 | 74.5 | 4.5 | 998 | 5 | PCT-US95-04681-20 | Sequence 20, Appli | 576 | 73.5 | 4.4 | 641 | 4 | US-10-267-311-51 | Sequence 51, Appli |
| 504 | 74.5 | 4.5 | 1638 | 4 | US-09-071-035-258 | Sequence 258, App | 577 | 73.5 | 4.4 | 646 | 4 | US-09-902-540-12044 | Sequence 12044, A |
| 505 | 74.5 | 4.5 | 1638 | 4 | US-09-071-035-258 | Sequence 258, App | 578 | 73.5 | 4.4 | 659 | 4 | US-09-543-681A-6013 | Sequence 6013, Ap |
| 506 | 74.5 | 4.5 | 1638 | 4 | US-09-071-035-266 | Sequence 266, App | 579 | 73.5 | 4.4 | 712 | 4 | US-09-949-016-10600 | Sequence 10600, A |
| 507 | 74.5 | 4.5 | 1747 | 4 | US-09-134-000C-5999 | Sequence 5999, Ap | 580 | 73.5 | 4.4 | 713 | 3 | US-08-899-437-2 | Sequence 2, Appli |
| 508 | 74 | 4.5 | 197 | 4 | US-09-513-995C-7852 | Sequence 7852, Ap | 581 | 73.5 | 4.4 | 713 | 3 | US-09-126-121-2 | Sequence 2, Appli |
| 509 | 74 | 4.5 | 257 | 4 | US-09-567-458A-2 | Sequence 2, Appli | 582 | 73.5 | 4.4 | 763 | 3 | US-08-961-083-66 | Sequence 66, Appli |
| 510 | 74 | 4.5 | 279 | 4 | US-09-248-796A-16859 | Sequence 16859, A | 583 | 73.5 | 4.4 | 763 | 4 | US-09-536-784-66 | Sequence 66, Appli |
| 511 | 74 | 4.5 | 299 | 4 | US-09-107-433-3811 | Sequence 3811, Ap | 584 | 73.5 | 4.4 | 780 | 4 | US-09-248-796A-16702 | Sequence 16702, A |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|--------------------|
| 585 | 73.5 | 4.4 | 795 | 3 | US-09-193-562B-11 | Sequence 11, Appl | 658 | 72.5 | 4.4 | 293 | 4 | US-09-496-120-5 | Sequence 5, Appli |
| 586 | 73.5 | 4.4 | 795 | 4 | US-10-055-412B-11 | Sequence 11, Appl | 659 | 72.5 | 4.4 | 315 | 4 | US-09-328-352-5948 | Sequence 5948, Ap |
| 587 | 73.5 | 4.4 | 819 | 4 | US-09-468-656A-10 | Sequence 10, Appl | 660 | 72.5 | 4.4 | 328 | 4 | US-09-489-039A-12803 | Sequence 12803, A |
| 588 | 73.5 | 4.4 | 821 | 3 | US-09-193-562D-12 | Sequence 12, Appl | 661 | 72.5 | 4.4 | 340 | 4 | US-09-492-709A-262 | Sequence 262, App |
| 589 | 73.5 | 4.4 | 821 | 4 | US-10-055-412B-12 | Sequence 12, Appl | 662 | 72.5 | 4.4 | 368 | 4 | US-09-248-796A-19000 | Sequence 19000, A |
| 590 | 73.5 | 4.4 | 905 | 3 | US-09-193-562B-2 | Sequence 2, Appli | 663 | 72.5 | 4.4 | 378 | 4 | US-09-248-796A-18526 | Sequence 18526, A |
| 591 | 73.5 | 4.4 | 905 | 4 | US-10-055-412B-2 | Sequence 2, Appli | 664 | 72.5 | 4.4 | 445 | 4 | US-09-710-279-1294 | Sequence 1294, Ap |
| 592 | 73.5 | 4.4 | 919 | 4 | US-09-949-016-6954 | Sequence 6954, Ap | 665 | 72.5 | 4.4 | 462 | 6 | 5171671-2 | Patent No. 5171671 |
| 593 | 73.5 | 4.4 | 922 | 4 | US-09-248-796A-16269 | Sequence 16269, A | 666 | 72.5 | 4.4 | 462 | 6 | 5171671-2 | Patent No. 5171671 |
| 594 | 73.5 | 4.4 | 1101 | 4 | US-09-561-709B-5 | Sequence 5, Appli | 667 | 72.5 | 4.4 | 463 | 2 | US-08-162-402B-9 | Sequence 9, Appli |
| 595 | 73.5 | 4.4 | 1761 | 4 | US-09-561-709B-1 | Sequence 1, Appli | 668 | 72.5 | 4.4 | 494 | 4 | US-09-902-540-9960 | Sequence 9960, Ap |
| 596 | 73.5 | 4.4 | 1876 | 4 | US-09-418-710-71 | Sequence 70, Appl | 669 | 72.5 | 4.4 | 510 | 3 | US-09-211-417-1 | Sequence 1, Appli |
| 597 | 73.5 | 4.4 | 1876 | 4 | US-09-839-479-70 | Sequence 70, Appl | 670 | 72.5 | 4.4 | 608 | 4 | US-09-949-016-11148 | Sequence 11148, A |
| 598 | 73.5 | 4.4 | 1878 | 4 | US-09-418-710-13 | Sequence 13, Appl | 671 | 72.5 | 4.4 | 608 | 4 | US-09-949-016-11149 | Sequence 11149, A |
| 599 | 73.5 | 4.4 | 1878 | 4 | US-09-839-479-13 | Sequence 13, Appl | 672 | 72.5 | 4.4 | 608 | 4 | US-09-949-016-11150 | Sequence 11150, A |
| 600 | 73 | 4.4 | 155 | 4 | US-09-252-991A-22634 | Sequence 22634, A | 673 | 72.5 | 4.4 | 608 | 4 | US-09-949-016-11151 | Sequence 11151, A |
| 601 | 73 | 4.4 | 162 | 3 | US-08-700-651-13 | Sequence 13, Appl | 674 | 72.5 | 4.4 | 652 | 3 | US-09-310-463-4 | Sequence 4, Appli |
| 602 | 73 | 4.4 | 326 | 4 | US-09-248-796A-19891 | Sequence 19891, A | 675 | 72.5 | 4.4 | 652 | 4 | US-08-842-248A-4 | Sequence 4, Appli |
| 603 | 73 | 4.4 | 332 | 4 | US-09-313-942-10 | Sequence 10, Appl | 676 | 72.5 | 4.4 | 707 | 3 | US-09-228-986-80 | Sequence 80, Appl |
| 604 | 73 | 4.4 | 340 | 4 | US-09-248-796A-24600 | Sequence 24600, A | 677 | 72.5 | 4.4 | 707 | 4 | US-10-101-464A-80 | Sequence 80, Appl |
| 605 | 73 | 4.4 | 380 | 4 | US-09-270-767-43387 | Sequence 43387, A | 678 | 72.5 | 4.4 | 719 | 4 | US-09-949-016-7766 | Sequence 7766, Ap |
| 606 | 73 | 4.4 | 428 | 4 | US-09-489-039A-10901 | Sequence 10901, A | 679 | 72.5 | 4.4 | 798 | 4 | US-09-270-767-42988 | Sequence 42988, A |
| 607 | 73 | 4.4 | 488 | 2 | US-08-599-455B-5 | Sequence 5, Appli | 680 | 72.5 | 4.4 | 806 | 1 | US-08-270-076A-11 | Sequence 11, Appl |
| 608 | 73 | 4.4 | 488 | 3 | US-09-069-781B-5 | Sequence 5, Appli | 681 | 72.5 | 4.4 | 827 | 4 | US-09-270-767-46276 | Sequence 46276, A |
| 609 | 73 | 4.4 | 488 | 3 | US-09-137-132-5 | Sequence 5, Appli | 682 | 72.5 | 4.4 | 841 | 4 | US-09-949-016-9669 | Sequence 9669, Ap |
| 610 | 73 | 4.4 | 488 | 3 | US-08-864-564A-5 | Sequence 5, Appli | 683 | 72.5 | 4.4 | 878 | 4 | US-09-556-706B-2 | Sequence 2, Appli |
| 611 | 73 | 4.4 | 488 | 4 | US-09-094-410-5 | Sequence 5, Appli | 684 | 72.5 | 4.4 | 878 | 4 | US-09-724-418A-2 | Sequence 2, Appli |
| 612 | 73 | 4.4 | 488 | 4 | US-08-708-123B-5 | Sequence 5, Appli | 685 | 72.5 | 4.4 | 907 | 3 | US-08-783-774-2 | Sequence 2, Appli |
| 613 | 73 | 4.4 | 488 | 4 | US-08-583-153A-5 | Sequence 5, Appli | 686 | 72.5 | 4.4 | 907 | 4 | US-09-328-599A-1 | Sequence 1, Appli |
| 614 | 73 | 4.4 | 488 | 4 | US-08-638-524B-5 | Sequence 5, Appli | 687 | 72.5 | 4.4 | 907 | 5 | PCT-US95-04611A-19 | Sequence 19, Appl |
| 615 | 73 | 4.4 | 497 | 4 | US-08-956-171B-5234 | Sequence 5234, Ap | 688 | 72.5 | 4.4 | 1306 | 4 | US-09-134-000C-6670 | Sequence 19, Appl |
| 616 | 73 | 4.4 | 497 | 4 | US-08-781-986A-5234 | Sequence 5234, Ap | 689 | 72.5 | 4.4 | 2308 | 1 | US-08-015-973-1 | Sequence 1, Appli |
| 617 | 73 | 4.4 | 502 | 4 | US-09-248-796A-15481 | Sequence 15481, A | 690 | 72.5 | 4.4 | 2308 | 2 | US-08-448-164-1 | Sequence 1, Appli |
| 618 | 73 | 4.4 | 579 | 4 | US-09-198-452A-918 | Sequence 918, App | 691 | 72.5 | 4.4 | 2308 | 3 | US-08-081-929-2 | Sequence 2, Appli |
| 619 | 73 | 4.4 | 606 | 4 | US-09-438-185A-853 | Sequence 853, App | 692 | 72.5 | 4.4 | 2308 | 4 | US-10-000-954-2 | Sequence 2, Appli |
| 620 | 73 | 4.4 | 645 | 4 | US-09-270-767-42233 | Sequence 42233, A | 693 | 72.5 | 4.4 | 2314 | 4 | US-09-816-703A-2 | Sequence 2, Appli |
| 621 | 73 | 4.4 | 650 | 3 | US-08-362-525-2 | Sequence 2, Appli | 694 | 72.5 | 4.4 | 3256 | 4 | US-09-919-039-21 | Sequence 21, Appl |
| 622 | 73 | 4.4 | 658 | 2 | US-08-825-558-4 | Sequence 4, Appli | 695 | 72.5 | 4.4 | 3256 | 4 | US-09-976-594-22 | Sequence 22, Appl |
| 623 | 73 | 4.4 | 658 | 3 | US-09-312-611-4 | Sequence 4, Appli | 696 | 72.5 | 4.4 | 3256 | 4 | US-09-919-039-21 | Sequence 21, Appl |
| 624 | 73 | 4.4 | 708 | 1 | US-07-797-556-2 | Sequence 2, Appli | 697 | 72 | 4.3 | 248 | 4 | US-09-248-796A-18840 | Sequence 18840, A |
| 625 | 73 | 4.4 | 708 | 2 | US-08-308-881-2 | Sequence 2, Appli | 698 | 72 | 4.3 | 295 | 4 | US-09-270-767-45025 | Sequence 45025, A |
| 626 | 73 | 4.4 | 708 | 2 | US-09-058-263-2 | Sequence 2, Appli | 699 | 72 | 4.3 | 303 | 4 | US-09-270-767-57613 | Sequence 57613, A |
| 627 | 73 | 4.4 | 708 | 3 | US-09-059-099-2 | Sequence 2, Appli | 700 | 72 | 4.3 | 317 | 4 | US-09-538-092-978 | Sequence 978, App |
| 628 | 73 | 4.4 | 708 | 3 | US-09-058-264-2 | Sequence 2, Appli | 701 | 72 | 4.3 | 327 | 4 | US-09-270-767-42324 | Sequence 42324, A |
| 629 | 73 | 4.4 | 708 | 4 | US-09-455-963-2 | Sequence 2, Appli | 702 | 72 | 4.3 | 342 | 4 | US-09-949-016-10365 | Sequence 10365, A |
| 630 | 73 | 4.4 | 708 | 5 | PCT-US95-06530-2 | Sequence 2, Appli | 703 | 72 | 4.3 | 372 | 4 | US-09-489-039A-13193 | Sequence 13193, A |
| 631 | 73 | 4.4 | 830 | 4 | US-09-107-433-4309 | Sequence 4309, Ap | 704 | 72 | 4.3 | 401 | 4 | US-09-270-767-44680 | Sequence 44680, A |
| 632 | 73 | 4.4 | 851 | 4 | US-09-583-110-3850 | Sequence 3850, Ap | 705 | 72 | 4.3 | 456 | 3 | US-09-058-389A-2 | Sequence 2, Appli |
| 633 | 73 | 4.4 | 852 | 4 | US-09-206-551-19 | Sequence 19, Appl | 706 | 72 | 4.3 | 456 | 3 | US-09-611-781-2 | Sequence 2, Appli |
| 634 | 73 | 4.4 | 859 | 2 | US-08-825-558-6 | Sequence 7, Appli | 707 | 72 | 4.3 | 457 | 4 | US-09-949-016-7211 | Sequence 7211, Ap |
| 635 | 73 | 4.4 | 918 | 2 | US-08-825-558-6 | Sequence 6, Appli | 708 | 72 | 4.3 | 462 | 2 | US-08-865-997A-2 | Sequence 2, Appli |
| 636 | 73 | 4.4 | 918 | 3 | US-09-312-611-6 | Sequence 3, Appli | 709 | 72 | 4.3 | 489 | 4 | US-09-545-814-29 | Sequence 29, Appl |
| 637 | 73 | 4.4 | 933 | 2 | US-09-853-180B-3 | Sequence 3, Appli | 710 | 72 | 4.3 | 559 | 4 | US-09-545-814-14 | Sequence 14, Appl |
| 638 | 73 | 4.4 | 933 | 2 | US-08-682-847-2 | Sequence 2, Appli | 711 | 72 | 4.3 | 583 | 4 | US-09-545-814-2 | Sequence 2, Appli |
| 639 | 73 | 4.4 | 951 | 4 | US-09-313-942-9 | Sequence 9, Appli | 712 | 72 | 4.3 | 583 | 4 | US-09-545-814-5 | Sequence 5, Appli |
| 640 | 73 | 4.4 | 1158 | 4 | US-09-313-942-26 | Sequence 26, Appl | 713 | 72 | 4.3 | 599 | 2 | US-08-910-551B-2 | Sequence 2, Appli |
| 641 | 73 | 4.4 | 1168 | 4 | US-09-313-942-24 | Sequence 24, Appl | 714 | 72 | 4.3 | 635 | 4 | US-09-545-814-32 | Sequence 32, Appl |
| 642 | 73 | 4.4 | 1702 | 3 | US-08-296-791-5 | Sequence 5, Appli | 715 | 72 | 4.3 | 785 | 3 | US-08-374-077C-3 | Sequence 3, Appli |
| 643 | 73 | 4.4 | 1702 | 4 | US-09-839-996-5 | Sequence 5, Appli | 716 | 72 | 4.3 | 785 | 3 | US-08-895-590-3 | Sequence 3, Appli |
| 644 | 73 | 4.4 | 1702 | 4 | US-10-080-503-5 | Sequence 5, Appli | 717 | 72 | 4.3 | 785 | 3 | US-08-895-590-3 | Sequence 3, Appli |
| 645 | 73 | 4.4 | 1702 | 4 | US-10-080-503-5 | Sequence 5, Appli | 718 | 72 | 4.3 | 801 | 1 | US-08-725-012-2 | Sequence 2, Appli |
| 646 | 73 | 4.4 | 1702 | 5 | PCT-US95-10661A-5 | Sequence 5, Appli | 719 | 72 | 4.3 | 903 | 3 | US-09-193-562D-46 | Sequence 46, Appl |
| 647 | 73 | 4.4 | 2285 | 3 | US-09-308-375-2 | Sequence 2, Appli | 720 | 72 | 4.3 | 903 | 3 | US-09-623-624-18 | Sequence 18, Appl |
| 648 | 73 | 4.4 | 2285 | 4 | US-09-932-183A-2 | Sequence 2, Appli | 721 | 72 | 4.3 | 903 | 4 | US-10-055-412B-46 | Sequence 46, Appl |
| 649 | 73 | 4.4 | 2736 | 4 | US-09-252-991A-30227 | Sequence 30227, A | 722 | 72 | 4.3 | 903 | 4 | US-10-270-595-18 | Sequence 18, Appl |
| 650 | 72.5 | 4.4 | 150 | 3 | US-08-928-361B-18 | Sequence 18, Appl | 723 | 72 | 4.3 | 903 | 4 | US-09-270-767-43656 | Sequence 43656, A |
| 651 | 72.5 | 4.4 | 150 | 4 | US-09-588-995A-18 | Sequence 18, Appl | 724 | 72 | 4.3 | 915 | 4 | US-09-023-905A-2 | Sequence 2, Appli |
| 652 | 72.5 | 4.4 | 167 | 4 | US-08-956-171B-5216 | Sequence 5216, App | 725 | 72 | 4.3 | 1129 | 3 | US-09-351-200-2 | Sequence 2, Appli |
| 653 | 72.5 | 4.4 | 167 | 4 | US-08-781-986A-5216 | Sequence 5216, App | 726 | 72 | 4.3 | 1389 | 2 | US-08-619-198-5 | Sequence 5, Appli |
| 654 | 72.5 | 4.4 | 185 | 4 | US-09-248-796A-18311 | Sequence 18311, A | 727 | 72 | 4.3 | 1512 | 3 | US-09-443-184-48 | Sequence 48, Appl |
| 655 | 72.5 | 4.4 | 204 | 4 | US-09-902-540-14080 | Sequence 14080, A | 728 | 72 | 4.3 | 2441 | 1 | US-08-194-468-2 | Sequence 2, Appli |
| 656 | 72.5 | 4.4 | 206 | 4 | US-09-198-452A-879 | Sequence 879, App | 729 | 72 | 4.3 | 2441 | 3 | US-08-961-739-2 | Sequence 2, Appli |
| 657 | 72.5 | 4.4 | 206 | 4 | US-09-438-185A-822 | Sequence 822, App | 730 | 72 | 4.3 | 2441 | 3 | US-09-514-247A-8 | Sequence 8, Appli |

| | | | | | | | | | | | |
|-----|------|---|----------------------|--------------------|-----|------|-----|------|---|----------------------|--------------------|
| 731 | 2441 | 4 | US-09-686-316-2 | Sequence 2, Appli | 804 | 70.5 | 4.3 | 292 | 1 | US-08-286-888B-6 | Sequence 6, Appli |
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| 733 | 142 | 4 | US-09-107-532A-6315 | Sequence 6315, Ap | 806 | 70.5 | 4.3 | 330 | 4 | US-09-248-796A-14853 | Sequence 14853, A |
| 734 | 232 | 4 | US-09-333-809-217 | Sequence 217, App | 807 | 70.5 | 4.3 | 401 | 4 | US-09-949-016-7956 | Sequence 7956, Ap |
| 735 | 232 | 4 | US-09-746-311B-366 | Sequence 366, App | 808 | 70.5 | 4.3 | 432 | 4 | US-09-134-000C-3498 | Sequence 3498, Ap |
| 736 | 240 | 4 | US-09-107-532A-4430 | Sequence 4430, Ap | 809 | 70.5 | 4.3 | 441 | 4 | US-09-248-796A-20171 | Sequence 20171, A |
| 737 | 326 | 4 | US-09-134-000C-5607 | Sequence 5607, Ap | 810 | 70.5 | 4.3 | 445 | 4 | US-09-270-767-44629 | Sequence 44629, A |
| 738 | 386 | 4 | US-09-248-796A-18312 | Sequence 18312, A | 811 | 70.5 | 4.3 | 462 | 1 | US-08-417-330A-16 | Sequence 16, Appl |
| 739 | 442 | 1 | US-08-363-255-4 | Sequence 4, Appli | 812 | 70.5 | 4.3 | 491 | 4 | US-09-248-796A-18483 | Sequence 18483, A |
| 740 | 442 | 1 | US-08-363-255-11 | Sequence 11, Appli | 813 | 70.5 | 4.3 | 522 | 4 | US-09-538-092-1096 | Sequence 1096, Ap |
| 741 | 442 | 2 | US-08-687-559-6 | Sequence 6, Appli | 814 | 70.5 | 4.3 | 574 | 4 | US-09-248-796A-16162 | Sequence 16162, A |
| 742 | 442 | 4 | US-09-401-415-6 | Sequence 6, Appli | 815 | 70.5 | 4.3 | 639 | 4 | US-09-252-991A-24474 | Sequence 24474, A |
| 743 | 540 | 4 | US-09-538-092-793 | Sequence 793, Appl | 816 | 70.5 | 4.3 | 676 | 3 | US-09-003-574-34 | Sequence 34, Appl |
| 744 | 650 | 4 | US-09-134-000C-5177 | Sequence 5177, Ap | 817 | 70.5 | 4.3 | 676 | 3 | US-09-003-570-34 | Sequence 34, Appl |
| 745 | 732 | 4 | US-09-134-000C-6359 | Sequence 6359, Ap | 818 | 70.5 | 4.3 | 763 | 3 | US-09-864-541A-34 | Sequence 34, Appl |
| 746 | 920 | 4 | US-09-538-092-1197 | Sequence 1197, Ap | 819 | 70.5 | 4.3 | 773 | 3 | US-09-588-256-10 | Sequence 10, Appl |
| 747 | 1709 | 4 | US-09-538-092-1197 | Sequence 1197, Ap | 820 | 70.5 | 4.3 | 942 | 4 | US-09-538-092-602 | Sequence 602, App |
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| 749 | 1751 | 4 | US-09-136-574A-44 | Sequence 44, Appl | 822 | 70.5 | 4.3 | 1014 | 4 | US-09-949-016-8229 | Sequence 8229, Ap |
| 750 | 3174 | 2 | US-08-477-451-3 | Sequence 3, Appli | 823 | 70.5 | 4.3 | 1168 | 4 | US-09-762-311-5 | Sequence 5, Appli |
| 751 | 144 | 4 | US-09-252-991A-23388 | Sequence 23388, A | 824 | 70.5 | 4.3 | 1187 | 4 | US-09-949-016-6513 | Sequence 6513, Ap |
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| 753 | 188 | 4 | US-09-248-796A-14699 | Sequence 14699, A | 826 | 70.5 | 4.3 | 1591 | 4 | US-09-914-272A-3 | Sequence 3, Appli |
| 754 | 189 | 4 | US-09-270-767-39457 | Sequence 39457, A | 827 | 70.5 | 4.3 | 1980 | 4 | US-10-638-333-3 | Sequence 3, Appli |
| 755 | 71 | 4 | US-09-270-767-54674 | Sequence 54674, A | 828 | 70.5 | 4.3 | 2169 | 4 | US-09-949-016-6930 | Sequence 6930, Ap |
| 756 | 230 | 4 | US-09-328-352-7443 | Sequence 7443, Ap | 829 | 70.5 | 4.3 | 2442 | 3 | US-09-514-247A-10 | Sequence 10, Appl |
| 757 | 230 | 4 | US-09-248-796A-22910 | Sequence 22910, A | 830 | 70.5 | 4.3 | 2442 | 4 | US-09-538-092-1370 | Sequence 1370, Ap |
| 758 | 239 | 4 | US-09-248-796A-16743 | Sequence 16743, A | 831 | 70 | 4.2 | 118 | 4 | US-09-252-991A-18728 | Sequence 18728, A |
| 759 | 251 | 4 | US-09-248-796A-20695 | Sequence 20695, A | 832 | 70 | 4.2 | 135 | 4 | US-09-270-767-35728 | Sequence 35728, A |
| 760 | 272 | 4 | US-09-248-796A-14774 | Sequence 14774, A | 833 | 70 | 4.2 | 135 | 4 | US-09-270-767-50945 | Sequence 50945, A |
| 761 | 316 | 3 | US-09-504-358-10 | Sequence 10, Appl | 834 | 70 | 4.2 | 222 | 4 | US-09-252-991A-27628 | Sequence 27628, A |
| 762 | 316 | 4 | US-09-954-314-10 | Sequence 10, Appl | 835 | 70 | 4.2 | 234 | 4 | US-09-492-709A-350 | Sequence 350, App |
| 763 | 316 | 4 | US-10-230-562-10 | Sequence 10, Appl | 836 | 70 | 4.2 | 236 | 4 | US-09-270-767-59225 | Sequence 59225, A |
| 764 | 385 | 4 | US-09-248-796A-23097 | Sequence 23097, A | 837 | 70 | 4.2 | 265 | 3 | US-08-918-288-39 | Sequence 39, Appl |
| 765 | 401 | 6 | 5252556-1 | Patent No. 5252556 | 838 | 70 | 4.2 | 265 | 3 | US-08-918-288-39 | Sequence 39, Appl |
| 766 | 401 | 6 | 5252556-1 | Patent No. 5252556 | 839 | 70 | 4.2 | 312 | 4 | US-10-101-464A-930 | Sequence 930, App |
| 767 | 437 | 3 | US-09-353-332-2 | Sequence 2, Appli | 840 | 70 | 4.2 | 317 | 6 | 5340934-11 | Patent No. 5340934 |
| 768 | 554 | 4 | US-09-599-360B-78 | Sequence 78, Appl | 841 | 70 | 4.2 | 317 | 6 | 5340934-11 | Patent No. 5340934 |
| 769 | 610 | 1 | US-07-821-717B-6 | Sequence 6, Appli | 842 | 70 | 4.2 | 352 | 3 | US-09-413-814-24 | Sequence 24, Appl |
| 770 | 610 | 1 | US-08-119-262B-6 | Sequence 6, Appli | 843 | 70 | 4.2 | 352 | 3 | US-09-902-540-9867 | Sequence 9867, Ap |
| 771 | 610 | 1 | US-08-135-929A-11 | Sequence 11, Appl | 844 | 70 | 4.2 | 355 | 2 | US-08-458-555-2 | Sequence 2, Appli |
| 772 | 610 | 1 | US-08-234-265A-11 | Sequence 11, Appl | 845 | 70 | 4.2 | 376 | 4 | US-09-248-796A-19334 | Sequence 19334, A |
| 773 | 630 | 4 | US-09-485-529-8 | Sequence 8, Appli | 846 | 70 | 4.2 | 410 | 4 | US-09-543-681A-5962 | Sequence 5962, Ap |
| 774 | 633 | 4 | US-09-248-796A-20407 | Sequence 20407, A | 847 | 70 | 4.2 | 413 | 4 | US-09-248-796A-15624 | Sequence 15624, A |
| 775 | 646 | 4 | US-09-248-796A-16701 | Sequence 16701, A | 848 | 70 | 4.2 | 423 | 4 | US-09-902-540-13157 | Sequence 13157, A |
| 776 | 883 | 3 | US-09-538-092-1320 | Sequence 1320, Ap | 849 | 70 | 4.2 | 461 | 4 | US-09-248-796A-17227 | Sequence 17227, A |
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| 778 | 1835 | 4 | US-09-457-571-15 | Sequence 15, Appl | 851 | 70 | 4.2 | 525 | 4 | US-09-107-532A-5095 | Sequence 5095, Ap |
| 779 | 2035 | 1 | US-09-949-016-6609 | Sequence 6609, Ap | 852 | 70 | 4.2 | 552 | 4 | US-09-248-796A-22710 | Sequence 22710, A |
| 780 | 2035 | 1 | US-08-046-585-5 | Sequence 5, Appli | 853 | 70 | 4.2 | 584 | 4 | US-09-693-746-22 | Sequence 22, Appl |
| 781 | 2035 | 1 | US-08-393-703-5 | Sequence 5, Appli | 854 | 70 | 4.2 | 631 | 4 | US-09-107-532A-4548 | Sequence 4548, Ap |
| 782 | 2035 | 5 | FCT-0593-11721-5 | Sequence 5, Appli | 855 | 70 | 4.2 | 692 | 3 | US-09-003-574-31 | Sequence 31, Appl |
| 783 | 2045 | 4 | US-09-949-016-10491 | Sequence 10491, A | 856 | 70 | 4.2 | 692 | 3 | US-09-003-570-31 | Sequence 31, Appl |
| 784 | 2090 | 4 | US-09-538-092-1081 | Sequence 1081, Ap | 857 | 70 | 4.2 | 692 | 3 | US-09-864-541A-31 | Sequence 31, Appl |
| 785 | 2120 | 4 | US-09-949-016-9768 | Sequence 9768, Ap | 858 | 70 | 4.2 | 722 | 4 | US-09-252-991A-26452 | Sequence 26452, A |
| 786 | 70.5 | 4 | US-09-270-767-38100 | Sequence 38100, A | 859 | 70 | 4.2 | 843 | 4 | US-09-252-991A-32668 | Sequence 32668, A |
| 787 | 157 | 4 | US-09-270-767-53317 | Sequence 53317, A | 860 | 70 | 4.2 | 915 | 2 | US-08-480-917-2 | Sequence 2, Appli |
| 788 | 173 | 4 | US-09-107-532A-4115 | Sequence 4115, Ap | 861 | 70 | 4.2 | 915 | 3 | US-09-138-736-2 | Sequence 2, Appli |
| 789 | 198 | 4 | US-09-489-039A-9988 | Sequence 9988, Ap | 862 | 70 | 4.2 | 915 | 3 | US-08-988-242-2 | Sequence 2, Appli |
| 790 | 213 | 4 | US-09-244-805-11 | Sequence 11, Appl | 863 | 70 | 4.2 | 3892 | 4 | US-09-328-352-5503 | Sequence 5503, Ap |
| 791 | 213 | 4 | US-09-538-092-1255 | Sequence 1255, Ap | 864 | 69.5 | 4.2 | 51 | 4 | US-09-902-540-15148 | Sequence 15148, A |
| 792 | 220 | 4 | US-09-198-452A-461 | Sequence 461, App | 865 | 69.5 | 4.2 | 139 | 4 | US-09-248-796A-14268 | Sequence 14268, A |
| 793 | 220 | 4 | US-09-438-185A-442 | Sequence 442, App | 866 | 69.5 | 4.2 | 184 | 4 | US-09-893-737-14 | Sequence 14, Appl |
| 794 | 232 | 4 | US-09-333-809-214 | Sequence 214, App | 867 | 69.5 | 4.2 | 219 | 1 | US-08-463-115-91 | Sequence 91, Appl |
| 795 | 232 | 4 | US-09-333-809-215 | Sequence 215, App | 868 | 69.5 | 4.2 | 219 | 1 | US-08-465-388-91 | Sequence 91, Appl |
| 796 | 232 | 4 | US-09-333-809-216 | Sequence 216, App | 869 | 69.5 | 4.2 | 290 | 2 | US-08-903-801-1 | Sequence 1, Appli |
| 797 | 232 | 4 | US-09-746-311B-363 | Sequence 363, App | 870 | 69.5 | 4.2 | 290 | 3 | US-09-295-035-1 | Sequence 1, Appli |
| 798 | 232 | 4 | US-09-746-311B-364 | Sequence 364, App | 871 | 69.5 | 4.2 | 291 | 6 | 5194600-2 | Patent No. 5194600 |
| 799 | 232 | 4 | US-09-746-311B-365 | Sequence 365, App | 872 | 69.5 | 4.2 | 291 | 6 | 5194600-2 | Patent No. 5194600 |
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| 801 | 244 | 4 | US-09-107-532A-4536 | Sequence 4536, Ap | 874 | 69.5 | 4.2 | 312 | 4 | US-09-254-465A-9 | Sequence 9, Appl |
| 802 | 256 | 4 | US-09-248-796A-14185 | Sequence 14185, A | 884 | 69.5 | 4.2 | 312 | 4 | US-09-953-499-9 | Sequence 9, Appli |
| 803 | 267 | 4 | US-09-270-767-60080 | Sequence 60080, A | 885 | 69.5 | 4.2 | 338 | 4 | US-09-538-092-144 | Sequence 144, App |

| | | | | | | | | | | | | | |
|-----|------|-----|------|---|----------------------|-------------------|------|------|-----|------|---|----------------------|--------------------|
| 886 | 69.5 | 4.2 | 339 | 1 | US-08-431-080-18 | Sequence 18, Appl | 959 | 68.5 | 4.1 | 253 | 4 | US-09-543-681A-8042 | Sequence 8042, Ap |
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| 888 | 69.5 | 4.2 | 339 | 3 | US-09-345-294-18 | Sequence 18, Appl | 961 | 68.5 | 4.1 | 325 | 1 | US-08-233-788A-55 | Sequence 55, Appl |
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| 890 | 69.5 | 4.2 | 406 | 4 | US-09-248-796A-20860 | Sequence 20860, A | 963 | 68.5 | 4.1 | 338 | 4 | US-09-328-352-4529 | Sequence 4529, Ap |
| 891 | 69.5 | 4.2 | 567 | 4 | US-09-773-877B-12 | Sequence 12, Appl | 964 | 68.5 | 4.1 | 371 | 4 | US-09-533-029-110 | Sequence 110, App |
| 892 | 69.5 | 4.2 | 633 | 4 | US-09-248-796A-18427 | Sequence 18427, A | 965 | 68.5 | 4.1 | 391 | 4 | US-09-200-090-4 | Sequence 4, Appl |
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| 894 | 69.5 | 4.2 | 651 | 4 | US-09-248-796A-18743 | Sequence 18743, A | 967 | 68.5 | 4.1 | 402 | 1 | US-08-087-772A-15 | Sequence 15, Appl |
| 895 | 69.5 | 4.2 | 812 | 4 | US-09-248-796A-20875 | Sequence 20875, A | 968 | 68.5 | 4.1 | 408 | 1 | US-07-916-901-2 | Sequence 2, Appl |
| 896 | 69.5 | 4.2 | 1020 | 4 | US-09-248-796A-17115 | Sequence 17115, A | 969 | 68.5 | 4.1 | 408 | 3 | US-08-450-962-2 | Sequence 2, Appl |
| 897 | 69.5 | 4.2 | 1059 | 4 | US-09-248-796A-15164 | Sequence 15164, A | 970 | 68.5 | 4.1 | 408 | 3 | US-08-450-962-5 | Sequence 5, Appl |
| 898 | 69.5 | 4.2 | 1105 | 3 | US-08-999-774A-2 | Sequence 2, Appl | 971 | 68.5 | 4.1 | 408 | 4 | US-08-848-631-2 | Sequence 2, Appl |
| 899 | 69.5 | 4.2 | 1308 | 4 | US-09-134-000C-6588 | Sequence 6588, Ap | 972 | 68.5 | 4.1 | 408 | 4 | US-08-848-631-5 | Sequence 5, Appl |
| 900 | 69.5 | 4.2 | 1323 | 3 | US-09-770-170-2 | Sequence 2, Appl | 973 | 68.5 | 4.1 | 440 | 4 | US-09-270-767-37864 | Sequence 37864, A |
| 901 | 69.5 | 4.2 | 1619 | 4 | US-09-328-352-7347 | Sequence 7347, Ap | 974 | 68.5 | 4.1 | 440 | 4 | US-09-270-767-53081 | Sequence 53081, A |
| 902 | 69.5 | 4.2 | 2468 | 4 | US-09-976-594-726 | Sequence 726, App | 975 | 68.5 | 4.1 | 498 | 4 | US-09-309-572-4 | Sequence 4, Appl |
| 903 | 69.5 | 4.2 | 2468 | 4 | US-09-538-092-1135 | Sequence 1135, Ap | 976 | 68.5 | 4.1 | 498 | 4 | US-09-718-096-4 | Sequence 4, Appl |
| 904 | 69.5 | 4.2 | 2522 | 4 | US-09-949-016-10237 | Sequence 10237, A | 977 | 68.5 | 4.1 | 499 | 3 | US-09-049-672A-1 | Sequence 1, Appl |
| 905 | 69 | 4.2 | 88 | 4 | US-09-252-991A-23868 | Sequence 23868, A | 978 | 68.5 | 4.1 | 529 | 3 | US-09-291-922-28 | Sequence 28, Appl |
| 906 | 69 | 4.2 | 111 | 4 | US-09-248-796A-14291 | Sequence 14291, A | 979 | 68.5 | 4.1 | 557 | 4 | US-09-773-877B-14 | Sequence 14, Appl |
| 907 | 69 | 4.2 | 153 | 4 | US-09-489-039A-12486 | Sequence 12486, A | 980 | 68.5 | 4.1 | 567 | 4 | US-09-773-877B-20 | Sequence 20, Appl |
| 908 | 69 | 4.2 | 171 | 4 | US-09-248-796A-19229 | Sequence 19229, A | 981 | 68.5 | 4.1 | 600 | 4 | US-09-693-746-2 | Sequence 2, Appl |
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| 910 | 69 | 4.2 | 189 | 4 | US-09-489-039A-11063 | Sequence 11063, A | 983 | 68.5 | 4.1 | 600 | 6 | 5240706-1 | Patent No. 5240706 |
| 911 | 69 | 4.2 | 211 | 1 | US-08-463-115-92 | Sequence 92, Appl | 984 | 68.5 | 4.1 | 680 | 2 | US-08-674-351-2 | Sequence 2, Appl |
| 912 | 69 | 4.2 | 218 | 1 | US-08-465-388-92 | Sequence 92, Appl | 985 | 68.5 | 4.1 | 687 | 4 | US-09-248-796A-23026 | Sequence 23026, A |
| 913 | 69 | 4.2 | 218 | 1 | US-08-465-388-92 | Sequence 92, Appl | 986 | 68.5 | 4.1 | 697 | 4 | US-09-270-767-41650 | Sequence 41650, A |
| 914 | 69 | 4.2 | 226 | 4 | US-09-721-908-3 | Sequence 3, Appl | 987 | 68.5 | 4.1 | 744 | 4 | US-09-021-560-2 | Sequence 2, Appl |
| 915 | 69 | 4.2 | 237 | 4 | US-09-721-908-4 | Sequence 4, Appl | 988 | 68.5 | 4.1 | 744 | 4 | US-09-021-560-2 | Sequence 2, Appl |
| 916 | 69 | 4.2 | 265 | 3 | US-08-918-288-3 | Sequence 3, Appl | 989 | 68.5 | 4.1 | 756 | 3 | US-09-085-199B-9 | Sequence 9, Appl |
| 917 | 69 | 4.2 | 265 | 3 | US-09-282-357-3 | Sequence 3, Appl | 990 | 68.5 | 4.1 | 756 | 4 | US-09-963-137-184 | Sequence 184, App |
| 918 | 69 | 4.2 | 288 | 4 | US-09-902-540-14377 | Sequence 14377, A | 991 | 68.5 | 4.1 | 763 | 4 | US-09-949-016-10382 | Sequence 10382, A |
| 919 | 69 | 4.2 | 341 | 4 | US-09-902-540-14167 | Sequence 14167, A | 992 | 68.5 | 4.1 | 773 | 4 | US-09-489-039A-11160 | Sequence 11160, A |
| 920 | 69 | 4.2 | 342 | 4 | US-09-252-991A-19903 | Sequence 19903, A | 993 | 68.5 | 4.1 | 887 | 4 | US-09-540-236-2911 | Sequence 2911, Ap |
| 921 | 69 | 4.2 | 347 | 4 | US-09-540-236-3596 | Sequence 3596, Ap | 994 | 68.5 | 4.1 | 888 | 4 | US-09-134-000C-5886 | Sequence 5886, Ap |
| 922 | 69 | 4.2 | 423 | 4 | US-09-248-796A-26813 | Sequence 26813, A | 995 | 68.5 | 4.1 | 906 | 4 | US-09-863-901-6 | Sequence 6, Appl |
| 923 | 69 | 4.2 | 430 | 4 | US-09-949-016-8782 | Sequence 8782, Ap | 996 | 68.5 | 4.1 | 1167 | 4 | US-10-274-409-2 | Sequence 2, Appl |
| 924 | 69 | 4.2 | 490 | 4 | US-09-292-225-41 | Sequence 41, Appl | 997 | 68.5 | 4.1 | 1167 | 4 | US-10-274-409-2 | Sequence 2, Appl |
| 925 | 69 | 4.2 | 490 | 4 | US-09-248-796A-20112 | Sequence 20112, A | 998 | 68.5 | 4.1 | 1187 | 4 | US-09-949-016-7933 | Sequence 7933, Ap |
| 926 | 69 | 4.2 | 509 | 4 | US-09-292-225-35 | Sequence 35, Appl | 999 | 68.5 | 4.1 | 1325 | 4 | US-09-270-767-43789 | Sequence 43789, A |
| 927 | 69 | 4.2 | 509 | 4 | US-09-292-225-38 | Sequence 38, Appl | 1000 | 68 | 4.1 | 1325 | 4 | US-09-252-991A-21137 | Sequence 21137, A |
| 928 | 69 | 4.2 | 552 | 4 | US-09-540-236-2610 | Sequence 2610, Ap | 1001 | 68 | 4.1 | 155 | 4 | US-10-101-464A-573 | Sequence 573, App |
| 929 | 69 | 4.2 | 556 | 4 | US-09-538-092-712 | Sequence 712, App | 1002 | 68 | 4.1 | 183 | 4 | US-09-270-767-35830 | Sequence 35830, A |
| 930 | 69 | 4.2 | 642 | 2 | US-08-245-511-48 | Sequence 48, Appl | 1003 | 68 | 4.1 | 183 | 4 | US-09-270-767-51047 | Sequence 51047, A |
| 931 | 69 | 4.2 | 642 | 2 | US-08-600-993A-48 | Sequence 48, Appl | 1004 | 68 | 4.1 | 191 | 3 | US-08-745-404-4 | Sequence 4, Appl |
| 932 | 69 | 4.2 | 696 | 3 | US-08-899-437-23 | Sequence 23, Appl | 1005 | 68 | 4.1 | 203 | 4 | US-09-059-625-85 | Sequence 85, Appl |
| 933 | 69 | 4.2 | 696 | 3 | US-09-126-121-23 | Sequence 23, Appl | 1006 | 68 | 4.1 | 204 | 4 | US-09-252-991A-29026 | Sequence 29026, A |
| 934 | 69 | 4.2 | 720 | 3 | US-08-899-437-6 | Sequence 6, Appl | 1007 | 68 | 4.1 | 269 | 3 | US-08-646-265A-109 | Sequence 109, App |
| 935 | 69 | 4.2 | 720 | 3 | US-09-126-121-6 | Sequence 6, Appl | 1008 | 68 | 4.1 | 284 | 4 | US-09-248-796A-18924 | Sequence 18924, A |
| 936 | 69 | 4.2 | 801 | 4 | US-09-248-796A-18375 | Sequence 18375, A | 1009 | 68 | 4.1 | 292 | 4 | US-09-248-796A-15095 | Sequence 15095, A |
| 937 | 69 | 4.2 | 813 | 3 | US-08-836-325-8 | Sequence 8, Appl | 1010 | 68 | 4.1 | 294 | 4 | US-09-248-796A-15817 | Sequence 15817, A |
| 938 | 69 | 4.2 | 813 | 3 | US-09-457-571-8 | Sequence 8, Appl | 1011 | 68 | 4.1 | 306 | 4 | US-09-107-532A-5552 | Sequence 5552, Ap |
| 939 | 69 | 4.2 | 817 | 4 | US-09-248-796A-20276 | Sequence 20276, A | 1012 | 68 | 4.1 | 307 | 4 | US-09-270-767-31716 | Sequence 31716, A |
| 940 | 69 | 4.2 | 845 | 3 | US-08-804-439A-94 | Sequence 94, Appl | 1013 | 68 | 4.1 | 312 | 4 | US-09-774-639-145 | Sequence 145, App |
| 941 | 69 | 4.2 | 845 | 3 | US-08-720-229-94 | Sequence 94, Appl | 1014 | 68 | 4.1 | 330 | 4 | US-09-248-796A-20142 | Sequence 20142, A |
| 942 | 69 | 4.2 | 861 | 4 | US-09-784-316-2 | Sequence 2, Appl | 1015 | 68 | 4.1 | 354 | 4 | US-09-949-016-10392 | Sequence 10392, A |
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| 944 | 69 | 4.2 | 882 | 4 | US-09-328-352-5232 | Sequence 5232, Ap | 1017 | 68 | 4.1 | 380 | 4 | US-09-902-540-10846 | Sequence 10846, A |
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| 946 | 69 | 4.2 | 903 | 1 | US-08-413-118-8 | Sequence 8, Appl | 1019 | 68 | 4.1 | 387 | 4 | US-09-991-138-11 | Sequence 11, Appl |
| 947 | 69 | 4.2 | 903 | 3 | US-08-473-446-8 | Sequence 8, Appl | 1020 | 68 | 4.1 | 422 | 3 | US-08-872-979-8 | Sequence 8, Appl |
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| 949 | 69 | 4.2 | 988 | 3 | US-08-980-357-19 | Sequence 19, Appl | 1022 | 68 | 4.1 | 516 | 2 | US-08-762-106-8 | Sequence 8, Appl |
| 950 | 69 | 4.2 | 1163 | 4 | US-09-949-016-11047 | Sequence 11047, A | 1023 | 68 | 4.1 | 516 | 3 | US-08-745-404-2 | Sequence 2, Appl |
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| 952 | 69 | 4.2 | 1311 | 3 | US-08-901-710-5 | Sequence 5, Appl | 1025 | 68 | 4.1 | 527 | 2 | US-08-762-106-9 | Sequence 9, Appl |
| 953 | 69 | 4.2 | 1311 | 4 | US-09-169-079-5 | Sequence 5, Appl | 1026 | 68 | 4.1 | 527 | 2 | US-08-823-516-144 | Sequence 144, App |
| 954 | 69 | 4.2 | 1455 | 3 | US-08-840-062-5 | Sequence 5, Appl | 1027 | 68 | 4.1 | 527 | 3 | US-09-320-774-9 | Sequence 9, Appl |
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| 956 | 68.5 | 4.1 | 189 | 4 | US-09-949-016-6682 | Sequence 6682, Ap | 1029 | 68 | 4.1 | 552 | 3 | US-08-745-404-3 | Sequence 3, Appl |
| 957 | 68.5 | 4.1 | 206 | 4 | US-09-949-016-10049 | Sequence 10049, A | 1030 | 68 | 4.1 | 562 | 6 | 5258502-2 | Patent No. 5258502 |
| 958 | 68.5 | 4.1 | 213 | 4 | US-09-949-016-6681 | Sequence 6681, Ap | 1031 | 68 | 4.1 | 562 | 6 | 5258502-2 | Patent No. 5258502 |

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|------|------|-----|------|---|----------------------|--------------------|------|------|-----|------|---|----------------------|--------------------|
| 1032 | 68 | 4.1 | 563 | 4 | US-09-949-016-7419 | Sequence 7419, Ap | 1105 | 67.5 | 4.1 | 140 | 4 | US-09-270-767-42846 | Sequence 42846, A |
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| 1034 | 68 | 4.1 | 599 | 3 | US-08-221-767-24 | Sequence 24, Appli | 1107 | 67.5 | 4.1 | 157 | 4 | US-09-248-796A-21632 | Sequence 21632, A |
| 1035 | 68 | 4.1 | 599 | 5 | PCT-US955-04075-2 | Sequence 2, Appli | 1108 | 67.5 | 4.1 | 159 | 4 | US-09-252-991A-20138 | Sequence 20138, A |
| 1036 | 68 | 4.1 | 654 | 4 | US-09-315-127-11 | Sequence 11, Appli | 1109 | 67.5 | 4.1 | 160 | 4 | US-09-270-767-59046 | Sequence 59046, A |
| 1037 | 68 | 4.1 | 654 | 4 | US-09-315-127-12 | Sequence 12, Appli | 1110 | 67.5 | 4.1 | 201 | 4 | US-09-408-020-54 | Sequence 54, Appli |
| 1038 | 68 | 4.1 | 672 | 4 | US-09-248-796A-26995 | Sequence 26995, A | 1111 | 67.5 | 4.1 | 223 | 4 | US-09-248-796A-17645 | Sequence 17645, A |
| 1039 | 68 | 4.1 | 699 | 4 | US-09-949-016-6158 | Sequence 6158, Ap | 1112 | 67.5 | 4.1 | 284 | 4 | US-09-270-767-46344 | Sequence 46344, A |
| 1040 | 68 | 4.1 | 702 | 4 | US-09-949-016-11476 | Sequence 11476, A | 1113 | 67.5 | 4.1 | 290 | 4 | US-09-270-767-35246 | Sequence 35246, A |
| 1041 | 68 | 4.1 | 702 | 4 | US-09-949-016-11477 | Sequence 11477, A | 1114 | 67.5 | 4.1 | 290 | 4 | US-09-270-767-50463 | Sequence 50463, A |
| 1042 | 68 | 4.1 | 709 | 4 | US-09-248-796A-19045 | Sequence 19045, A | 1115 | 67.5 | 4.1 | 291 | 4 | US-09-248-796A-14273 | Sequence 14273, A |
| 1043 | 68 | 4.1 | 833 | 4 | US-09-949-016-9530 | Sequence 9530, Ap | 1116 | 67.5 | 4.1 | 301 | 5 | PCT-US93-08528-72 | Sequence 72, Appli |
| 1044 | 68 | 4.1 | 859 | 4 | US-09-538-092-717 | Sequence 717, Appl | 1117 | 67.5 | 4.1 | 301 | 5 | PCT-US93-08528-72 | Sequence 72, Appli |
| 1045 | 68 | 4.1 | 863 | 2 | US-08-380-182-20 | Sequence 20, Appli | 1118 | 67.5 | 4.1 | 313 | 4 | US-09-270-767-43688 | Sequence 43688, A |
| 1046 | 68 | 4.1 | 873 | 1 | US-08-571-758-6 | Sequence 6, Appli | 1119 | 67.5 | 4.1 | 319 | 3 | US-08-832-399-2 | Sequence 2, Appli |
| 1047 | 68 | 4.1 | 873 | 1 | US-08-909-984A-6 | Sequence 6, Appli | 1120 | 67.5 | 4.1 | 319 | 3 | US-09-372-498-2 | Sequence 2, Appli |
| 1048 | 68 | 4.1 | 873 | 1 | US-08-909-983-6 | Sequence 6, Appli | 1121 | 67.5 | 4.1 | 362 | 1 | US-08-437-027-21 | Sequence 21, Appli |
| 1049 | 68 | 4.1 | 877 | 4 | US-09-328-352-8162 | Sequence 8162, Ap | 1122 | 67.5 | 4.1 | 365 | 1 | US-08-437-027-20 | Sequence 20, Appli |
| 1050 | 68 | 4.1 | 878 | 3 | US-09-141-213-8 | Sequence 8, Appli | 1123 | 67.5 | 4.1 | 380 | 4 | US-09-252-991A-16840 | Sequence 16840, A |
| 1051 | 68 | 4.1 | 878 | 3 | US-09-561-138-8 | Sequence 8, Appli | 1124 | 67.5 | 4.1 | 383 | 4 | US-09-107-532A-5105 | Sequence 5105, Ap |
| 1052 | 68 | 4.1 | 879 | 3 | US-09-141-212-6 | Sequence 6, Appli | 1125 | 67.5 | 4.1 | 394 | 4 | US-09-949-016-9565 | Sequence 9565, Ap |
| 1053 | 68 | 4.1 | 879 | 3 | US-09-561-138-6 | Sequence 6, Appli | 1126 | 67.5 | 4.1 | 401 | 4 | US-09-248-796A-26759 | Sequence 26759, A |
| 1054 | 68 | 4.1 | 884 | 1 | US-07-718-575-12 | Sequence 12, Appli | 1127 | 67.5 | 4.1 | 405 | 4 | US-09-902-540-11954 | Sequence 11954, A |
| 1055 | 68 | 4.1 | 884 | 2 | US-08-481-206-12 | Sequence 12, Appli | 1128 | 67.5 | 4.1 | 410 | 3 | US-08-858-876A-2 | Sequence 2, Appli |
| 1056 | 68 | 4.1 | 884 | 2 | US-08-486-269A-12 | Sequence 12, Appli | 1129 | 67.5 | 4.1 | 410 | 3 | US-09-472-880-2 | Sequence 2, Appli |
| 1057 | 68 | 4.1 | 908 | 3 | US-08-855-146-2 | Sequence 2, Appli | 1130 | 67.5 | 4.1 | 410 | 4 | US-09-826-509-537 | Sequence 537, App |
| 1058 | 68 | 4.1 | 966 | 4 | US-09-949-016-6669 | Sequence 6669, Ap | 1131 | 67.5 | 4.1 | 424 | 4 | US-09-248-796A-24117 | Sequence 24117, A |
| 1059 | 68 | 4.1 | 974 | 2 | US-08-868-786-6 | Sequence 6, Appli | 1132 | 67.5 | 4.1 | 427 | 4 | US-09-328-352-5205 | Sequence 5205, Ap |
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| 1061 | 68 | 4.1 | 1026 | 4 | US-09-949-016-6777 | Sequence 6777, Ap | 1134 | 67.5 | 4.1 | 455 | 4 | US-09-489-039A-14133 | Sequence 14133, A |
| 1062 | 68 | 4.1 | 1034 | 4 | US-09-949-016-10870 | Sequence 10870, A | 1135 | 67.5 | 4.1 | 498 | 4 | US-09-718-096-26 | Sequence 26, Appli |
| 1063 | 68 | 4.1 | 1155 | 1 | US-08-286-889-46 | Sequence 46, Appli | 1136 | 67.5 | 4.1 | 498 | 4 | US-09-583-110-2949 | Sequence 2949, Ap |
| 1064 | 68 | 4.1 | 1155 | 1 | US-08-485-618-46 | Sequence 46, Appli | 1137 | 67.5 | 4.1 | 510 | 4 | US-09-107-433-2618 | Sequence 2618, Ap |
| 1065 | 68 | 4.1 | 1155 | 2 | US-08-362-652-46 | Sequence 46, Appli | 1138 | 67.5 | 4.1 | 522 | 4 | US-09-198-452A-480 | Sequence 480, App |
| 1066 | 68 | 4.1 | 1155 | 2 | US-08-605-672-46 | Sequence 46, Appli | 1139 | 67.5 | 4.1 | 549 | 3 | US-08-325-071-61 | Sequence 61, Appli |
| 1067 | 68 | 4.1 | 1155 | 2 | US-08-482-293A-46 | Sequence 46, Appli | 1140 | 67.5 | 4.1 | 549 | 3 | US-08-461-004A-61 | Sequence 61, Appli |
| 1068 | 68 | 4.1 | 1155 | 2 | US-08-943-363-46 | Sequence 46, Appli | 1141 | 67.5 | 4.1 | 555 | 4 | US-09-107-532A-6422 | Sequence 6422, Ap |
| 1069 | 68 | 4.1 | 1155 | 3 | US-09-193-043-46 | Sequence 46, Appli | 1142 | 67.5 | 4.1 | 591 | 4 | US-09-949-016-10914 | Sequence 10914, A |
| 1070 | 68 | 4.1 | 1155 | 4 | US-09-688-307A-46 | Sequence 46, Appli | 1143 | 67.5 | 4.1 | 591 | 4 | US-09-949-016-10915 | Sequence 10915, A |
| 1071 | 68 | 4.1 | 1155 | 4 | US-09-350-259-46 | Sequence 46, Appli | 1144 | 67.5 | 4.1 | 614 | 4 | US-09-248-796A-17642 | Sequence 17642, A |
| 1072 | 68 | 4.1 | 1161 | 1 | US-08-485-618-53 | Sequence 53, Appli | 1145 | 67.5 | 4.1 | 630 | 2 | US-08-797-366-3 | Sequence 3, Appli |
| 1073 | 68 | 4.1 | 1161 | 1 | US-08-485-618-55 | Sequence 55, Appli | 1146 | 67.5 | 4.1 | 630 | 2 | US-08-956-268-3 | Sequence 3, Appli |
| 1074 | 68 | 4.1 | 1161 | 1 | US-08-362-652-53 | Sequence 53, Appli | 1147 | 67.5 | 4.1 | 630 | 4 | US-09-499-522-16 | Sequence 16, Appli |
| 1075 | 68 | 4.1 | 1161 | 1 | US-08-362-652-53 | Sequence 53, Appli | 1148 | 67.5 | 4.1 | 630 | 4 | US-09-269-939A-10 | Sequence 10, Appli |
| 1076 | 68 | 4.1 | 1161 | 2 | US-08-605-672-53 | Sequence 53, Appli | 1149 | 67.5 | 4.1 | 649 | 4 | US-09-499-522-14 | Sequence 14, Appli |
| 1077 | 68 | 4.1 | 1161 | 2 | US-08-605-672-55 | Sequence 55, Appli | 1150 | 67.5 | 4.1 | 649 | 4 | US-09-269-939A-8 | Sequence 8, Appli |
| 1078 | 68 | 4.1 | 1161 | 2 | US-08-482-293A-53 | Sequence 53, Appli | 1151 | 67.5 | 4.1 | 650 | 1 | US-08-325-071-63 | Sequence 63, Appli |
| 1079 | 68 | 4.1 | 1161 | 2 | US-08-482-293A-55 | Sequence 55, Appli | 1152 | 67.5 | 4.1 | 656 | 3 | US-08-461-004A-63 | Sequence 63, Appli |
| 1080 | 68 | 4.1 | 1161 | 2 | US-08-943-363-53 | Sequence 53, Appli | 1153 | 67.5 | 4.1 | 656 | 2 | US-08-343-443B-2 | Sequence 2, Appli |
| 1081 | 68 | 4.1 | 1161 | 2 | US-08-943-363-55 | Sequence 55, Appli | 1154 | 67.5 | 4.1 | 656 | 3 | US-09-214-564A-4 | Sequence 4, Appli |
| 1082 | 68 | 4.1 | 1161 | 3 | US-09-193-043-53 | Sequence 53, Appli | 1155 | 67.5 | 4.1 | 656 | 4 | US-09-538-052-1250 | Sequence 1250, Ap |
| 1083 | 68 | 4.1 | 1161 | 4 | US-09-688-307A-53 | Sequence 53, Appli | 1156 | 67.5 | 4.1 | 664 | 4 | US-09-107-532A-7252 | Sequence 7252, Ap |
| 1084 | 68 | 4.1 | 1161 | 4 | US-09-350-259-53 | Sequence 53, Appli | 1157 | 67.5 | 4.1 | 802 | 3 | US-09-081-345-18 | Sequence 18, Appli |
| 1085 | 68 | 4.1 | 1181 | 4 | US-09-540-236-3804 | Sequence 3804, Ap | 1158 | 67.5 | 4.1 | 812 | 1 | US-08-446-794A-4 | Sequence 4, Appli |
| 1086 | 68 | 4.1 | 1341 | 4 | US-09-949-016-6890 | Sequence 6890, Ap | 1159 | 67.5 | 4.1 | 877 | 2 | US-08-916-917-2 | Sequence 2, Appli |
| 1087 | 68 | 4.1 | 1344 | 4 | US-09-949-016-10925 | Sequence 10925, A | 1160 | 67.5 | 4.1 | 877 | 2 | US-08-972-631-2 | Sequence 2, Appli |
| 1088 | 68 | 4.1 | 1440 | 3 | US-09-357-251-37 | Sequence 37, Appli | 1161 | 67.5 | 4.1 | 877 | 2 | US-08-972-631-2 | Sequence 2, Appli |
| 1089 | 68 | 4.1 | 1541 | 3 | US-08-296-791-3 | Sequence 3, Appli | 1162 | 67.5 | 4.1 | 877 | 2 | US-08-972-630-2 | Sequence 2, Appli |
| 1090 | 68 | 4.1 | 1541 | 3 | US-09-839-996-3 | Sequence 3, Appli | 1163 | 67.5 | 4.1 | 877 | 2 | US-08-672-211-2 | Sequence 2, Appli |
| 1091 | 68 | 4.1 | 1541 | 4 | US-10-080-505-3 | Sequence 3, Appli | 1164 | 67.5 | 4.1 | 877 | 3 | US-09-225-170-2 | Sequence 2, Appli |
| 1092 | 68 | 4.1 | 1541 | 4 | US-10-645-655-3 | Sequence 3, Appli | 1165 | 67.5 | 4.1 | 933 | 4 | US-09-430-723-2 | Sequence 2, Appli |
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| 1094 | 68 | 4.1 | 1545 | 3 | US-08-296-791-4 | Sequence 4, Appli | 1167 | 67.5 | 4.1 | 1014 | 4 | US-10-101-464A-807 | Sequence 807, App |
| 1095 | 68 | 4.1 | 1545 | 4 | US-09-839-996-4 | Sequence 4, Appli | 1168 | 67.5 | 4.1 | 1020 | 4 | US-09-538-092-911 | Sequence 911, App |
| 1096 | 68 | 4.1 | 1545 | 4 | US-10-080-505-4 | Sequence 4, Appli | 1169 | 67.5 | 4.1 | 1150 | 2 | US-08-589-756-3 | Sequence 3, Appli |
| 1097 | 68 | 4.1 | 1545 | 4 | US-10-645-655-4 | Sequence 4, Appli | 1170 | 67.5 | 4.1 | 1150 | 3 | US-09-206-800-3 | Sequence 3, Appli |
| 1098 | 68 | 4.1 | 1545 | 5 | PCT-US95-10661A-4 | Sequence 4, Appli | 1171 | 67.5 | 4.1 | 1150 | 3 | US-09-206-898-3 | Sequence 3, Appli |
| 1099 | 68 | 4.1 | 1675 | 2 | US-09-540-236-1994 | Sequence 1994, Ap | 1172 | 67.5 | 4.1 | 1301 | 4 | US-09-071-035-234 | Sequence 234, App |
| 1100 | 68 | 4.1 | 3457 | 2 | US-08-416-603-4 | Sequence 4, Appli | 1173 | 67.5 | 4.1 | 1301 | 4 | US-09-071-035-238 | Sequence 238, App |
| 1101 | 68 | 4.1 | 8991 | 4 | US-08-714-741-32 | Sequence 32, Appli | 1174 | 67.5 | 4.1 | 1301 | 4 | US-09-071-035-242 | Sequence 242, App |
| 1102 | 67.5 | 4.1 | 107 | 3 | US-08-961-083-150 | Sequence 150, App | 1175 | 67.5 | 4.1 | 1574 | 4 | US-09-302-626B-179 | Sequence 179, App |
| 1103 | 67.5 | 4.1 | 107 | 4 | US-09-536-784-150 | Sequence 150, App | 1176 | 67.5 | 4.1 | 1978 | 4 | US-09-302-626B-60 | Sequence 60, Appli |
| 1104 | 67.5 | 4.1 | 137 | 4 | US-09-583-110-4762 | Sequence 4762, Ap | 1177 | 67.5 | 4.1 | 3913 | 4 | US-09-949-016-10933 | Sequence 10933, A |

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| 1178 | 67 | 4.0 | 135 | 3 | US-08-981-392-51 | Sequence 51, Appl | 1251 | 67 | 4.0 | 661 | 2 | US-08-786-164-12 | Sequence 12, Appl |
| 1179 | 67 | 4.0 | 135 | 4 | US-09-908-322-51 | Sequence 51, Appl | 1252 | 67 | 4.0 | 668 | 4 | US-09-134-000C-5289 | Sequence 5289, Ap |
| 1180 | 67 | 4.0 | 149 | 4 | US-09-513-999C-4813 | Sequence 4813, Ap | 1253 | 67 | 4.0 | 784 | 4 | US-09-538-092-1254 | Sequence 1254, Ap |
| 1181 | 67 | 4.0 | 185 | 4 | US-09-902-540-13687 | Sequence 13687, A | 1254 | 67 | 4.0 | 786 | 4 | US-09-949-016-10170 | Sequence 10170, A |
| 1182 | 67 | 4.0 | 197 | 4 | US-09-107-532A-7229 | Sequence 7229, Ap | 1255 | 67 | 4.0 | 863 | 2 | US-08-380-182-19 | Sequence 19, Appl |
| 1183 | 67 | 4.0 | 206 | 4 | US-09-328-352-6224 | Sequence 6224, Ap | 1256 | 67 | 4.0 | 886 | 4 | US-09-784-316-4 | Sequence 4, Appl |
| 1184 | 67 | 4.0 | 210 | 1 | US-07-667-276A-2 | Sequence 2, Appl | 1257 | 67 | 4.0 | 886 | 4 | US-10-229-124-4 | Sequence 4, Appl |
| 1185 | 67 | 4.0 | 226 | 4 | US-09-107-532A-3715 | Sequence 3715, Ap | 1258 | 67 | 4.0 | 908 | 1 | US-07-903-456-2 | Sequence 2, Appl |
| 1186 | 67 | 4.0 | 246 | 1 | US-08-286-888B-1 | Sequence 1, Appl | 1259 | 67 | 4.0 | 908 | 3 | US-08-666-221B-6 | Sequence 6, Appl |
| 1187 | 67 | 4.0 | 246 | 1 | US-08-294-386C-3 | Sequence 3, Appl | 1260 | 67 | 4.0 | 908 | 3 | US-08-666-221B-12 | Sequence 12, Appl |
| 1188 | 67 | 4.0 | 246 | 1 | US-08-294-386C-3 | Sequence 3, Appl | 1261 | 67 | 4.0 | 908 | 3 | US-08-666-221B-14 | Sequence 14, Appl |
| 1189 | 67 | 4.0 | 246 | 1 | US-08-299-249A-1 | Sequence 1, Appl | 1262 | 67 | 4.0 | 908 | 3 | US-08-666-221B-12 | Sequence 12, Appl |
| 1190 | 67 | 4.0 | 246 | 1 | US-08-299-249A-10 | Sequence 10, Appl | 1263 | 67 | 4.0 | 908 | 3 | US-08-249-241-2 | Sequence 2, Appl |
| 1191 | 67 | 4.0 | 246 | 1 | US-08-590-708-1 | Sequence 1, Appl | 1264 | 67 | 4.0 | 908 | 3 | US-09-949-016-7025 | Sequence 7025, Ap |
| 1192 | 67 | 4.0 | 246 | 5 | PCT-US94-06543-1 | Sequence 1, Appl | 1265 | 67 | 4.0 | 915 | 4 | US-09-949-016-9697 | Sequence 9697, Ap |
| 1193 | 67 | 4.0 | 246 | 5 | PCT-US95-10224-3 | Sequence 1, Appl | 1266 | 67 | 4.0 | 976 | 2 | US-08-449-016-6806 | Sequence 18, Appl |
| 1194 | 67 | 4.0 | 246 | 5 | PCT-US95-10224-3 | Sequence 1, Appl | 1267 | 67 | 4.0 | 976 | 2 | US-08-449-016-6806 | Sequence 18, Appl |
| 1195 | 67 | 4.0 | 267 | 4 | US-09-949-016-7941 | Sequence 7941, Ap | 1268 | 67 | 4.0 | 976 | 5 | US-09-949-016-6499 | Sequence 6499, Ap |
| 1196 | 67 | 4.0 | 272 | 4 | US-09-248-796A-16689 | Sequence 16689, A | 1269 | 67 | 4.0 | 976 | 5 | PCT-US95-04681-18 | Sequence 18, Appl |
| 1197 | 67 | 4.0 | 273 | 3 | US-08-482-918-54 | Sequence 54, Appl | 1270 | 67 | 4.0 | 1013 | 4 | US-09-949-016-7991 | Sequence 7991, Ap |
| 1198 | 67 | 4.0 | 273 | 3 | US-09-224-681-54 | Sequence 54, Appl | 1271 | 67 | 4.0 | 1132 | 4 | US-09-528-784A-87 | Sequence 87, Appl |
| 1199 | 67 | 4.0 | 273 | 4 | US-09-635-251-54 | Sequence 54, Appl | 1272 | 67 | 4.0 | 1132 | 4 | US-09-569-098A-87 | Sequence 87, Appl |
| 1200 | 67 | 4.0 | 277 | 4 | US-08-469-633A-4 | Sequence 4, Appl | 1273 | 67 | 4.0 | 1231 | 4 | US-09-071-035-420 | Sequence 420, App |
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| 1202 | 67 | 4.0 | 289 | 4 | US-09-536-778A-2 | Sequence 20, Appl | 1275 | 67 | 4.0 | 1278 | 4 | US-09-134-000C-6043 | Sequence 6043, Ap |
| 1203 | 67 | 4.0 | 309 | 4 | US-09-270-767-46802 | Sequence 20, Appl | 1276 | 67 | 4.0 | 1279 | 4 | US-09-710-279-3188 | Sequence 3188, Ap |
| 1204 | 67 | 4.0 | 320 | 4 | US-09-248-796A-20167 | Sequence 46802, A | 1277 | 67 | 4.0 | 1336 | 4 | US-09-949-016-6806 | Sequence 6806, Ap |
| 1205 | 67 | 4.0 | 342 | 4 | US-09-107-433-3903 | Sequence 20167, A | 1278 | 67 | 4.0 | 1339 | 4 | US-09-949-016-10448 | Sequence 10448, A |
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| 1208 | 67 | 4.0 | 387 | 4 | US-09-570-778A-2 | Sequence 2, Appl | 1281 | 67 | 4.0 | 2005 | 3 | US-08-836-325-7 | Sequence 7, Appl |
| 1209 | 67 | 4.0 | 387 | 4 | US-09-570-778A-2 | Sequence 2, Appl | 1282 | 67 | 4.0 | 2005 | 4 | US-09-457-571-7 | Sequence 7, Appl |
| 1210 | 67 | 4.0 | 387 | 4 | US-09-570-778A-8 | Sequence 8, Appl | 1283 | 67 | 4.0 | 2476 | 2 | US-08-276-967-2 | Sequence 2, Appl |
| 1211 | 67 | 4.0 | 387 | 4 | US-09-570-778A-9 | Sequence 9, Appl | 1284 | 67 | 4.0 | 3696 | 3 | US-09-134-001C-5080 | Sequence 5080, Ap |
| 1212 | 67 | 4.0 | 387 | 4 | US-09-991-138-2 | Sequence 2, Appl | 1285 | 67 | 4.0 | 4377 | 3 | US-09-949-016-6978 | Sequence 6978, Ap |
| 1213 | 67 | 4.0 | 387 | 4 | US-09-991-138-7 | Sequence 7, Appl | 1286 | 66.5 | 4.0 | 91 | 3 | US-08-700-651-14 | Sequence 14, Appl |
| 1214 | 67 | 4.0 | 387 | 4 | US-09-991-138-8 | Sequence 8, Appl | 1287 | 66.5 | 4.0 | 91 | 3 | US-08-928-361B-19 | Sequence 19, Appl |
| 1215 | 67 | 4.0 | 387 | 4 | US-09-991-138-9 | Sequence 9, Appl | 1288 | 66.5 | 4.0 | 154 | 4 | US-09-252-991A-32034 | Sequence 32034, A |
| 1216 | 67 | 4.0 | 387 | 4 | US-10-037-677A-4 | Sequence 4, Appl | 1289 | 66.5 | 4.0 | 173 | 4 | US-09-328-352-5235 | Sequence 5235, Ap |
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| 1221 | 67 | 4.0 | 416 | 4 | US-09-601-478-4 | Sequence 4, Appl | 1294 | 66.5 | 4.0 | 206 | 4 | US-09-417-264-6 | Sequence 6, Appl |
| 1222 | 67 | 4.0 | 435 | 4 | US-09-949-016-9133 | Sequence 9133, Ap | 1295 | 66.5 | 4.0 | 235 | 3 | US-09-247-155-126 | Sequence 126, App |
| 1223 | 67 | 4.0 | 454 | 4 | US-09-949-016-9823 | Sequence 9823, Ap | 1296 | 66.5 | 4.0 | 236 | 4 | US-09-148-545-202 | Sequence 202, App |
| 1224 | 67 | 4.0 | 465 | 3 | US-08-845-258-30 | Sequence 30, Appl | 1297 | 66.5 | 4.0 | 239 | 4 | US-09-248-796A-21096 | Sequence 21096, A |
| 1225 | 67 | 4.0 | 465 | 3 | US-08-990-571-30 | Sequence 30, Appl | 1298 | 66.5 | 4.0 | 249 | 3 | US-09-189-760-6 | Sequence 6, Appl |
| 1226 | 67 | 4.0 | 465 | 3 | US-08-723-142A-30 | Sequence 30, Appl | 1299 | 66.5 | 4.0 | 249 | 3 | US-09-188-811-6 | Sequence 6, Appl |
| 1227 | 67 | 4.0 | 465 | 4 | US-09-528-784A-30 | Sequence 30, Appl | 1300 | 66.5 | 4.0 | 249 | 3 | US-09-514-422-6 | Sequence 6, Appl |
| 1228 | 67 | 4.0 | 465 | 4 | US-09-569-098A-30 | Sequence 30, Appl | 1301 | 66.5 | 4.0 | 252 | 4 | US-09-270-767-43125 | Sequence 43125, A |
| 1229 | 67 | 4.0 | 474 | 2 | US-08-650-000-4 | Sequence 4, Appl | 1302 | 66.5 | 4.0 | 284 | 4 | US-09-248-796A-20639 | Sequence 20639, A |
| 1230 | 67 | 4.0 | 474 | 3 | US-09-042-785A-8 | Sequence 8, Appl | 1303 | 66.5 | 4.0 | 305 | 4 | US-09-134-001C-5038 | Sequence 5038, Ap |
| 1231 | 67 | 4.0 | 474 | 3 | US-09-042-785A-8 | Sequence 8, Appl | 1304 | 66.5 | 4.0 | 306 | 4 | US-09-252-991A-17153 | Sequence 17153, A |
| 1232 | 67 | 4.0 | 474 | 4 | US-09-758-124-4 | Sequence 4, Appl | 1305 | 66.5 | 4.0 | 319 | 4 | US-09-107-532A-4723 | Sequence 4723, Ap |
| 1233 | 67 | 4.0 | 474 | 6 | 5395760-4 | Patent No. 5395760 | 1306 | 66.5 | 4.0 | 326 | 3 | US-09-058-389A-3 | Sequence 3, Appl |
| 1234 | 67 | 4.0 | 491 | 4 | US-09-270-767-44430 | Sequence 44430, A | 1307 | 66.5 | 4.0 | 326 | 4 | US-09-611-781-3 | Sequence 3, Appl |
| 1235 | 67 | 4.0 | 503 | 3 | US-08-123-934A-10 | Sequence 10, Appl | 1308 | 66.5 | 4.0 | 331 | 3 | US-08-808-720-5 | Sequence 5, Appl |
| 1236 | 67 | 4.0 | 503 | 4 | US-09-874-628-10 | Sequence 10, Appl | 1309 | 66.5 | 4.0 | 331 | 4 | US-09-467-638-5 | Sequence 5, Appl |
| 1237 | 67 | 4.0 | 503 | 5 | PCT-US94-10080-10 | Sequence 10, Appl | 1310 | 66.5 | 4.0 | 362 | 3 | US-08-899-437-3 | Sequence 3, Appl |
| 1238 | 67 | 4.0 | 541 | 4 | US-09-248-796A-25057 | Sequence 25057, A | 1311 | 66.5 | 4.0 | 362 | 3 | US-09-126-121-3 | Sequence 3, Appl |
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| 1240 | 67 | 4.0 | 570 | 3 | US-08-826-246-2 | Sequence 2, Appl | 1313 | 66.5 | 4.0 | 381 | 4 | US-09-270-767-38365 | Sequence 38365, A |
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| 1242 | 67 | 4.0 | 570 | 3 | US-08-126-640-7 | Sequence 7, Appl | 1315 | 66.5 | 4.0 | 387 | 4 | US-09-489-847-372 | Sequence 372, App |
| 1243 | 67 | 4.0 | 570 | 3 | US-08-925-588-2 | Sequence 2, Appl | 1316 | 66.5 | 4.0 | 407 | 2 | US-08-776-585-3 | Sequence 3, Appl |
| 1244 | 67 | 4.0 | 570 | 3 | US-09-288-292A-7 | Sequence 7, Appl | 1317 | 66.5 | 4.0 | 408 | 1 | US-08-351-473B-3 | Sequence 3, Appl |
| 1245 | 67 | 4.0 | 570 | 4 | US-09-372-044-2 | Sequence 2, Appl | 1318 | 66.5 | 4.0 | 429 | 4 | US-09-328-352-4392 | Sequence 4392, Ap |
| 1246 | 67 | 4.0 | 570 | 4 | US-08-825-486-2 | Sequence 2, Appl | 1319 | 66.5 | 4.0 | 436 | 4 | US-09-248-796A-17505 | Sequence 17505, A |
| 1247 | 67 | 4.0 | 570 | 4 | US-08-826-248-2 | Sequence 2, Appl | 1320 | 66.5 | 4.0 | 459 | 4 | US-09-691-220-4 | Sequence 4, Appl |
| 1248 | 67 | 4.0 | 598 | 4 | US-09-538-092-1083 | Sequence 1083, Ap | 1321 | 66.5 | 4.0 | 459 | 6 | 5194375-2 | Patent No. 5194375 |
| 1249 | 67 | 4.0 | 623 | 4 | US-09-485-529-7 | Sequence 7, Appl | 1322 | 66.5 | 4.0 | 459 | 6 | 5194375-2 | Patent No. 5194375 |
| 1250 | 67 | 4.0 | 661 | 1 | US-08-232-538-12 | Sequence 12, Appl | 1323 | 66.5 | 4.0 | 496 | 4 | US-09-540-236-2266 | Sequence 2266, Ap |

| | | | | | | | | | | | | | |
|------|------|-----|------|---|----------------------|-------------------|------|----|-----|------|---|----------------------|--------------------|
| 1324 | 66.5 | 4.0 | 517 | 3 | US-09-189-760-2 | Sequence 2, Appli | 1407 | 66 | 4.0 | 533 | 1 | US-08-040-548-1 | Sequence 1, Appli |
| 1325 | 66.5 | 4.0 | 517 | 3 | US-09-514-422-2 | Sequence 2, Appli | 1408 | 66 | 4.0 | 533 | 1 | US-08-466-344-1 | Sequence 1, Appli |
| 1326 | 66.5 | 4.0 | 567 | 3 | US-09-188-811-2 | Sequence 2, Appli | 1409 | 66 | 4.0 | 533 | 4 | US-09-546-013-21 | Sequence 21, Appl |
| 1327 | 66.5 | 4.0 | 573 | 4 | US-09-328-352-6420 | Sequence 6420, Ap | 1410 | 66 | 4.0 | 533 | 6 | 5206152-2 | Patent No. 5206152 |
| 1328 | 66.5 | 4.0 | 582 | 4 | US-09-187-999-13 | Sequence 13, Appl | 1411 | 66 | 4.0 | 533 | 6 | 5206152-2 | Patent No. 5206152 |
| 1329 | 66.5 | 4.0 | 582 | 4 | US-09-489-039A-12055 | Sequence 12055, A | 1412 | 66 | 4.0 | 540 | 3 | US-08-461-722-3 | Sequence 3, Appli |
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| 1331 | 66.5 | 4.0 | 619 | 4 | US-08-372-652-5 | Sequence 5, Appli | 1414 | 66 | 4.0 | 540 | 4 | US-09-468-041-3 | Sequence 3, Appli |
| 1332 | 66.5 | 4.0 | 619 | 5 | PCT-US95-16311-5 | Sequence 5, Appli | 1415 | 66 | 4.0 | 540 | 5 | PCT-US94-06362-3 | Sequence 3, Appli |
| 1333 | 66.5 | 4.0 | 620 | 1 | US-08-325-071-65 | Sequence 65, Appl | 1416 | 66 | 4.0 | 548 | 4 | US-09-543-681A-6561 | Sequence 6561, Ap |
| 1334 | 66.5 | 4.0 | 620 | 3 | US-08-461-004A-65 | Sequence 65, Appl | 1417 | 66 | 4.0 | 550 | 4 | US-09-075-505-7 | Sequence 7, Appli |
| 1335 | 66.5 | 4.0 | 650 | 1 | US-08-325-071-67 | Sequence 67, Appl | 1418 | 66 | 4.0 | 561 | 4 | US-09-248-796A-24349 | Sequence 24349, A |
| 1336 | 66.5 | 4.0 | 650 | 3 | US-08-461-004A-67 | Sequence 67, Appl | 1419 | 66 | 4.0 | 580 | 4 | US-09-248-796A-26639 | Sequence 26639, A |
| 1337 | 66.5 | 4.0 | 655 | 4 | US-09-632-538C-36 | Sequence 36, Appl | 1420 | 66 | 4.0 | 613 | 4 | US-09-270-767-45961 | Sequence 45961, A |
| 1338 | 66.5 | 4.0 | 681 | 3 | US-08-760-615-6 | Sequence 6, Appli | 1421 | 66 | 4.0 | 624 | 4 | US-09-248-796A-24363 | Sequence 24363, A |
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| 1340 | 66.5 | 4.0 | 691 | 4 | US-09-949-016-10422 | Sequence 10422, A | 1432 | 66 | 4.0 | 655 | 3 | US-09-228-986-70 | Sequence 70, Appl |
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| 1342 | 66.5 | 4.0 | 694 | 3 | US-09-138-236-2 | Sequence 2, Appli | 1434 | 66 | 4.0 | 655 | 4 | US-09-107-433-3033 | Sequence 3033, Ap |
| 1343 | 66.5 | 4.0 | 815 | 4 | US-09-914-259-18 | Sequence 18, Appl | 1435 | 66 | 4.0 | 661 | 4 | US-09-583-110-2948 | Sequence 2948, Ap |
| 1344 | 66.5 | 4.0 | 872 | 3 | US-08-337-797A-2 | Sequence 2, Appli | 1436 | 66 | 4.0 | 686 | 4 | US-09-538-092-1037 | Sequence 1037, Ap |
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| 1347 | 66.5 | 4.0 | 980 | 1 | US-08-220-151-5 | Sequence 5, Appli | 1439 | 66 | 4.0 | 720 | 4 | US-09-097-681-22 | Sequence 22, Appl |
| 1348 | 66.5 | 4.0 | 980 | 3 | US-08-413-118-5 | Sequence 5, Appli | 1440 | 66 | 4.0 | 726 | 4 | US-09-583-110-2782 | Sequence 2782, Ap |
| 1349 | 66.5 | 4.0 | 980 | 3 | US-08-473-446-5 | Sequence 5, Appli | 1441 | 66 | 4.0 | 726 | 4 | US-09-107-433-3906 | Sequence 3906, Ap |
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| 1357 | 66.5 | 4.0 | 1416 | 1 | US-08-061-465-4 | Sequence 4, Appli | 1449 | 66 | 4.0 | 806 | 4 | US-09-976-594-321 | Sequence 321, App |
| 1358 | 66.5 | 4.0 | 1457 | 4 | US-09-436-874-2 | Sequence 2, Appli | 1450 | 66 | 4.0 | 816 | 1 | US-08-038-760-3 | Sequence 3, Appli |
| 1359 | 66.5 | 4.0 | 1457 | 3 | US-09-713-273A-18 | Sequence 18, Appl | 1451 | 66 | 4.0 | 816 | 2 | US-08-470-091-3 | Sequence 3, Appli |
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| 1363 | 66.5 | 4.0 | 2466 | 5 | PCT-US94-09943-2 | Sequence 2, Appli | 1455 | 66 | 4.0 | 880 | 3 | US-09-141-212-2 | Sequence 2, Appli |
| 1364 | 66.5 | 4.0 | 2485 | 3 | US-09-290-640-46 | Sequence 46, Appl | 1456 | 66 | 4.0 | 880 | 3 | US-09-141-212-4 | Sequence 4, Appli |
| 1365 | 66.5 | 4.0 | 2485 | 4 | US-09-665-615B-46 | Sequence 46, Appl | 1457 | 66 | 4.0 | 880 | 3 | US-09-552-351-4 | Sequence 4, Appli |
| 1366 | 66.5 | 4.0 | 3594 | 4 | US-09-911-842A-4 | Sequence 4, Appli | 1458 | 66 | 4.0 | 880 | 3 | US-09-251-372-6 | Sequence 6, Appli |
| 1367 | 66 | 4.0 | 137 | 4 | US-09-248-796A-26561 | Sequence 26561, A | 1459 | 66 | 4.0 | 880 | 3 | US-09-561-138-2 | Sequence 2, Appli |
| 1368 | 66 | 4.0 | 187 | 4 | US-09-248-796A-21855 | Sequence 21855, A | 1460 | 66 | 4.0 | 880 | 3 | US-09-561-138-4 | Sequence 4, Appli |
| 1369 | 66 | 4.0 | 194 | 4 | US-09-489-039A-14065 | Sequence 14065, A | 1461 | 66 | 4.0 | 880 | 3 | US-09-715-336-6 | Sequence 6, Appli |
| 1370 | 66 | 4.0 | 198 | 4 | US-09-252-991A-29162 | Sequence 29162, A | 1462 | 66 | 4.0 | 880 | 3 | US-09-811-241-6 | Sequence 6, Appli |
| 1371 | 66 | 4.0 | 208 | 4 | US-09-248-796A-21781 | Sequence 21781, A | 1463 | 66 | 4.0 | 880 | 3 | US-08-802-839-4 | Sequence 4, Appli |
| 1372 | 66 | 4.0 | 231 | 4 | US-09-717-364A-13 | Sequence 13, Appl | 1464 | 66 | 4.0 | 928 | 1 | US-08-204-329-1 | Sequence 1, Appli |
| 1373 | 66 | 4.0 | 234 | 4 | US-09-248-796A-20570 | Sequence 20570, A | 1465 | 66 | 4.0 | 928 | 2 | US-08-959-638-8 | Sequence 8, Appli |
| 1374 | 66 | 4.0 | 235 | 4 | US-09-949-016-6661 | Sequence 6661, Ap | 1466 | 66 | 4.0 | 928 | 2 | US-08-482-627-5 | Sequence 5, Appli |
| 1375 | 66 | 4.0 | 268 | 3 | US-08-961-083-208 | Sequence 208, App | 1467 | 66 | 4.0 | 928 | 3 | US-08-801-092-4 | Sequence 4, Appli |
| 1376 | 66 | 4.0 | 268 | 4 | US-09-536-784-208 | Sequence 208, App | 1468 | 66 | 4.0 | 928 | 3 | US-08-328-673A-8 | Sequence 8, Appli |
| 1377 | 66 | 4.0 | 309 | 2 | US-08-715-131-2 | Sequence 2, Appli | 1469 | 66 | 4.0 | 928 | 3 | US-09-315-113-4 | Sequence 4, Appli |
| 1378 | 66 | 4.0 | 309 | 3 | US-09-221-753-2 | Sequence 2, Appli | 1470 | 66 | 4.0 | 928 | 4 | US-09-354-221-8 | Sequence 8, Appli |
| 1379 | 66 | 4.0 | 309 | 4 | US-09-754-809-2 | Sequence 2, Appli | 1471 | 66 | 4.0 | 928 | 5 | PCT-US94-10357-3 | Sequence 3, Appli |
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| 1381 | 66 | 4.0 | 334 | 4 | US-09-902-545-13842 | Sequence 13842, A | 1473 | 66 | 4.0 | 1070 | 3 | US-08-922-635-22 | Sequence 22, Appl |
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| 1383 | 66 | 4.0 | 344 | 4 | US-09-904-615-131 | Sequence 131, App | 1475 | 66 | 4.0 | 1085 | 4 | US-09-734-674-4 | Sequence 4, Appli |
| 1384 | 66 | 4.0 | 349 | 4 | US-09-270-767-44336 | Sequence 44336, A | 1476 | 66 | 4.0 | 1210 | 4 | US-09-949-016-6801 | Sequence 6801, Ap |
| 1385 | 66 | 4.0 | 385 | 1 | US-08-416-756A-3 | Sequence 3, Appli | 1477 | 66 | 4.0 | 1219 | 4 | US-09-344-624-4 | Sequence 4, Appli |
| 1386 | 66 | 4.0 | 385 | 4 | US-08-880-865-3 | Sequence 3, Appli | 1478 | 66 | 4.0 | 1220 | 2 | US-08-680-326-38 | Sequence 38, Appl |
| 1387 | 66 | 4.0 | 396 | 4 | US-09-328-352-5040 | Sequence 5040, Ap | 1479 | 66 | 4.0 | 1323 | 4 | US-09-949-016-6553 | Sequence 6553, Ap |
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| 1389 | 66 | 4.0 | 409 | 3 | US-08-404-381-2 | Sequence 2, Appli | 1481 | 66 | 4.0 | 1435 | 4 | US-09-949-016-9943 | Sequence 9943, Ap |
| 1390 | 66 | 4.0 | 417 | 3 | US-09-355-115-2 | Sequence 2, Appli | 1482 | 66 | 4.0 | 1435 | 4 | US-09-949-016-9944 | Sequence 9944, Ap |
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| 1393 | 66 | 4.0 | 475 | 4 | US-09-740-002-27 | Sequence 27, Appl | 1485 | 66 | 4.0 | 1564 | 4 | US-10-144-198-2 | Sequence 2, Appli |
| 1394 | 66 | 4.0 | 495 | 4 | US-09-248-796A-14275 | Sequence 14275, A | 1486 | 66 | 4.0 | 1622 | 4 | US-09-231-899-72 | Sequence 72, Appl |
| 1405 | 66 | 4.0 | 496 | 2 | US-08-224-482-2 | Sequence 2, Appli | 1487 | 66 | 4.0 | 1667 | 4 | US-09-270-767-41425 | Sequence 41425, A |
| 1406 | 66 | 4.0 | 508 | 3 | US-09-457-040B-16 | Sequence 16, Appl | 1488 | 66 | 4.0 | 1979 | 4 | US-09-949-016-6468 | Sequence 6468, Ap |

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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
DB 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
DB 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
QY 121 SRQFAAYCYNSSDWTNNSCIPEIITTKDPIFNQTQTATQTFEIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDWTNNSCIPEIITTKDPIFNQTQTATQTFEIVSDSTYSVASPYSTIPA 180
QY 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPVENKAAAFKNEAAGFGVPTAL 240
DB 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPVENKAAAFKNEAAGFGVPTAL 240
QY 241 LVLLALLFCAAGLFCYVKRYKVAFFPFTNKNQCKEMIETKVVKKEKANDSNPNESKKT 300
DB 241 LVLLALLFCAAGLFCYVKRYKVAFFPFTNKNQCKEMIETKVVKKEKANDSNPNESKKT 300
QY 301 DKNPEESKSPSKTTVRCLAEV 322
DB 301 DKNPEESKSPSKTTVRCLAEV 322

RESULT 6
; Sequence 201, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903,603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
DB 1 MARCFSLVLLLTISIWTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTPEAKEA 60
QY 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
DB 61 CRLGLSLAGKQDVETALKASFETCSYGVWGDGFVVISRISPNKCGKNGVGLWKVPV 120
QY 121 SRQFAAYCYNSSDWTNNSCIPEIITTKDPIFNQTQTATQTFEIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDWTNNSCIPEIITTKDPIFNQTQTATQTFEIVSDSTYSVASPYSTIPA 180
QY 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPVENKAAAFKNEAAGFGVPTAL 240

Db 181 PTTTPAPASTSIPRRKLLICVTEVFMETSTMTEPFFVENKAAFNKNEAGGGVPTAL 240
Qy 241 LVLALLFFGAAAGLFCYVKRYVKAFFFTNKNQOKEMIETKVVKKEKANDSNPNESKKT 300
Db 241 LVLALLFFGAAAGLFCYVKRYVKAFFFTNKNQOKEMIETKVVKKEKANDSNPNESKKT 300
Qy 301 DKNPEESKSPSKTTVRCLEAEV 322
Db 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 7

; Sequence 201, Application US/09904920A
; Patent No. 6806352
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,920A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16

; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARCFSLVLLTSTIWTTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTKEA 60
Db 1 MARCFSLVLLTSTIWTTRLLVQGSRLABELSIQVSCRIMGITLVSKKANQQLNFTKEA 60

Qy 61 CELLGSLAGKDOVETALKASFETCSYGWVGDFVVISRISPNKCGKNGVGLWKVPV 120
Db 61 CELLGSLAGKDOVETALKASFETCSYGWVGDFVVISRISPNKCGKNGVGLWKVPV 120

Qy 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNQTATOTTEFIVSDTSYVASPYSTIPA 180
Db 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNQTATOTTEFIVSDTSYVASPYSTIPA 180

Qy 181 PTTTPAPASTSIPRRKLLICVTEVFMETSTMTEPFFVENKAAFNKNEAGGGVPTAL 240
Db 181 PTTTPAPASTSIPRRKLLICVTEVFMETSTMTEPFFVENKAAFNKNEAGGGVPTAL 240

Qy 241 LVLALLFFGAAAGLFCYVKRYVKAFFFTNKNQOKEMIETKVVKKEKANDSNPNESKKT 300
Db 241 LVLALLFFGAAAGLFCYVKRYVKAFFFTNKNQOKEMIETKVVKKEKANDSNPNESKKT 300

Qy 301 DKNPEESKSPSKTTVRCLEAEV 322
Db 301 DKNPEESKSPSKTTVRCLEAEV 322

RESULT 8

; Sequence 201, Application US/09909064
; Patent No. 6818449
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/909,064
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCSLVLLLSIWTRLLVQGSRAEELSIOVSCRINGITLVSKKANQQLNFTAEKEA 60
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 CRLGLSLAGKQOVETALKASFTETCSYGVWGVDFVVISRISPNKCGKNGVGLVWKVPV 120
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 SRQFAAYCVNSDWTNNSCIPRIITKDPINFNTQTATQTEFIVSDSTYSVASPYSTIPA 180
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 181 PTTTPAPASTSIPRRKLLICVTEVFMETSTMTETEPVENKAAFKQEAAGFGVPTAL 240
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 241 LVLALLFFGAAAGLFCYVKRVKAPFPFTNKNQKQEMIEITKVVKBEKANDSNPNESKKT 300
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 301 DKNPEESKSPSKTTVRCLEAEV 322
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
; Sequence 201, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,381A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match      100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGLSLRAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 60
DB 1 MARCFSLVLLLTISIWTRLLVQGLSLRAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 60

QY 61 CRLLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
DB 61 CRLLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120

QY 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNQTQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNQTQTATOTTEFIVSDSTYSVASPYSTIPA 180

QY 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPYPTAL 240
DB 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPYPTAL 240

QY 241 LVIALFFGAAAGLGFYVYKRYVKAFFPTNKNQOKKEMIEYKVVKEEKANDSNPNESKKT 300
DB 241 LVIALFFGAAAGLGFYVYKRYVKAFFPTNKNQOKKEMIEYKVVKEEKANDSNPNESKKT 300

QY 301 DKNPEESKSPSKTIVRCLEAEV 322
DB 301 DKNPEESKSPSKTIVRCLEAEV 322
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RESULT 10

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; Sequence 201, Application US/09906618
; Patent No. 6828146
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,618
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
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; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
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; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 201
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein

Query Match      100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGLSLRAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 60
DB 1 MARCFSLVLLLTISIWTRLLVQGLSLRAEELSIQVSCRIMGITLVSKKANQQLNFTTEAKEA 60

QY 61 CRLLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120
DB 61 CRLLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLIWKVPV 120

QY 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNQTQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDTWNSCIPEIITTKDPIFNQTQTATOTTEFIVSDSTYSVASPYSTIPA 180

QY 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPYPTAL 240
DB 181 PTTTPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKNAAAGFGGVPYPTAL 240

QY 241 LVIALFFGAAAGLGFYVYKRYVKAFFPTNKNQOKKEMIEYKVVKEEKANDSNPNESKKT 300
DB 241 LVIALFFGAAAGLGFYVYKRYVKAFFPTNKNQOKKEMIEYKVVKEEKANDSNPNESKKT 300

QY 301 DKNPEESKSPSKTIVRCLEAEV 322
DB 301 DKNPEESKSPSKTIVRCLEAEV 322

RESULT 11
US-09-949-016-7765
; Sequence 7765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

;; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;; FILE REFERENCE: CL001307
;; CURRENT APPLICATION NUMBER: US/09/949,016
;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7765
;; LENGTH: 344
;; TYPE: PRT
;; ORGANISM: Human
US-09-949-016-7765

Query Match 100.0%; Score 1657; DB 4; Length 344;
Best Local Similarity 100.0%; Pred No. 2.2e-159;
Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTPEAKEA 60
DB 23 MARCFSLVLLLTISIWTRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTPEAKEA 82
QY 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 120
DB 83 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 142
QY 121 SRQFAAYCYNSSDWTNISCIPILITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 143 SRQFAAYCYNSSDWTNISCIPILITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 202
QY 181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAFAFNKAAAGFGGVPPTAL 240
DB 203 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAFAFNKAAAGFGGVPPTAL 262
QY 241 LVALLFFGAAAGLFCYVKRYKAFPTNKNQOKEMIETKVVEKANDSNPNESKKT 300
DB 263 LVALLFFGAAAGLFCYVKRYKAFPTNKNQOKEMIETKVVEKANDSNPNESKKT 322
QY 301 DKNPEESKPSKTTVRCLAEAV 322
DB 323 DKNPEESKPSKTTVRCLAEAV 344

RESULT 12
US-08-892-880-2
; Sequence 2, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERewith
; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/021,762
;; FILING DATE: 15-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: STEFFE, ERIC K
;; REGISTRATION NUMBER: 36,688
;; REFERENCE/DOCKET NUMBER: 1488.0490001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-2600
;; TELEFAX: 202-371-2540
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 322 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-892-880-2

Query Match 99.6%; Score 1651; DB 2; Length 322;
Best Local Similarity 99.7%; Pred No. 8.1e-159;
Matches 321; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARCFSLVLLLTISIWTRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTPEAKEA 60
DB 1 MARCFSLVLLLTISIWTRLLVQGSRAEELSIVQSCRIMGITLVSKKANQQLNFTPEAKEA 60
QY 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 120
DB 61 CRLGLSLAGKQOVETALKASFETCSYGVWGDGFVVISRISPNPKCGKNGVGLWKVPV 120
QY 121 SRQFAAYCYNSSDWTNISCIPILITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 180
DB 121 SRQFAAYCYNSSDWTNISCIPILITTKDPIFNTQTATOTTEFIVSDSTYSVASPYSTIPA 180
QY 181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAFAFNKAAAGFGGVPPTAL 240
DB 181 PTTTPPAPASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAFAFNKAAAGFGGVPPTAL 240
QY 241 LVALLFFGAAAGLFCYVKRYKAFPTNKNQOKEMIETKVVEKANDSNPNESKKT 300
DB 241 LVALLFFGAAAGLFCYVKRYKAFPTNKNQOKEMIETKVVEKANDSNPNESKKT 300
QY 301 DKNPEESKPSKTTVRCLAEAV 322
DB 301 DKNPEESKPSKTTVRCLAEAV 322

RESULT 13
US-09-724-864-60
; Sequence 60, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-60

Query Match 66.6%; Score 1103; DB 3; Length 318;
Best Local Similarity 69.7%; Pred. No. 2.6e-103;
Matches 221; Conservative 30; Mismatches 62; Indels 4; Gaps 3;

QY 6 SLVLLTSTWTRLLVQGSRAEELSIOVSCRIMGITLVSKKANQQLNFTKEAKCRLLG 65
Db 6 SLVLLTSTWTRLLVQGSRAEELSIOVSCRIMGITLVSKKANQQLNFTKEAKCRLLG 64
QY 66 LSLAGDQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSROFA 125
Db 65 LILASRDQVESAKSFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSROFA 124
QY 126 AYCNSDDTWNISCIPEIITTKDPIFNTOATOTTEFIVSDSTYSVASPSTIPAPTTTP 185
Db 125 AYCNSDDTWNISCIPEIITTKDPIFNTOATOTTEFIVSDSTYSVASPSTIPAPTTTP 181
QY 186 PAPASTISPRKCLICVTEFVEMTSTMTSTETETEFVFNKAFAKNEAAGFGVPTALLVLAL 245
Db 182 RAPPLTSMARKTKKICITVTEPEITWATETAFVAGAAFKNEAAGFGVPTALLVLAL 241
QY 246 LRFGAAGLGFVCKVYKRYKAFPTNKNQOKEMIETKVVKKEKANDSNPNESKKTDKNPE 305
Db 242 LRFGAAGLGFVCKVYKRYKAFPTNKNQOKEMIETKVVKKEKANDSNPNESKKTDKNPE 301
QY 306 ESKSPSKTTVRCLAEV 322
Db 302 EAKSPKTTVRCLAEV 318

RESULT 14
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
US-07-946-497-7

Query Match 14.0%; Score 231.5; DB 1; Length 363;
Best Local Similarity 24.9%; Pred. No. 6.2e-15;

Matches 89; Conservative 57; Mismatches 148; Indels 63; Gaps 14;
QY 15 WTR---LIVQGSRAEELSIOVSCRIMGITLVSKKANQQLNFTKEAKCRLLGLSLACK 71
Db 6 WTAGLCLLQLSLAHQQLDNLVTRYAGVFCVKNKGRYSISRTEAADI,COAFNSTLPTM 65
QY 72 DQVETALKASFETCSYGVGDGFVVISRISPNPKCGKNGVGLIWKVPVSROFAAYCYN 131
Db 66 DQKLALSKGFETCYGFI-EGNVVPIRHPNAICAAHNTGVVILVTSNTSHYDTCFNA 124
QY 132 SDTWNISCIPEIITTKDPIFNTOATOTTEFIVSDSTYSVASPSTIPAPTTTP 182
Db 125 SAPPEDC-----TSVTDLPNSFDGFTVITIVNRDGRYSKKGERTHOEDIDASNIID 179
QY 183 -----TTPPA-PASTSIPRKKLICVTEFVEMTSTMTST-ETEPFVENKAAPK--- 227
Db 180 DVSSGSTTEKSTPEGYILHTYLTPEQTGDDQDSFFIRSTLATRDSDSKDGRSRTVT 239
QY 228 --NEAGFGG-----VPTALLVLALFFGAAAGLGFVCKVYKRYKAF 267
Db 240 HGSSELAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASL-LALALILAVC-----IAVNS 293
QY 268 PTNKNQOKEMI---ETKVVKKEKANDSNPNESKKTDKNPEESKSPSKTTVRCLAE 321
Db 294 RRRCGKKLVINGNGTVEDRKPSELN-GEASKSQEMVHLVYNKEPSETPDQCMTAD 349

RESULT 15
US-08-483-322-7
; Sequence 7, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHERT, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; TITLE OF INVENTION: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

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; CLONE: mCD44
US-08-483-322-7

Query Match      14.0%; Score 231.5; DB 1; Length 363;
Best Local Similarity 24.9%; Pred. No. 6.2e-15;
Matches 89; Conservative 57; Mismatches 148; Indels 63; Gaps 14;

QY 15 WTR--LIVQSLRAEELSIQVSCRIMGITLVSKKANQQLNFTBAKEACRLGLSLAGK 71
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 72 DQVETALKASFETCSYGWYGDGFVVISRISPNPKCKNGVGLIWKVPVSRQFAAYCYN 131
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 66 DQMKLALSKGFETCRYGFI-EGNVVPIRIHPNAICAAHNTGVYILVTSNTSHYDYCFNA 124
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 132 SDTWNSCIPELIITTKDPIFNQTQTQTFEFIVSDST-YSVASPYST----IPAPT--- 182
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 125 SAPPEEDC-----TSVTDLPNSFGDFVTITIVNRDGTTRYKKGEYRTHQEDIDASNIIDD 179
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 183 -----TTPPA-PASTSIPIRRKKLICVTEFEMETSTMTST-ETEPFVENKAAPK--- 227
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 180 DVSSGSTIEKSTPEGYILHTYLTPTQPTGDDDSFFIRSTLATRDSDSKDSRGSRTVT 239
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 228 --NEAGFGG-----VPTALLVLALFFGAAAGLGFYVYKRVYKAPP 267
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 240 HGSELAGHSSANQDSGVTTTSGPMRRPQIPEWLIILASL-LALALILAVC-----IAVNS 293
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 268 FTKNQOQKEMI---ETKVVKEEKANDSNPNESKKTDDKNPBEKSPSKTTVVRCLEAE 321
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 294 RRCGQKKKLIVNGGNGTVEDRKPSELN-GEASKSQEMVHLVKNKBPSETPDQCMTAD 349
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: October 5, 2005, 17:26:07
Job time : 54.4704 secs

OM protein - protein search, using sw model
Run on: October 5, 2005, 17:07:32 ; Search time 138.341 Seconds
(without alignments)
900.218 Million cell updates/sec

Title: US-10-063-510-6
Perfect score: 1657
Sequence: 1 MARCSLVLLTSIWTRLL.....NPEESKSPKTTVRCLEAFV 322
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Total number of hits satisfying chosen parameters: 2105692
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Database :
Listing first 1500 summaries
A_Geneseq_16Dec04: *
1: Geneseq_1980s: *
2: Geneseq_1990s: *
3: Geneseq_2000s: *
4: Geneseq_2001s: *
5: Geneseq_2002s: *
6: Geneseq_2003as: *
7: Geneseq_2003bs: *
8: Geneseq_2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No. Score Match Length DB ID Description

RESULT 1
ID AAY13379 standard; protein; 322 AA.
DE Amino acid sequence of protein PRO263.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 2; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 2
ID AAY87287 standard; protein; 322 AA.
DE Human signal peptide containing protein HSP-64 SEQ ID NO:64.
PN WO20000610-A2.
PD 06-JAN-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 100.0%; Score 1657; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 3
ID ADC78521 standard; protein; 322 AA.
DE Human PRO263 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 3; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 4
ID AAB80247 standard; protein; 322 AA.
DE Human PRO263 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 5
ID AAB87528 standard; protein; 322 AA.
DE Human PRO263.
PN WO200116318-A2.
PD 08-MAR-2001.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 6
ID AAB88391 standard; protein; 322 AA.

DE Human membrane or secretory protein clone PSEC0135.
PN EP1067182-A2.
PD 10-JAN-2001.
PA (HELI-) HELIX RES INST.
Query Match 100.0%; Score 1657; DB 4; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 7
ID ABG95853 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2002119130-A1.
PD 29-AUG-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 8
ID ABB84832 standard; protein; 322 AA.
DE Human PRO263 protein sequence SEQ ID NO:32.
PN WO200200690-A2.
PD 03-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 9
ID ABB95438 standard; protein; 322 AA.
DE Human angiogenesis related protein PRO263 SEQ ID NO: 32.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 5; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 10
ID ABU71625 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 11
ID ABU71480 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 12
ID ABU71926 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 13
ID ABO01809 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002197671-A1.

PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 14
ID ABU90878 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003018173-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 15
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 16
ID ABO33937 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003009013-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 17
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 18
ID ABO47397 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 19
ID ABO71508 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003013855-A1.
PD 16-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 20
ID ABU7289 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 21
ID ABU90962 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 22
ID ABO27283 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO263.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 23
ID ABU64534 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #38.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 24
ID ABU67380 standard; protein; 322 AA.
DE Human secreted protein PRO263.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 25
ID ABU92478 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 26
ID ABO14900 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 27
ID ABU81148 standard; protein; 322 AA.
DE Human secreted polypeptide PRO263.
PN US2003027212-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 28
ID ABO33263 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 29
ID ABU98265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 30
ID ABU99270 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 31
ID ABU82477 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.

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Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 32
ID ABU69657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 33
ID ABU96441 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 34
ID ABU72111 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 35
ID ABO14839 standard; protein; 322 AA.
DE Human secreted / transmembrane polypeptide PRO263.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 36
ID ADB29406 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 37
ID ADB17063 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 38
ID ABO44241 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 39
ID ADA18262 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 40
ID ABO32791 standard; protein; 322 AA.
DE Human secreted/transmembrane protein PRO263.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 41
ID ADA19868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 42
ID ADB17251 standard; protein; 322 AA.
DE Human transmembrane PRO polypeptide (SeqID 6).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 43
ID ABO34851 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 44
ID ADA16237 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 45
ID ADA20040 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 46
ID ABO34169 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 47
ID ADA42382 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 48
ID ABO17529 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 49
ID ADA00337 standard; protein; 322 AA.
DE Human secreted/transmembrane polypeptide PRO 263.
PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match      100.0%; Score 1657; DB 6; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
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RESULT 50
ID ADA16661 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US200303969-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 51
ID ADA13090 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 52
ID ADA1958 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 53
ID ADA17305 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 54
ID ADA42808 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 55
ID ABO17590 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 56
ID ADB85579 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 57
ID ADB77727 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 58
ID ADB74863 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 59
ID ADB68258 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 60
ID ADB68065 standard; protein; 322 AA.
DE Human PRO263 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 61
ID ADB90882 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 62
ID ADC28509 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 63
ID ADC39709 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 64
ID ADC40223 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 65
ID ADC19047 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 66
ID ADC34347 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 67
ID ADC29402 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 68
ID ADC28933 standard; protein; 322 AA.
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DE Human secreted/transmembrane protein, #40.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 69
ID ADC40818 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 70
ID ADC19475 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 71
ID ADC06962 standard; protein; 322 AA.
DE Human secreted/transmembrane protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 72
ID ADC17141 standard; protein; 322 AA.
DE Mammalian PRO polypeptide (SeqID 6).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 73
ID ADC33923 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 74
ID ADC12993 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 75
ID ADC14839 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 76
ID ADC52334 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 77
ID ADC12445 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003078387-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 78
ID ADD10321 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 79
ID ADD05000 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 80
ID ADD11281 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 81
ID ADD04006 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 82
ID ADD03582 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 83
ID ADD37074 standard; protein; 322 AA.
DE Human secreted/transmembrane PRO polypeptide #16.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 84
ID ADD36010 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 85
ID ADE34834 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 86
ID ADG01011 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO363.
PN US2003078387-A1.

PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 87
ID ADG08564 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 88
ID ADP95185 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 89
ID ADH24038 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 90
ID ADH34064 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 91
ID ADH29897 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 92
ID ADH23868 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 93
ID ADG85272 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 94
ID ADH24548 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 95
ID ADH37404 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181646-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 96
ID ADH01993 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 97
ID ADH37574 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 98
ID ADG85612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 99
ID ADH24208 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 100
ID ADH38502 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 101
ID ADG83623 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 102
ID ADH29431 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 103
ID ADH27547 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 104
ID ADH37744 standard; protein; 322 AA.
DE Human secreted and transmembrane protein PRO263.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.

DE Novel human secreted and transmembrane protein PRO263.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 142
ID ADH79442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 143
ID ADI19399 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 144
ID ADI05200 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 145
ID ADH79612 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 146
ID ADI01438 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 147
ID ADI01608 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 148
ID ADI01778 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 149
ID ADH79782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 150
ID ADI04600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.

PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 151
ID ADI02736 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 152
ID ADH78055 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 153
ID ADI25694 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 154
ID ADI25864 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 155
ID ADK65376 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 156
ID ADH98718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 157
ID ADH79959 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 158
ID ADJ26364 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 7; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 159
ID ADJ93690 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003040013-A1.

PD 27-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 7; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 160
 ID ADC52144 standard; protein; 322 AA.
 DE Novel human secreted and transmembrane protein PRO263.
 PN US2003130483-A1.
 PD 10-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 161
 ID ADE79279 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003135025-A1.
 PD 17-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 162
 ID ADE79703 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003130489-A1.
 PD 10-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 163
 ID ADE73379 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003129592-A1.
 PD 10-JUL-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 164
 ID ADE41282 standard; protein; 322 AA.
 DE Human secreted/transmembrane PRO polypeptide #16.
 PN US2003100497-A1.
 PD 29-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 165
 ID ADE71444 standard; protein; 322 AA.
 DE Human PDEBC Incyte 3044710CD1.
 PN US2003124543-A1.
 PD 03-JUL-2003.
 PA (STUA/) STUART S G.
 PA (STRE/) STREETER D G.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 166
 ID ADE73914 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003148370-A1.
 PD 07-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 167
 ID ADE99468 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003211576-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 168
 ID ADE98587 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003211569-A1.

PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 169
 ID ADE99014 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003211568-A1.
 PD 13-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 170
 ID ADG40484 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003225253-A1.
 PD 04-DEC-2003.
 PA (DESN/) DESNOYERS L.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GURN/) GURNEY A L.
 PA (MATH/) MATHER J P.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 171
 ID ADF73878 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003180312-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 172
 ID ADF73454 standard; protein; 322 AA.
 DE Human secreted/transmembrane protein, #40.
 PN US2003166051-A1.
 PD 04-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 173
 ID ADH06576 standard; protein; 322 AA.
 DE Novel human secreted and transmembrane protein PRO263.
 PN US2003180852-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 174
 ID ADH06406 standard; protein; 322 AA.
 DE Novel human secreted and transmembrane protein PRO263.
 PN US2003180853-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 175
 ID ADG68827 standard; protein; 322 AA.
 DE Novel human secreted and transmembrane protein PRO263.
 PN US2003180855-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 176
 ID ADH27717 standard; protein; 322 AA.
 DE Novel human secreted and transmembrane protein PRO263.
 PN US2003180912-A1.
 PD 25-SEP-2003.
 PA (GETH) GENENTECH INC.
 Query Match 100.0%; Score 1657; DB 8; Length 322;
 Best Local Similarity 100.0%; Pred. No. 8.7e-148;
 RESULT 177

Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 177
ID ADH25058 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180913-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 178
ID ADH33690 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181645-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 179
ID ADG92297 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 180
ID ADH02333 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180839-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 181
ID ADH07940 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180845-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 182
ID ADG9337 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180846-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 183
ID ADH39158 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180917-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 184
ID ADG22724 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 185
ID ADG83898 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180842-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 186
ID ADG85442 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003166848-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 187
ID ADH06236 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180854-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 188
ID ADH30066 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180856-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 189
ID ADH24378 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180910-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 190
ID ADG69507 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180844-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 191
ID ADH07770 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180851-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 192
ID ADG85782 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180861-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 193
ID ADH39328 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180916-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 194
ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 195
ID ADH33520 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181637-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;

ID ADH33860 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181644-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 196
ID ADH01070 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180838-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 197
ID ADG69677 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180843-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 198
ID ADH02163 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180841-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 199
ID ADG9167 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180847-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 200
ID ADG95952 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180862-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 201
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180909-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 202
ID ADH24888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180915-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 203
ID ADH02503 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003180840-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 204
ID ADG68997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003180849-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 205
ID ADH07600 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180850-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 206
ID ADG86122 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180863-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 207
ID ADH24718 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180908-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 208
ID ADH25766 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180911-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 209
ID ADH38332 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180922-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 210
ID ADH20513 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 211
ID ADH57171 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181642-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 212
ID ADH43465 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 213
ID ADH07368 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.

PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 214
ID ADH52159 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180921-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 215
ID ADH59913 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 216
ID ADH49525 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003180857-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 217
ID ADH06941 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 218
ID ADH90487 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181700-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 219
ID ADI11223 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003181683-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 220
ID ADI18683 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 221
ID ADH98888 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190698-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 222
ID ADI65403 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 223
ID ADI02118 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003190699-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 224
ID ADH90657 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181701-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 225
ID ADI37666 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 226
ID ADH97462 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 227
ID ADI65830 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 228
ID ADH60573 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN/) DESNOYERS L.
PA (GODO/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 229
ID ADJ99630 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.

PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 230
ID ADL08823 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein, #40.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 231
ID ADJ98532 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187197-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 232
ID ADJ98702 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187228-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 233
ID ADH78861 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181703-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 234
ID ADJ99095 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 235
ID ADJ99265 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 236
ID ADJ98883 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 237
ID ADH79031 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 238
ID ADK00891 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2003186407-A1.

PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 239
ID ADK14412 standard; protein; 322 AA.
DE Novel human secreted and transmembrane protein PRO263.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 240
ID ADM25164 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 241
ID ADM29914 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 242
ID ADK82810 standard; protein; 322 AA.
DE Human PRO polypeptide #16.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 243
ID ADM80861 standard; protein; 322 AA.
DE Human PRO polypeptide #3.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 244
ID ADO06236 standard; protein; 322 AA.
DE Human PRO polypeptide #36.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 245
ID ADL11088 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1657; DB 8; Length 322;
Best Local Similarity 100.0%; Pred. No. 8.7e-148;
RESULT 246
ID ADL17997 standard; protein; 322 AA.
DE Human secreted/transmembrane protein, #40.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.

PA (ZERR/) ZERHUSEN B D.
 Query Match 90.6%; Score 1500.5; DB 8; Length 297;
 Best Local Similarity 91.9%; Pred. No. 4.9e-133;
 RESULT 257
 ID AAB34702 standard; protein; 250 AA.
 DE Human secreted protein encoded by DNA clone vb28 1.
 PN WO20005375-A1.
 PD 21-SEP-2000.
 PA (ALPH-) ALPHAGENE INC.
 Query Match 73.5%; Score 1218.5; DB 3; Length 250;
 Best Local Similarity 92.0%; Pred. No. 1.8e-106;
 RESULT 258
 ID AAE05364 standard; protein; 318 AA.
 DE Mouse lymphatic endothelium-specific hyaluronan receptor LYVE-1 protein.
 PN WO200148192-A1.
 PD 05-JUL-2001.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Query Match 66.6%; Score 1103; DB 4; Length 318;
 Best Local Similarity 69.7%; Pred. No. 2e-95;
 RESULT 259
 ID ABB72376 standard; protein; 255 AA.
 DE Murine protein isolated from skin cells SEQ ID NO: 700.
 PN WO200190357-A1.
 PD 29-NOV-2001.
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 Query Match 49.5%; Score 821; DB 5; Length 255;
 Best Local Similarity 65.0%; Pred. No. 6.9e-69;
 RESULT 260
 ID AAY12323 standard; protein; 116 AA.
 DE Human 5' EST secreted protein SEQ ID NO: 354.
 PN WO9906548-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 35.7%; Score 592; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 1e-47;
 RESULT 261
 ID AAY12853 standard; protein; 58 AA.
 DE Human 5' EST secreted protein SEQ ID NO: 443.
 PN WO9906549-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 16.7%; Score 277; DB 2; Length 58;
 Best Local Similarity 98.3%; Pred. No. 2.5e-18;
 RESULT 262
 ID AAY12170 standard; protein; 69 AA.
 DE Human 5' EST secreted protein SEQ ID NO: 483.
 PN WO9906554-A2.
 PD 11-FEB-1999.
 PA (GEST) GENSET.
 Query Match 15.8%; Score 261; DB 2; Length 69;
 Best Local Similarity 96.4%; Pred. No. 1e-16;
 RESULT 263
 ID ABB81033 standard; protein; 364 AA.
 DE Rat glycoprotein CD44 polypeptide.
 PN WO200238794-A2.
 PD 16-MAY-2002.
 PA (EGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 13.8%; Score 229; DB 5; Length 364;
 Best Local Similarity 24.3%; Pred. No. 1.1e-12;
 RESULT 264
 ID AAR07355 standard; protein; 362 AA.
 DE B7 adhesion receptor.
 PN WO9011365-A.
 PD 04-OCT-1990.
 PA (HUTC-) HUTCHINSON F CANCER.
 Query Match 13.4%; Score 222.5; DB 2; Length 362;
 Best Local Similarity 25.5%; Pred. No. 4.3e-12;
 RESULT 265
 ID ABU79109 standard; protein; 365 AA.
 DE CD44 protein.
 PN US2002177551-A1.
 PD 28-NOV-2002.
 PA (TERM/) TERMAN D S.

Query Match 13.4%; Score 222.5; DB 6; Length 365;
 Best Local Similarity 24.5%; Pred. No. 4.4e-12;
 RESULT 266
 ID ADF4353 standard; protein; 365 AA.
 DE CD44 receptor polypeptide seq id 73.
 PN US2003157113-A1.
 PD 21-AUG-2003.
 PA (TERM/) TERMAN D S.
 Query Match 13.4%; Score 222.5; DB 7; Length 365;
 Best Local Similarity 24.5%; Pred. No. 4.4e-12;
 RESULT 267
 ID AAR14768 standard; protein; 503 AA.
 DE Metastasis-specific variant of CD44 glycoprotein.
 PN DE4014510-A.
 PD 14-NOV-1991.
 PA (GESL) KERNFORSCHUNGSZENT KARLSRUHE.
 PA (UYKA-) UNIV KARLSRUHE.
 PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
 Query Match 13.4%; Score 222; DB 2; Length 503;
 Best Local Similarity 25.7%; Pred. No. 7.5e-12;
 RESULT 268
 ID ADE57911 standard; protein; 503 AA.
 DE Rat Protein P26051, SEQ ID NO 3777.
 PN WO2003016475-A2.
 PD 27-FEB-2003.
 PA (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 Query Match 13.4%; Score 222; DB 7; Length 503;
 Best Local Similarity 25.7%; Pred. No. 7.5e-12;
 RESULT 269
 ID ABU04619 standard; protein; 668 AA.
 DE Human expressed protein tag (EPT) #1285.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match 12.6%; Score 208.5; DB 6; Length 668;
 Best Local Similarity 29.3%; Pred. No. 2.1e-10;
 RESULT 270
 ID ADQ39384 standard; protein; 668 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1047.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match 12.6%; Score 208.5; DB 8; Length 668;
 Best Local Similarity 29.3%; Pred. No. 2.1e-10;
 RESULT 271
 ID AAR20816 standard; protein; 361 AA.
 DE Haematopoietic CD44 Antigen.
 PN WO9201049-A.
 PD 23-JAN-1992.
 PA (GHEO) GEN HOSPITAL CORP.
 Query Match 12.5%; Score 207; DB 2; Length 361;
 Best Local Similarity 24.4%; Pred. No. 1.3e-10;
 RESULT 272
 ID AAR91444 standard; protein; 361 AA.
 DE Human haematopoietic CD44 antigen.
 PN US5506126-A.
 PD 09-APR-1996.
 PA (GHEO) GEN HOSPITAL CORP.
 Query Match 12.5%; Score 207; DB 2; Length 361;
 Best Local Similarity 24.4%; Pred. No. 1.3e-10;
 RESULT 273
 ID AAW80453 standard; protein; 361 AA.
 DE Human CD44 antigen (membrane form).
 PN US5830731-A.
 PD 03-NOV-1998.
 PA (GHEO) GEN HOSPITAL CORP.
 Query Match 12.5%; Score 207; DB 2; Length 361;
 Best Local Similarity 24.4%; Pred. No. 1.3e-10;
 RESULT 274
 ID AAW86200 standard; protein; 361 AA.
 DE Human CD44 antigen (membrane form).

PN US5849898-A.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 2; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 275
ID RAY96139 standard; protein; 361 AA.
DE Human haematopoietic CD44.5.
PN US6111093-A.
PD 29-AUG-2000.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 276
ID AAU02448 standard; protein; 361 AA.
DE Human haematopoietic antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.5%; Score 207; DB 4; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 277
ID ABU04632 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1298.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 278
ID ABU04610 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1276.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 279
ID ABU04638 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1304.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 280
ID ABU04634 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1300.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 281
ID ABU04626 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1292.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 282
ID ABU04630 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1296.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 283
ID ABU04636 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1302.
PN WO200278524-A2.

PN US2004058052-A2.
PA (ZYCO-) ZYCOS INC.
Query Match 12.5%; Score 207; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 284
ID ADO49373 standard; protein; 361 AA.
DE Human CD44 #1.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUE/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (COUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 12.5%; Score 207; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.3e-10;
RESULT 285
ID RAY9851 standard; protein; 361 AA.
DE Human CD44 cell surface adhesion receptor.
PN WO200035935-A1.
PD 22-JUN-2000.
PA (ISIS-) ISIS PHARM INC.
Query Match 12.4%; Score 205; DB 3; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 286
ID ABU04643 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1309.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 287
ID ABU04609 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1275.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 288
ID ABU04644 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1310.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.4%; Score 205; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 1.9e-10;
RESULT 289
ID ABU04622 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1388.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.4e-10;
RESULT 290
ID AAE30338 standard; protein; 361 AA.
DE Human CD44 antigen.
PN WO200276510-A1.
PD 03-OCT-2002.
PA (AGYT-) AGY THERAPEUTICS INC.
Query Match 12.3%; Score 204; DB 6; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.4e-10;
RESULT 291
ID ADQ39385 standard; protein; 361 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1048.
PN WO2004058052-A2.

PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.3%; Score 204; DB 8; Length 361;
Best Local Similarity 24.4%; Pred. No. 2.4e-10;
RESULT 292
ID ABP72424 standard; protein; 608 AA.
DE Human CD44 variant CD44VRA associated with rheumatoid arthritis.
PN WO2003014160-A2.
PD 20-FEB-2003.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203.5; DB 6; Length 608;
Best Local Similarity 21.8%; Pred. No. 5.5e-10;
RESULT 293
ID AAY97579 standard; protein; 700 AA.
DE Human CD44 splice variant (RA-CD44) protein sequence.
PN WO200075312-A1.
PD 14-DEC-2000.
PA (YISS) YISSUM RES & DEV CO.
Query Match 12.3%; Score 203.5; DB 4; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.7e-10;
RESULT 294
ID ABU04640 standard; protein; 700 AA.
DE Human expressed protein tag (EPT) #1306.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203.5; DB 6; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.7e-10;
RESULT 295
ID ADD90594 standard; protein; 700 AA.
DE Human CD44v glycoprotein SEQ ID NO:4.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203.5; DB 7; Length 700;
Best Local Similarity 21.8%; Pred. No. 6.7e-10;
RESULT 296
ID ADD90592 standard; protein; 361 AA.
DE Human CD44std glycoprotein SEQ ID NO:2.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.3%; Score 203; DB 7; Length 361;
Best Local Similarity 24.4%; Pred. No. 3e-10;
RESULT 297
ID AAY97651 standard; protein; 436 AA.
DE CD44Hextra/tmfASCyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.3%; Score 203; DB 4; Length 436;
Best Local Similarity 25.4%; Pred. No. 3.9e-10;
RESULT 298
ID ABU04642 standard; protein; 436 AA.
DE Human expressed protein tag (EPT) #1308.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203; DB 6; Length 436;
Best Local Similarity 25.4%; Pred. No. 3.9e-10;
RESULT 299
ID ABU04653 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1319.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.3%; Score 203; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 300
ID ABU04616 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1282.
Query Match 12.2%; Score 202; DB 6; Length 361;
Best Local Similarity 25.1%; Pred. No. 2.9e-10;
RESULT 301
ID ADP65295 standard; protein; 742 AA.
DE Human CD44 antigen (homing function and Indian blood group system), CD44.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 12.3%; Score 203; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 302
ID ADL61252 standard; protein; 742 AA.
DE Human protein tyrosine kinase biomarker CD44 antigen protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 303
ID ADQ39391 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1054.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 304
ID ADR67253 standard; protein; 742 AA.
DE Human bladder cancer associated amino acid sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Query Match 12.3%; Score 203; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 8e-10;
RESULT 305
ID ADH18988 standard; protein; 330 AA.
DE Human cell adhesion and extracellular matrix CADECM-25 protein - SEQ 25.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match 12.2%; Score 202.5; DB 8; Length 330;
Best Local Similarity 25.1%; Pred. No. 2.9e-10;
RESULT 306
ID AAY97650 standard; protein; 431 AA.
DE CD44HextraFAStm/cyto protein sequence.
PN WO200100854-A2.
PD 04-JAN-2001.
PA (ANGI-) ANGIOGENE PHARM LTD.
Query Match 12.2%; Score 202.5; DB 4; Length 431;
Best Local Similarity 24.7%; Pred. No. 4.3e-10;
RESULT 307
ID ABU04641 standard; protein; 431 AA.
DE Human expressed protein tag (EPT) #1307.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202.5; DB 6; Length 431;
Best Local Similarity 24.7%; Pred. No. 4.3e-10;
RESULT 308
ID ABU04607 standard; protein; 361 AA.
DE Human expressed protein tag (EPT) #1273.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 361;

Best Local Similarity 24.4%; Pred. No. 3.7e-10;
RESULT 309
ID ADL93508 standard; protein; 361 AA.
DE Human CD44 isoform exons 1-5, 15-17 and 19 SEQ ID NO:3.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.2%; Score 202; DB 8; Length 361;
Best Local Similarity 24.1%; Pred. No. 3.7e-10;
RESULT 310
ID ABU04618 standard; protein; 675 AA.
DE Human expressed protein tag (EPT) #1284.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 675;
Best Local Similarity 26.0%; Pred. No. 8.8e-10;
RESULT 311
ID ABU04621 standard; protein; 691 AA.
DE Human expressed protein tag (EPT) #1287.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 691;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 312
ID ADQ39390 standard; protein; 691 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1053.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 691;
Best Local Similarity 26.0%; Pred. No. 9.1e-10;
RESULT 313
ID ABU04620 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1286.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 314
ID ABU04645 standard; protein; 742 AA.
DE Human expressed protein tag (EPT) #1311.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.2%; Score 202; DB 6; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 315
ID ADN95511 standard; protein; 742 AA.
DE Human BCC/LEC-related protein sequence SeqID434.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 12.2%; Score 202; DB 7; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 316
ID ADL93506 standard; protein; 742 AA.
DE Human CD44 isoform exons 1-17 and 19 SEQ ID NO:1.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 317
ID ADO55181 standard; protein; 742 AA.
DE Protein #83 with increased gene expression in renal cell carcinoma.
PN WO2004032842-A2.
PD 22-APR-2004.
PA (VAND-) VAN ANDEL INST.
Query Match 12.2%; Score 202; DB 8; Length 742;

Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 318
ID ADQ39383 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1046.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 319
ID ADQ39386 standard; protein; 742 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1049.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 12.2%; Score 202; DB 8; Length 742;
Best Local Similarity 26.0%; Pred. No. 1e-09;
RESULT 320
ID ABU04617 standard; protein; 425 AA.
DE Human expressed protein tag (EPT) #1283.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.1%; Score 201; DB 6; Length 425;
Best Local Similarity 22.0%; Pred. No. 5.8e-10;
RESULT 321
ID ADD90596 standard; protein; 699 AA.
DE Human CD44v glycoprotein SEQ ID NO:6.
PN WO2003072606-A2.
PD 04-SEP-2003.
PA (YEDA) YEDA RES & DEV CO LTD.
PA (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
Query Match 12.1%; Score 200.5; DB 7; Length 699;
Best Local Similarity 25.2%; Pred. No. 1.3e-09;
RESULT 322
ID AAR20817 standard; protein; 493 AA.
DE Epithelial CD44 Antigen.
PN WO9201049-A.
PD 23-JAN-1992.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 323
ID AAR91445 standard; protein; 493 AA.
DE Human epithelial CD44 antigen.
PN US5506126-A.
PD 09-APR-1996.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 324
ID AAW80454 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5830731-A.
PD 03-NOV-1998.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 325
ID AAW89151 standard; protein; 493 AA.
DE Human CD44 antigen (epithelial form).
PN US5849898-A.
PD 15-DEC-1998.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 2; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 326
ID AAY96140 standard; protein; 493 AA.
DE Human epithelial CD44.
PN US6111033-A.
PD 29-AUG-2000.
PA (GHEO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 3; Length 493;

Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 327
ID AAU02449 standard; protein; 493 AA.
DE Human epithelial antigen CD44 polypeptide.
PN US6218525-B1.
PD 17-APR-2001.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 12.0%; Score 199.5; DB 4; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 328
ID AAU99123 standard; protein; 493 AA.
DE Haematopoietic cell E-selectin/L-selectin ligand (HCELL) protein.
PN WO200244342-A2.
PD 06-JUN-2002.
PA (EGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 12.0%; Score 199.5; DB 5; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 329
ID ABU04637 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1303.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 330
ID ABU04627 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1293.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 331
ID ABU04639 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1305.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 332
ID ABU04623 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1289.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 333
ID ABU04631 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1297.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 334
ID ABU04633 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1299.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 335
ID ABU04612 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1278.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 336
ID ABU04635 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1301.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 337
ID ABU04613 standard; protein; 493 AA.
DE Human expressed protein tag (EPT) #1279.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199.5; DB 6; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 338
ID ADL93507 standard; protein; 493 AA.
DE Human CD44 isoform exons 1-5, 2-17 and 19 SEQ ID NO:2.
PN WO2004024750-A2.
PD 25-MAR-2004.
PA (DYAX-) DYAX CORP.
Query Match 12.0%; Score 199.5; DB 8; Length 493;
Best Local Similarity 22.2%; Pred. No. 9.8e-10;
RESULT 339
ID ADO49375 standard; protein; 493 AA.
DE Human CD44 #2.
PN US2004072283-A1.
PD 15-APR-2004.
PA (SEED/) SEED B.
PA (ALLE/) ALLEN J.
PA (ARUF/) ARUFFO A.
PA (CAME/) CAMERINI D.
PA (LAUF/) LAUFFER L.
PA (OQUE/) OQUENDO C.
PA (SIMM/) SIMMONS D.
PA (STAM/) STAMENKOVIC I.
PA (STEN/) STENGELIN S.
PA (AMIO/) AMIOT M.
Query Match 12.0%; Score 199.5; DB 8; Length 493;
Best Local Similarity 23.6%; Pred. No. 9.8e-10;
RESULT 340
ID ABU04649 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1315.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 6.5e-10;
RESULT 341
ID ABU04605 standard; protein; 338 AA.
DE Human expressed protein tag (EPT) #1271.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 12.0%; Score 199; DB 6; Length 338;
Best Local Similarity 24.6%; Pred. No. 6.5e-10;
RESULT 342
ID ABU04615 standard; protein; 395 AA.
DE Human expressed protein tag (EPT) #1281.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 198; DB 6; Length 395;
Best Local Similarity 23.0%; Pred. No. 1e-09;
RESULT 343
ID ABU04604 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1270.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 2.8e-09;

RESULT 344
ID ABU04650 standard; protein; 719 AA.
DE Human expressed protein tag (EPT) #1316.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 197; DB 6; Length 719;
Best Local Similarity 26.3%; Pred. No. 2.8e-09;
RESULT 345
ID ABM83594 standard; protein; 535 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3843.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 11.9%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.1e-09;
RESULT 346
ID ADQ39381 standard; protein; 535 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1044.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.9%; Score 196.5; DB 8; Length 535;
Best Local Similarity 25.4%; Pred. No. 2.1e-09;
RESULT 347
ID ABU56470 standard; protein; 699 AA.
DE Lung cancer-associated polypeptide #63.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 348
ID ABU04647 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1313.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 349
ID ABU04614 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1280.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 350
ID ABU04608 standard; protein; 699 AA.
DE Human expressed protein tag (EPT) #1274.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.9%; Score 196.5; DB 6; Length 699;
Best Local Similarity 25.4%; Pred. No. 3e-09;
RESULT 351
ID ADI60182 standard; protein; 261 AA.
DE Secreted polypeptide #66.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 11.8%; Score 196; DB 7; Length 261;
Best Local Similarity 30.9%; Pred. No. 8.8e-10;
RESULT 352
ID ABU04611 standard; protein; 293 AA.
DE Human expressed protein tag (EPT) #1277.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 293;
Best Local Similarity 30.9%; Pred. No. 1e-09;
RESULT 353
ID ABU04602 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1290.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1e-09;
RESULT 354
ID ABU04646 standard; protein; 294 AA.
DE Human expressed protein tag (EPT) #1312.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.8%; Score 196; DB 6; Length 294;
Best Local Similarity 30.9%; Pred. No. 1e-09;
RESULT 355
ID ADQ39389 standard; protein; 395 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1052.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 395;
Best Local Similarity 30.9%; Pred. No. 1.6e-09;
RESULT 356
ID ADQ39382 standard; protein; 425 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1045.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 425;
Best Local Similarity 30.9%; Pred. No. 1.7e-09;
RESULT 357
ID ADQ39388 standard; protein; 493 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1051.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 11.8%; Score 196; DB 8; Length 493;
Best Local Similarity 30.9%; Pred. No. 2.1e-09;
RESULT 358
ID ABG17071 standard; protein; 742 AA.
DE Novel human diagnostic protein #17062.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 11.7%; Score 194.5; DB 4; Length 742;
Best Local Similarity 25.4%; Pred. No. 5.1e-09;
RESULT 359
ID AAM48306 standard; protein; 194 AA.
DE Protein R2 SEQ ID 29.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 194;
Best Local Similarity 30.8%; Pred. No. 9e-10;
RESULT 360
ID AAM48307 standard; protein; 200 AA.
DE Protein R3 SEQ ID 30.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 200;
Best Local Similarity 30.8%; Pred. No. 9.4e-10;
RESULT 361
ID AAM48308 standard; protein; 273 AA.
DE Protein R4 SEQ ID 31.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.7%; Score 194; DB 5; Length 273;
Best Local Similarity 30.8%; Pred. No. 1.4e-09;
RESULT 362
ID ABU04602 standard; protein; 676 AA.

DE Human expressed protein tag (EPT) #1268.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.6%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 8.6e-09;
RESULT 363
ID ABU04652 standard; protein; 676 AA.
DE Human expressed protein tag (EPT) #1318.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.6%; Score 191.5; DB 6; Length 676;
Best Local Similarity 25.8%; Pred. No. 8.6e-09;
RESULT 364
ID ABU04648 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1314.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 2.7e-09;
RESULT 365
ID ABU04606 standard; protein; 271 AA.
DE Human expressed protein tag (EPT) #1272.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 271;
Best Local Similarity 31.5%; Pred. No. 2.7e-09;
RESULT 366
ID ABU04651 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1317.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 5.9e-09;
RESULT 367
ID ABU04603 standard; protein; 470 AA.
DE Human expressed protein tag (EPT) #1269.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 11.5%; Score 191; DB 6; Length 470;
Best Local Similarity 31.5%; Pred. No. 5.9e-09;
RESULT 368
ID AAM48305 standard; protein; 170 AA.
DE Protein R1 SEQ ID 28.
PN WO200192507-A1.
PD 06-DEC-2001.
PA (FUJI-) FUJICHEMICO LTD.
Query Match 11.3%; Score 188; DB 5; Length 170;
Best Local Similarity 35.7%; Pred. No. 2.8e-09;
RESULT 369
ID ABP73148 standard; protein; 112 AA.
DE Amino acid sequence of a human CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.3%; Score 187; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 2e-09;
RESULT 370
ID ABP73150 standard; protein; 113 AA.
DE Amino acid sequence of a chicken CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.3%; Score 186.5; DB 6; Length 113;
Best Local Similarity 36.0%; Pred. No. 2e-09;
Best Local Similarity 36.3%; Pred. No. 2.2e-09;
RESULT 371
ID ABP73151 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.2%; Score 185; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 3e-09;
RESULT 372
ID ABP73152 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.0%; Score 183; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 4.7e-09;
RESULT 373
ID ABP73149 standard; protein; 112 AA.
DE Amino acid sequence of a dog CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 11.0%; Score 182; DB 6; Length 112;
Best Local Similarity 34.2%; Pred. No. 5.8e-09;
RESULT 374
ID ABP73153 standard; protein; 112 AA.
DE Amino acid sequence of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOGEL/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 10.9%; Score 181; DB 6; Length 112;
Best Local Similarity 36.0%; Pred. No. 7.2e-09;
RESULT 375
ID ABG17067 standard; protein; 920 AA.
DE Novel human diagnostic protein #17058.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.9%; Score 180; DB 4; Length 920;
Best Local Similarity 25.6%; Pred. No. 1.6e-07;
RESULT 376
ID AD160410 standard; protein; 920 AA.
DE Secreted polypeptide encoded by gene splice variant #46.
PN WO2003025142-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 10.9%; Score 180; DB 7; Length 920;
Best Local Similarity 25.6%; Pred. No. 1.6e-07;
RESULT 377
ID AAM28056 standard; protein; 34 AA.
DE Peptide #2093 encoded by probe for measuring placental gene expression.
PN WO200157272-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.3%; Score 170; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
RESULT 378
ID ABG37308 standard; peptide; 34 AA.
DE Human peptide encoded by genome-derived single exon probe SEQ ID 26973.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Query Match 10.3%; Score 170; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;

RESULT 379
ID ADB64426 standard; protein; 510 AA.
DE Human protein encoded by clone FEBRA20038970.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 9.1%; Score 150; DB 7; Length 510;
Best Local Similarity 23.6%; Pred. No. 4.9e-05;
RESULT 380
ID ABP73154 standard; protein; 80 AA.
DE Deletion mutant of a CD44-hyaluronic acid binding domain.
PN WO2003018044-A1.
PD 06-MAR-2003.
PA (STRO/) STROEMBLAD S.
PA (KOG/) KOGERMAN P.
PA (PAEL/) PAELL T.
Query Match 9.0%; Score 148.5; DB 6; Length 80;
Best Local Similarity 37.0%; Pred. No. 5.4e-06;
RESULT 381
ID ADP07712 standard; protein; 162 AA.
DE Human secreted protein, seq id 195.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 8.8%; Score 145; DB 8; Length 162;
Best Local Similarity 33.0%; Pred. No. 3e-05;
RESULT 382
ID ADM80807 standard; protein; 237 AA.
DE Human CADECM-36 protein SEQ ID NO:36.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 8.8%; Score 145; DB 8; Length 237;
Best Local Similarity 33.0%; Pred. No. 5.1e-05;
RESULT 383
ID AAR26044 standard; protein; 277 AA.
DE Tumour necrosis factor-induced glycoprotein TSG-6.
PN WO9212175-A1.
PD 23-JUL-1992.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 384
ID AAU3654 standard; protein; 277 AA.
DE Tumour necrosis factor-stimulated gene-6 protein.
PN WO9704075-A1.
PD 06-FEB-1997.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 385
ID AAW84087 standard; protein; 277 AA.
DE Tumour necrosis factor stimulated gene 6 (TSG-6) protein.
PN US5846763-A.
PD 08-DEC-1998.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 2; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 386
ID AAE02361 standard; protein; 277 AA.
DE Human tumour necrosis factor (TNF) stimulated gene-6 (TSG-6) protein.
PN US6210905-B1.
PD 03-APR-2001.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 4; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 387
ID ABG70870 standard; protein; 277 AA.
DE Human tumour necrosis factor stimulated gene 6, TSG-6, protein.
PN US2002090708-A1.
PD 11-JUL-2002.
PA (UYNY) UNIV NEW YORK STATE.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 0.0014;
RESULT 388
ID ABR58556 standard; protein; 277 AA.
DE Human cancer related protein SEQ ID NO:213.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 389
ID ABUS6653 standard; protein; 277 AA.
DE Lung cancer-associated polypeptide #246.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 6; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 390
ID ADE25781 standard; protein; 277 AA.
DE Human protein differentially expressed in foam cells #58.
PN US2003194721-A1.
PD 16-OCT-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 391
ID ADN39919 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C289.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 392
ID ADN38974 standard; protein; 277 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:292.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 8.8%; Score 145; DB 7; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 393
ID ADQ21506 standard; protein; 277 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 4356.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 394
ID ADR51534 standard; protein; 277 AA.
DE Human lipopolysaccharide-sensitive polypeptide #14.
PN WO2004069870-A2.
PD 19-AUG-2004.
PA (UYLE-) RIJKSUNIV LEIDEN.
Query Match 8.8%; Score 145; DB 8; Length 277;
Best Local Similarity 33.0%; Pred. No. 6.3e-05;
RESULT 395
ID ADK67822 standard; protein; 2626 AA.
DE Human BRCC300 polypeptide.
PN WO2004012755-A1.
PD 12-FEB-2004.
PA (WIST-) WISTAR INST.
Query Match 8.8%; Score 145; DB 8; Length 2626;
Best Local Similarity 33.0%; Pred. No. 0.0014;
RESULT 396
ID ADS85081 standard; protein; 275 AA.
DE Mouse atopic dermatitis-related protein sequence SeqID83.
PN WO2004031366-A1.
PD 15-APR-2004.
PA (GENO-) GENOX RES INC.
PA (UYJU-) UNIV JUNTENDO.

Query Match 8.7%; Score 144; DB 8; Length 275;
 Best Local Similarity 33.0%; Pred. No. 7.8e-05;
 RESULT 397
 ID ADO09968 standard; protein; 897 AA.
 DE Human NOV1C CDNA.
 PN US2004018970-A1.
 PD 29-JAN-2004.
 PA (SHIM/) SHIMKETS R A.
 PA (PATT/) PATTURAJAN M.
 PA (VERN/) VERNET C A M.
 PA (CASM/) CASMAN S J.
 PA (MALLY/) MALYANKAR U M.
 PA (SHEN/) SHENOY S G.
 PA (SPYT/) SPYTEK K A.
 PA (GANG/) GANGOLLI E A.
 PA (MILL/) MILLER C E.
 PA (BOLD/) BOLDOG F L.
 PA (LILL/) LI L.
 PA (TAUP/) TAUPIER R J.
 PA (KEKU/) KEKUDA R.
 PA (SMIT/) SMITHSON G.
 PA (ZERH/) ZERHUSEN B D.
 PA (LIUX/) LIU X.
 PA (COLM/) COLMAN S D.
 PA (SPYT/) SPYTEK K A.
 PA (GANG/) GANGOLLI E A.
 PA (MILL/) MILLER C E.
 PA (BOLD/) BOLDOG F L.
 PA (LILL/) LI L.
 PA (TAUP/) TAUPIER R J.
 PA (KEKU/) KEKUDA R.
 PA (SMIT/) SMITHSON G.
 PA (ZERH/) ZERHUSEN B D.
 PA (LIUX/) LIU X.
 PA (COLM/) COLMAN S D.
 PA (TCHER/) TCHERNEV V T.
 PA (SIJ/) SI J.
 PA (EDIN/) EDINGER S R.
 PA (STON/) STONE D J.
 PA (SCIO/) SCIORE P.
 PA (MILL/) MILLET I.
 PA (ROTH/) ROTHENBERG M E.
 Query Match 8.2%; Score 136; DB 8; Length 897;
 Best Local Similarity 21.2%; Pred. No. 0.0023;
 RESULT 398
 ID ABJ10588 standard; protein; 897 AA.
 DE Human novel protein NOV1C SEQ ID NO: 211.
 PN WO200259315-A2.
 PD 01-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.1%; Score 134; DB 5; Length 897;
 Best Local Similarity 20.7%; Pred. No. 0.0035;
 RESULT 399
 ID ADH71312 standard; protein; 897 AA.
 DE Human protein of the invention NOV9a SEQ ID NO:208.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.1%; Score 134; DB 8; Length 897;
 Best Local Similarity 20.7%; Pred. No. 0.0035;
 RESULT 400
 ID ADH71356 standard; protein; 1502 AA.
 DE Human protein of the invention NOV9w SEQ ID NO:252.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.1%; Score 134; DB 8; Length 1502;
 Best Local Similarity 20.7%; Pred. No. 0.0071;
 RESULT 401
 ID ABJ10586 standard; protein; 2675 AA.
 DE Human novel protein NOV1a SEQ ID NO: 2.
 PN WO200259315-A2.
 PD 01-AUG-2002.
 PA (CURA-) CURAGEN CORP.
 Query Match 8.1%; Score 134; DB 5; Length 2675;
 Best Local Similarity 17.8%; Pred. No. 0.016;
 RESULT 402
 ID ADO09971 standard; protein; 2675 AA.
 DE Human NOV1a variant.
 PN US2004018970-A1.
 PD 29-JAN-2004.
 PA (SHIM/) SHIMKETS R A.
 PA (PATT/) PATTURAJAN M.
 PA (VERN/) VERNET C A M.

PA (CASM/) CASMAN S J.
 PA (MALLY/) MALYANKAR U M.
 PA (SHEN/) SHENOY S G.
 PA (SPYT/) SPYTEK K A.
 PA (GANG/) GANGOLLI E A.
 PA (MILL/) MILLER C E.
 PA (BOLD/) BOLDOG F L.
 PA (LILL/) LI L.
 PA (TAUP/) TAUPIER R J.
 PA (KEKU/) KEKUDA R.
 PA (SMIT/) SMITHSON G.
 PA (ZERH/) ZERHUSEN B D.
 PA (LIUX/) LIU X.
 PA (COLM/) COLMAN S D.
 PA (TCHER/) TCHERNEV V T.
 PA (SIJ/) SI J.
 PA (EDIN/) EDINGER S R.
 PA (STON/) STONE D J.
 PA (SCIO/) SCIORE P.
 PA (MILL/) MILLET I.
 PA (ROTH/) ROTHENBERG M E.
 Query Match 8.1%; Score 134; DB 8; Length 2675;
 Best Local Similarity 17.8%; Pred. No. 0.016;
 RESULT 403
 ID ADO09836 standard; protein; 2675 AA.
 DE Human NOV1a.
 PN US2004018970-A1.
 PD 29-JAN-2004.
 PA (SHIM/) SHIMKETS R A.
 PA (PATT/) PATTURAJAN M.
 PA (VERN/) VERNET C A M.
 PA (CASM/) CASMAN S J.
 PA (MALLY/) MALYANKAR U M.
 PA (SHEN/) SHENOY S G.
 PA (SPYT/) SPYTEK K A.
 PA (GANG/) GANGOLLI E A.
 PA (MILL/) MILLER C E.
 PA (BOLD/) BOLDOG F L.
 PA (LILL/) LI L.
 PA (TAUP/) TAUPIER R J.
 PA (KEKU/) KEKUDA R.
 PA (SMIT/) SMITHSON G.
 PA (ZERH/) ZERHUSEN B D.
 PA (LIUX/) LIU X.
 PA (COLM/) COLMAN S D.
 PA (TCHER/) TCHERNEV V T.
 PA (SIJ/) SI J.
 PA (EDIN/) EDINGER S R.
 PA (STON/) STONE D J.
 PA (SCIO/) SCIORE P.
 PA (MILL/) MILLET I.
 PA (ROTH/) ROTHENBERG M E.
 Query Match 8.1%; Score 134; DB 8; Length 2675;
 Best Local Similarity 17.8%; Pred. No. 0.016;
 RESULT 404
 ID AAM47684 standard; protein; 1394 AA.
 DE Human Hyaluronic Acid Receptor for Endocytosis, HARE.
 PN WO200181544-A2.
 PD 01-NOV-2001.
 PA (WEIG/) WEIGEL P A.
 PA (ZHOU/) ZHOU B.
 PA (WEIG/) WEIGEL J A.
 Query Match 8.0%; Score 133; DB 5; Length 1394;
 Best Local Similarity 20.7%; Pred. No. 0.0079;
 RESULT 405
 ID ABG72499 standard; protein; 1416 AA.
 DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #1.
 PN WO200286091-A2.
 PD 31-OCT-2002.
 PA (WEIG/) WEIGEL P H.
 PA (WEIG/) WEIGEL J A.
 Query Match 8.0%; Score 133; DB 6; Length 1416;
 Best Local Similarity 20.7%; Pred. No. 0.0081;

RESULT 406
ID AAM47675 standard; protein; 1431 AA.
DE Rat Hyaluronic Acid Receptor for Endocytosis, HARE.
PN WO200181544-A2.
PD 01-NOV-2001.
PA (WEIG/) WEIGEL P A.
PA (ZHOU/) ZHOU B.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 8.0%; Score 133; DB 5; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0082;
RESULT 407
ID ABG72498 standard; protein; 1431 AA.
DE Rat 175kDa Hyaluronan receptor for endocytosis (HARE).
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 8.0%; Score 133; DB 6; Length 1431;
Best Local Similarity 18.5%; Pred. No. 0.0082;
RESULT 408
ID ADH71358 standard; protein; 1510 AA.
DE Human protein of the invention NOV9x SEQ ID NO:254.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.0%; Score 133; DB 8; Length 1510;
Best Local Similarity 20.7%; Pred. No. 0.0088;
RESULT 409
ID ABG72514 standard; protein; 1653 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) #2.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match
Best Local Similarity 8.0%; Score 133; DB 6; Length 1653;
Best Local Similarity 20.7%; Pred. No. 0.01;
RESULT 410
ID ADM90835 standard; protein; 1895 AA.
DE Human pharmaceutically useful protein SeqID 228.
PN WO2004020595-A2.
PD 11-MAR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.
PA (DNAF-) DNAFORM KK.
Query Match
Best Local Similarity 8.0%; Score 133; DB 8; Length 1895;
Best Local Similarity 20.7%; Pred. No. 0.012;
RESULT 411
ID ADH71360 standard; protein; 2551 AA.
DE Human protein of the invention NOV9y SEQ ID NO:256.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 8.0%; Score 133; DB 8; Length 2551;
Best Local Similarity 20.7%; Pred. No. 0.018;
RESULT 412
ID ABM84174 standard; protein; 2285 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4423.
PN WO20040231973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 8.0%; Score 132.5; DB 8; Length 2285;
Best Local Similarity 27.4%; Pred. No. 0.017;
RESULT 413
ID ABM84173 standard; protein; 2384 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4422.
PN WO20040231973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 8.0%; Score 132.5; DB 8; Length 2384;
Best Local Similarity 27.4%; Pred. No. 0.018;
RESULT 414
ID ABP72603 standard; protein; 883 AA.
DE Rat mutant brain-enriched hyaluronan binding protein.

PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (MATT/) MATTHEWS R T.
Query Match
Best Local Similarity 7.9%; Score 131.5; DB 6; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0059;
RESULT 415
ID ADK67779 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding (BEHAB) mutant.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match
Best Local Similarity 7.9%; Score 131.5; DB 8; Length 883;
Best Local Similarity 24.3%; Pred. No. 0.0059;
RESULT 416
ID AAB61236 standard; protein; 649 AA.
DE Mature human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 4; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 417
ID ABO32673 standard; protein; 649 AA.
DE Secreted polypeptide-related protein #74.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (MACK/) MACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match
Best Local Similarity 7.9%; Score 131; DB 6; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 418
ID ADB90778 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 419
ID ADF71513 standard; protein; 649 AA.
DE Human TANGO 332 mature protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 7; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 420
ID ADQ10331 standard; protein; 649 AA.
DE Human polypeptide #167.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 649;
Best Local Similarity 20.4%; Pred. No. 0.0043;
RESULT 421
ID AAB61234 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 4; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;

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RESULT 422
ID ABO32671 standard; protein; 671 AA.
DE Secreted polypeptide-related protein #73.
PN US2003022279-A1.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.
PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (WACK/) WACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match
Best Local Similarity 20.4%; Score 131; DB 6; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 423
ID ADB90776 standard; protein; 671 AA.
DE Human TANGO 332 protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 424
ID ADF1511 standard; protein; 671 AA.
DE Human TANGO 332.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 425
ID ADQ10329 standard; protein; 671 AA.
DE Human polypeptide #165.
PN US2004121396-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 8; Length 671;
Best Local Similarity 20.4%; Pred. No. 0.0045;
RESULT 426
ID ADH18892 standard; protein; 806 AA.
DE Human cell adhesion and extracellular matrix CADECM-19 protein - SEQ 19.
PN WO2003094843-A2.
PD 20-NOV-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 20.4%; Score 131; DB 8; Length 806;
Best Local Similarity 20.4%; Pred. No. 0.0058;
RESULT 427
ID AAY97583 standard; protein; 911 AA.
DE Human secreted protein PRO6018.
PN WO200075317-A2.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 4; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 428
ID ABG34055 standard; protein; 911 AA.
DE Human Pro peptide #26.
PN WO200224888-A2.
PD 28-MAR-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 429
ID ADI28032 standard; protein; 911 AA.
DE ECMCAD protein 6755002CD1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 5; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 430
ID ADA01320 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068779-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 431
ID ADA43749 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064474-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 432
ID ADA43517 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073196-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 433
ID ADA01192 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068782-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 6; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 434
ID ADA01076 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003068780-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 435
ID ADA43633 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073190-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 436
ID ADA06895 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068781-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 437
ID ADA08383 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003068783-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 438
ID ADB99676 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003082728-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
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RESULT 439
ID ADB86959 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082726-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 440
ID ADB66114 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082729-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 441
ID ADB99792 standard; protein; 911 AA.
DE Human PRO polypeptide SEQ ID 52.
PN US2003073192-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 442
ID ADB99447 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003082731-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 443
ID ADB65998 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003082732-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 444
ID ADC23396 standard; protein; 911 AA.
DE Human transmembrane PRO polypeptide (SeqID 52).
PN US2003073193-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 445
ID ADC26089 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003073194-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 446
ID ADE62583 standard; protein; 911 AA.
DE Human Protein NP_068767, SEQ ID NO 8514.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 447
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 448
ID ADE11222 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073191-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 449
ID ADD88153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003082733-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 450
ID ADD95448 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003064473-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 451
ID ADE06378 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073195-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 452
ID ADE38153 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119120-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 453
ID ADD88269 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003073189-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 454
ID ADD90850 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003073188-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 455
ID ADF99405 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003078401-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 456
ID ADG06498 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003077742-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
RESULT 457
ID ADE04916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003068778-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 20.4%; Score 131; DB 7; Length 911;
Pred. No. 0.0068;
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ID ADG05449 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US200307741-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 458
ID ADG02450 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US200307744-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 459
ID ADE51703 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104560-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 7; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 460
ID ADE51819 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104561-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 461
ID ADE37677 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104564-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 462
ID ADE37561 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104565-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 463
ID ADD95332 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138901-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 464
ID ADE38032 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003104566-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 465
ID ADE76121 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124665-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 466
ID ADE39444 standard; protein; 911 AA.

DE Human PRO polypeptide #26.
PN US2003119117-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 467
ID ADE04248 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003096364-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 468
ID ADEJ9845 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138896-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 469
ID ADE19710 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138903-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 470
ID ADE77288 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124666-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 471
ID ADE65396 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119116-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 472
ID ADE76005 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003124663-A1.
PD 03-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 473
ID ADEJ7916 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119119-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 474
ID ADE64526 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119114-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 475
ID ADE38861 standard; protein; 911 AA.
DE Human PRO polypeptide #26.

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PN US2003096363-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 475
ID ADE51935 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104562-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 477
ID ADD90966 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138902-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 478
ID ADE38745 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003108996-A1.
PD 12-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 479
ID ADE37445 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104563-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 480
ID ADE06262 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138898-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 481
ID ADD90121 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003138904-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 482
ID ADE38629 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119086-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 483
ID ADE39560 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119118-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 484
ID ADD89165 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138897-A1.

PN US2003096363-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 485
ID ADD88932 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138899-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 486
ID ADE19826 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003138900-A1.
PD 24-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 487
ID ADE77404 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003124667-A1.
PD 03-JUL-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 488
ID ADE65280 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119113-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 489
ID ADE39328 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119115-A1.
PD 26-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 490
ID ADE38513 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003104559-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 491
ID ADG11066 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003170809-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 492
ID ADG10950 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003077743-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.9%; Score 131; DB 8; Length 911;
RESULT 493
ID ADH31478 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119139-A1.
PD 26-JUN-2003.
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PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 494
ID ADH38726 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119140-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 495
ID ADH29361 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119137-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 496
ID ADH23664 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119143-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 497
ID ADH26994 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119135-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 498
ID ADH38262 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119124-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 499
ID ADH26878 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119134-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 500
ID ADH38146 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119123-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 501
ID ADH38842 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119141-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 502
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 503
ID ADH40156 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119132-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 504
ID ADH40040 standard; protein; 911 AA.
DE Human PRO6018 protein.
PN US2003119133-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 505
ID ADH31362 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003119138-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 506
ID ADH29240 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119136-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 507
ID ADH49455 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119127-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 508
ID ADH51919 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119125-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 509
ID ADH49774 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119128-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 510
ID ADH52375 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119130-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 511
ID ADH52491 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119129-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 512
ID ADH23780 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003119142-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 512
ID ADH5488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 513
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 514
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 515
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 516
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 517
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 518
ID ABM0156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 519
ID RAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 520
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.

Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 512
ID ADH5488 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119121-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 513
ID ADH51803 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119126-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 514
ID ADH58364 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119122-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 515
ID ADI13561 standard; protein; 911 AA.
DE Novel human secreted and transmembrane protein PRO6018.
PN US2003119131-A1.
PD 26-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 516
ID ADK00817 standard; protein; 911 AA.
DE Human PRO polypeptide #26.
PN US2003186373-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 517
ID ADL08558 standard; protein; 911 AA.
DE Human secreted/transmembrane polypeptide PRO6018.
PN US2003186372-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 518
ID ABM0156 standard; protein; 911 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO6018, SEQ:395.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 7.9%; Score 131; DB 8; Length 911;
Best Local Similarity 20.4%; Pred. No. 0.0068;
RESULT 519
ID RAB61242 standard; protein; 883 AA.
DE Murine brevidin protein.
PN WO200100638-A2.
PD 04-JAN-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 4; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 520
ID ABO32678 standard; protein; 883 AA.
DE Secreted polypeptide-related protein #119.
PN US2003022279-A1.
PD 30-JAN-2003.
PA (FRAS/) FRASER C C.
PA (BARN/) BARNES T M.
PA (SHAR/) SHARP J D.

PA (KIRS/) KIRST S J.
PA (MYER/) MYERS P S.
PA (LEIB/) LEIBY K R.
PA (HOLT/) HOLTZMAN D A.
PA (MCCA/) MCCARTHY S A.
PA (WRIG/) WRIGHTON N.
PA (WACK/) WACKAY C R.
PA (GOOD/) GOODEARL A D J.
Query Match 7.9%; Score 130.5; DB 6; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 521
ID ABP72604 standard; protein; 883 AA.
DE Rat brain-enriched hyaluronan binding protein.
PN WO2003007880-A2.
PD 30-JAN-2003.
PA (UYVA) UNIV YALE.
PA (HOCK/) HOCKFIELD S.
PA (WAT7/) MATTHEWS R T.
Query Match 7.9%; Score 130.5; DB 6; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0073;
RESULT 522
ID ADB90787 standard; protein; 883 AA.
DE Mouse brevicin protein.
PN US2003082586-A1.
PD 01-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 523
ID ADE62581 standard; protein; 883 AA.
DE Rat Protein P55068, SEQ ID NO 8512.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0073;
RESULT 524
ID ADF71522 standard; protein; 883 AA.
DE Murine brevidin protein.
PN US2003175733-A1.
PD 18-SEP-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 7; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 525
ID ADK67782 standard; protein; 883 AA.
DE Rat glycosylation-variant BEHAB isoform.
PN WO2004013356-A1.
PD 12-FEB-2004.
PA (UYVA) UNIV YALE.
Query Match 7.9%; Score 130.5; DB 8; Length 883;
Best Local Similarity 23.3%; Pred. No. 0.0073;
RESULT 526
ID ADQ10338 standard; protein; 883 AA.
DE Human polypeptide #172.
PN US2004121356-A1.
PD 24-JUN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 7.9%; Score 130.5; DB 8; Length 883;
Best Local Similarity 24.4%; Pred. No. 0.0073;
RESULT 527
ID ABB90349 standard; protein; 1082 AA.
DE Human polypeptide SEQ ID NO 2725.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.9%; Score 130.5; DB 5; Length 1082;
Best Local Similarity 20.6%; Pred. No. 0.0096;
RESULT 528
ID ABM80463 standard; protein; 2570 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO80999, SEQ:1164.
PN WO2004030615-A2.

PD 15-APR-2004.
 PA (GENE) GENENTECH INC. 7.9%; Score 130.5; DB 8; Length 2570;
 Query Match
 Best Local Similarity 20.6%; Pred. No. 0.032;
 RESULT 529
 ID AAY93911 standard; protein; 457 AA.
 DE A human hyaluronan-binding protein, designated WF-HABP.
 PN WO200039166-A1.
 PD 06-JUL-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (AMNA-) AMERICAN NAT RED CROSS.
 Query Match
 Best Local Similarity 7.8%; Score 129.5; DB 3; Length 457;
 Best Local Similarity 20.9%; Pred. No. 0.0037;
 RESULT 530
 ID ABM83434 standard; protein; 761 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3683.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 7.8%; Score 129.5; DB 8; Length 761;
 Best Local Similarity 22.8%; Pred. No. 0.0074;
 RESULT 531
 ID AAY93910 standard; protein; 2157 AA.
 DE A human hyaluronan-binding protein, designated WF-HABP.
 PN WO200039166-A1.
 PD 06-JUL-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (AMNA-) AMERICAN NAT RED CROSS.
 Query Match
 Best Local Similarity 7.8%; Score 129.5; DB 3; Length 2157;
 Best Local Similarity 20.9%; Pred. No. 0.031;
 RESULT 532
 ID ABR82200 standard; protein; 2570 AA.
 DE Human CLEVER-1 protein SEQ ID NO:1.
 PN WO20003057130-A2.
 PD 17-JUL-2003.
 PA (JALK/) JALKANEN S.
 PA (IRJA/) IRJALA H.
 PA (SALM/) SALMI M.
 Query Match
 Best Local Similarity 7.8%; Score 129.5; DB 6; Length 2570;
 Best Local Similarity 20.9%; Pred. No. 0.039;
 RESULT 533
 ID AAB08023 standard; protein; 95 AA.
 DE The domain of hyaluronic acid which interacts with CD44.
 PN WO200047163-A2.
 PD 17-AUG-2000.
 PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
 Query Match
 Best Local Similarity 7.8%; Score 128.5; DB 3; Length 95;
 Best Local Similarity 28.7%; Pred. No. 0.00053;
 RESULT 534
 ID ABU04625 standard; protein; 95 AA.
 DE Human expressed protein tag (EPT) #1291.
 PN WO200278524-A2.
 PD 10-OCT-2002.
 PA (ZYCO-) ZYCOS INC.
 Query Match
 Best Local Similarity 7.8%; Score 128.5; DB 6; Length 95;
 Best Local Similarity 28.7%; Pred. No. 0.00053;
 RESULT 535
 ID AAR85442 standard; protein; 912 AA.
 DE Bovine brevican core protein.
 PN WO9526201-A1.
 PD 05-OCT-1995.
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 Query Match
 Best Local Similarity 7.8%; Score 128.5; DB 2; Length 912;
 Best Local Similarity 22.0%; Pred. No. 0.012;
 RESULT 536
 ID ABM83431 standard; protein; 825 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3680.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 8; Length 825;
 Best Local Similarity 24.7%; Pred. No. 0.013;
 RESULT 537

ID ABM83430 standard; protein; 863 AA.
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:3679.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 8; Length 863;
 Best Local Similarity 24.7%; Pred. No. 0.014;
 RESULT 538
 ID AAE30340 standard; protein; 911 AA.
 DE Human chondroitin sulphate proteoglycan BEHAB/brevican protein.
 PN WO200276510-A1.
 PD 03-OCT-2002.
 PA (AGYT-) AGY THERAPEUTICS INC.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 6; Length 911;
 Best Local Similarity 24.7%; Pred. No. 0.015;
 RESULT 539
 ID ADN38942 standard; protein; 911 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:260.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 7; Length 911;
 Best Local Similarity 24.7%; Pred. No. 0.015;
 RESULT 540
 ID ADK67784 standard; protein; 911 AA.
 DE Human glycosylation-variant BEHAB isoform.
 PN WO2004013356-A1.
 PD 12-FEB-2004.
 PA (UYVA) UNIV YALE.
 Query Match
 Best Local Similarity 7.7%; Score 127.5; DB 8; Length 911;
 Best Local Similarity 24.7%; Pred. No. 0.015;
 RESULT 541
 ID ABR58557 standard; protein; 277 AA.
 DE Human cancer related protein SEQ ID NO:214.
 PN WO2003025138-A2.
 PD 27-MAR-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 6; Length 277;
 Best Local Similarity 30.7%; Pred. No. 0.0032;
 RESULT 542
 ID ABUS6654 standard; protein; 277 AA.
 DE Lung cancer-associated polypeptide #247.
 PN WO200286443-A2.
 PD 31-OCT-2002.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 6; Length 277;
 Best Local Similarity 30.7%; Pred. No. 0.0032;
 RESULT 543
 ID ADN38976 standard; protein; 277 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:294.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 7; Length 277;
 Best Local Similarity 30.7%; Pred. No. 0.0032;
 RESULT 544
 ID ADO24439 standard; protein; 277 AA.
 DE Human PRO87335 protein SEQ ID NO:78.
 PN WO2004043397-A2.
 PD 27-MAY-2004.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 8; Length 277;
 Best Local Similarity 30.7%; Pred. No. 0.0032;
 RESULT 545
 ID ADRI4117 standard; protein; 277 AA.
 DE Human NF-kappaB pathway-associated protein SegID118.
 PN WO2004065577-A2.
 PD 05-AUG-2004.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match
 Best Local Similarity 7.7%; Score 127; DB 8; Length 277;
 Best Local Similarity 30.7%; Pred. No. 0.0032;
 RESULT 546
 ID ADB47827 standard; protein; 457 AA.

DE Novel human secreted protein #3.
PN US2003054443-A1.
PD 20-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (SOPP/) SOPPET D R.
PA (EBNE/) EBNER R.
PA (OLSE/) OLSEN H S.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (YUGG/) YU G.
PA (NIJU/) NI J.
PA (ROSE/) ROSEN C A.
PA (BREW/) BREWER L A.
PA (JANA/) JANAT F.
PA (BIRS/) BIRSE C E.
Query Match
Best Local Similarity 7.6%; Score 126.5; DB 7; Length 457;
RESULT 547
ID ADJ5382 standard; protein; 457 AA.
DE Novel human secreted protein #3.
PN US2004023283-A1.
PD 05-FEB-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 7.6%; Score 126.5; DB 8; Length 457;
RESULT 548
ID ADO24485 standard; protein; 277 AA.
DE Human PRO87343 protein SEQ ID NO:124.
PN WO2004043397-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.6%; Score 126; DB 8; Length 277;
RESULT 549
ID ADB65640 standard; protein; 482 AA.
DE Human protein encoded by clone THYMU20143230.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 7.5%; Score 124.5; DB 7; Length 482;
RESULT 550
ID ADM80804 standard; protein; 259 AA.
DE Human CADECM-33 protein SEQ ID NO:33.
PN WO2004015396-A2.
PD 19-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 259;
RESULT 551
ID AAY13381 standard; protein; 360 AA.
DE Amino acid sequence of protein PRO271.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 2; Length 360;
RESULT 552
ID ADC78533 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 3; Length 360;
RESULT 553
ID AAB80249 standard; protein; 360 AA.
DE Human PRO271 protein.
PN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 4; Length 360;
RESULT 554
ID AAU29037 standard; protein; 360 AA.
DE Human PRO polypeptide sequence #14.
PN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 4; Length 360;
RESULT 555
ID AAM38965 standard; protein; 360 AA.
DE Human polypeptide SEQ ID NO 2110.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 4; Length 360;
RESULT 556
ID ABUS8413 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027272-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 557
ID ABU71627 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 558
ID ABUS7961 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032127-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 559
ID ABUS4276 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032112-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 560
ID ABR66150 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027278-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 561
ID ABR65540 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036159-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 562
ID ABUS9480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040070-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 563
ID ABUS2719 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032113-A1.
PD 13-FEB-2003.

Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 564
ID ABU99840 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036147-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 565
ID ABU71482 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 566
ID ABR68089 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027284-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 567
ID ABU96142 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036144-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 568
ID ABU92573 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036149-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 569
ID ABO08650 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044923-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 570
ID ABO02702 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040062-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 571
ID ABR74856 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040056-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 572
ID ABR94618 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044926-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 573
ID ABU95591 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036140-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 574
ID ABU99751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003013153-A1.
PD 16-JAN-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 575
ID ABU97966 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017544-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 576
ID ABU91672 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003027277-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 577
ID ABU71928 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 578
ID ABU99365 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036141-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 579
ID ABU86206 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 580
ID ABU67419 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 581
ID ABU80447 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 582
ID ABO01811 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 583
ID ABR99365 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040063-A1.

PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 584
ID ABR98755 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 585
ID ABO16278 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 586
ID ABR92178 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 587
ID ABO18819 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 588
ID ABR78240 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 589
ID ABU84976 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 590
ID ABO00115 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 591
ID ABO11447 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 592
ID ABO02092 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 593
ID ABU54384 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.

Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 594
ID ABU8666 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 595
ID ABU83361 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 596
ID ABO06162 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 597
ID ABR59198 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 598
ID ABO09260 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 599
ID ABO19124 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 600
ID ABO1142 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 601
ID ABR66760 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 602
ID ABO15973 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 603
ID ABO13679 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 604
ID ABO47399 standard; protein; 360 AA.
DE Human secreted/transmembrane polypeptide PRO271.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 605
ID ABUS582 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, SEQ ID 28.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 606
ID ABO07430 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 607
ID ABO3617 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 608
ID ABR67065 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 609
ID ABO15668 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 610
ID ABUS5949 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 611
ID ABUS5277 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 612
ID ABUS9522 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 613
ID ABU71125 standard; protein; 360 AA.
DE Human PRO271 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 614

ID ABO07735 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 615
ID ABR69976 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 616
ID ABR69309 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 617
ID ABO01450 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 618
ID ABU81252 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 619
ID ABR60049 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 620
ID ABR67784 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 621
ID ABR65172 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 622
ID ABR68394 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 623
ID ABR71806 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 624

ID ABU85286 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 625
ID ABU88976 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 626
ID ABU83056 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 627
ID ABU94912 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 628
ID ABU90460 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 629
ID ABU83971 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 630
ID ABU93622 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 631
ID ABR64867 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 632
ID ABR68699 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 633
ID ABO06515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 634
ID ABR99060 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 635
ID ABU56944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 636
ID ABU64536 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 637
ID ABU85896 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 638
ID ABU67382 standard; protein; 360 AA.
DE Human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 639
ID ABU82183 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 640
ID ABU87194 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 641
ID ABU83666 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 642
ID ABO08040 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 643
ID ABO14902 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 644
ID ABU81751 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.

PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 645
ID ABU94605 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 656
ID ABO04532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 657
ID ABR70281 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 658
ID ABU98446 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 659
ID ABR65845 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 660
ID ABR64562 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027362-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 661
ID ABU79487 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 662
ID ABU92878 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 663
ID ABU95837 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 664
ID ABU91057 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 645
ID ABU65915 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 646
ID ABR59744 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 647
ID ABU93932 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 648
ID ABU99785 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 649
ID ABR66455 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 650
ID ABR90873 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 651
ID ABU94300 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 652
ID ABU79182 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 653
ID ABU86511 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 654
ID ABU86816 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032131-A1.
PD 13-FEB-2003.

RESULT 665
ID ABU90150 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 666
ID ABO09565 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 667
ID ABO10837 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 668
ID ABR70891 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 669
ID ABU87499 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 670
ID ABU91367 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 671
ID ABU84581 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 672
ID ABR69671 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 673
ID ABU80048 standard; protein; 360 AA.
DE Human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 674
ID ABU69659 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 675
ID ABU93317 standard; protein; 360 AA.

DE Human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 676
ID ABO09870 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 677
ID ABO08955 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 678
ID ABU10523 standard; protein; 360 AA.
DE Human secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 679
ID ABU95532 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 680
ID ABU96741 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 681
ID ABR70586 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 682
ID ABO04937 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 683
ID ABO08345 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 684
ID ABO14841 standard; protein; 360 AA.
DE Human secreted / transmembrane polypeptide PRO271.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 685

ID ABO5552 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 686
ID ABR73941 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 687
ID ABR95533 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 688
ID ABR80830 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 689
ID ABR81135 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 690
ID ABO00831 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 691
ID ABR88433 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 692
ID ABO287254 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 693
ID ABO28738 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 694
ID ABO31483 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068725-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 695
ID ABO07900 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 696
ID ABO40380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 697
ID ABO35805 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 698
ID ABO43944 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 699
ID ADA77780 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 700
ID ABO24739 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 701
ID ADB29418 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 702
ID ABO03007 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 703
ID ABR90263 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

RESULT 704
ID ABM17177 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 705
ID ABR94923 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 706
ID ABR95228 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 707
ID ABR97730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 708
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 709
ID ABR87518 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 710
ID ABM77559 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 711
ID ABM27789 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 712
ID ABM06070 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 713
ID ABM03576 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 714
ID ABM35027 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 715
ID ABM26264 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 716
ID ABO48046 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 717
ID ABR92788 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 718
ID ABO24549 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 719
ID ABM1560 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 720
ID ABM02661 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 721
ID ABM15957 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 722
ID ABO27518 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

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PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 723
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 732
ID ABM25654 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 733
ID ABM25959 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 734
ID ABO03312 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 735
ID ABO02397 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 736
ID ABR90568 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 737
ID ABR73636 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 738
ID ABO16888 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 739
ID ABR94313 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 740
ID ABR75820 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 741
ID ADA18274 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.

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Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 742
ID ABO32793 standard; protein; 360 AA.
DE Human secreted/transmembrane protein PRO271.
PN US2003045693-A1.
PD 08-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 743
ID ABR71196 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 744
ID ABR93093 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 745
ID ABR93398 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 746
ID ABR7823 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 747
ID ABO27823 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 748
ID ABO29958 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003084461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 749
ID ABO33167 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 750
ID ABO4855 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 751
ID ABO8815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 752
ID ABO36415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 753
ID ABO35500 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 754
ID ABO39465 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 755
ID ABM10340 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 756
ID ABM1865 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 757
ID ABO52011 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 758
ID ABO52316 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 759
ID ABO23634 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032134-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 760
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 760

ID ABR97120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 761
ID ABR96908 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 762
ID ABM10950 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 763
ID ABM28094 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 764
ID ABO32093 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 765
ID ABM15220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 766
ID ABM06375 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 767
ID ABM04186 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 768
ID ABM22299 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 769
ID ABM07595 standard; protein; 360 AA.

DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 770
ID ABO40685 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 771
ID ABM35332 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 772
ID ABM33095 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 773
ID ABO52621 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 774
ID ABO50181 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 775
ID ABU99175 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 776
ID ABO04227 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 777
ID ABO05857 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 778
ID ABO34853 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 779
ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 780
ID ADA16249 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 781
ID ABR97425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 782
ID ABR80525 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 783
ID ABO41136 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 784
ID ABR88738 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 785
ID ABM13390 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 786
ID ABM20774 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 787
ID ABO41905 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 788

ID ABO42515 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 789
ID ABM10035 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 790
ID ABO38550 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 791
ID ABM32790 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 792
ID ABM22604 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 793
ID ABM74815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 794
ID ADA79572 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 795
ID ABR96205 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 796
ID ABM02356 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 797
ID ABR86298 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049758-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.

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Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 798
ID ABR86603 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 799
ID ABM16567 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 800
ID ABM29619 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 801
ID ABO29043 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068693-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 802
ID ABM23824 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 803
ID ABM23214 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 804
ID ABM21994 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 805
ID ABO37635 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 806
ID ABM28399 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 807
ID ABM28704 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 808
ID ABM66348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 809
ID ABM75730 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 810
ID ABM34010 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 811
ID ABM34315 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 812
ID ABO20246 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 813
ID ABO21161 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 814
ID ABO22076 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054477-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 815
ID ABR96510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
Pred. No. 0.015;
RESULT 816
ID ABR85688 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049753-A1.
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PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 817
ID ABR99670 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 818
ID ABM00221 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 819
ID ABM00526 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 820
ID ABO29653 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 821
ID ABM23519 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 822
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 823
ID ABO38245 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 824
ID ABO45545 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 825
ID ABM20469 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 826
ID ADA42394 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 827
ID ADA81299 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 828
ID ABO16593 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 829
ID ABO18209 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 830
ID ABO22636 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003027285-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 831
ID ABO22941 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 832
ID ABR92483 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 833
ID ABR81440 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 834
ID ABO17531 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 835
ID ABM77864 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

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PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 845
ID ABO35195 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 846
ID ABM25044 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 847
ID ABO47436 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 848
ID ABO47741 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 849
ID ABO48351 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 850
ID ABO51401 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 851
ID ABO51706 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 852
ID ABO50486 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 853
ID ABR79610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 854
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 836
ID ABR89653 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 837
ID ABM26569 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 838
ID ABM13695 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 839
ID ABO28433 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 840
ID ABO30263 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 841
ID ABM07290 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 842
ID ABM03881 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 843
ID ABO37025 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 6; Length 360;
RESULT 844
ID ABO41600 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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ID ABM16872 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 855
ID ABO17904 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 856
ID ABO20856 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 857
ID ABR96815 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 858
ID ABM12170 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 859
ID ABM16262 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 860
ID ABM24129 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 861
ID ABM14610 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 862
ID ABM04491 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 863
ID ABM06680 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068730-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 864
ID ABM09120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 865
ID ABO39160 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 866
ID ABM75425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 867
ID ABM25349 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 868
ID ABM19859 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 869
ID ABO46765 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 870
ID ABO47070 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 871
ID ADA83097 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 872
ID ABR71501 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 873

ID ABR72111 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003032136-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 874
ID ABR98450 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036129-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 875
ID ABO06820 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040053-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 876
ID ABR84773 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040057-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 877
ID ABR7331 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 878
ID ABR76425 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044932-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 879
ID ABR73026 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027270-A1.
PD 06-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 880
ID ABM18092 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 881
ID ABO20551 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032126-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 882
ID ABO25294 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 883

ID ABO25599 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 884
ID ABR94008 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 885
ID ABR79915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049738-A1.
PD 13-MAR-2003.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 886
ID ABM11255 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 887
ID ABO32862 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 888
ID ABO30568 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 889
ID ABO30873 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064468-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 890
ID ABM27179 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 891
ID ABM29924 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 6; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 892
ID ABM05460 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.

PN US2003045700-A1.
 PD 06-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 893
 ID ABM15525 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068698-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 894
 ID ABM08510 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068759-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 895
 ID ABO42210 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049748-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 896
 ID ABO37940 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068765-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 897
 ID ABO45850 standard; protein; 360 AA.
 DE Human PRO polypeptide #14.
 PN US2003049754-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 898
 ID ABM66653 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068688-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 899
 ID ADB20140 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003082767-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 900
 ID ABM19554 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003104552-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 901
 ID ABO49266 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049774-A1.
 PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 902
 ID ABO49571 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049775-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 903
 ID ADA78392 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003073181-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 904
 ID ABR88128 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068720-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 905
 ID ABM26874 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068739-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 906
 ID ABM03271 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068763-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 907
 ID ABO39770 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068689-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 6; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 908
 ID ABO49876 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049776-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 909
 ID ABO50791 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049780-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 910
 ID ABO05247 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003061266-A1.
 PD 20-FEB-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;

Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 911
ID ABR74551 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044924-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 912
ID ABR77030 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044927-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 913
ID ADA16673 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 914
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 915
ID ABR95838 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 916
ID ADA13102 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 917
ID ABO21771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 918
ID ABO19941 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 919
ID ABO24244 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 920
ID ABR85993 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049759-A1.
PD 13-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 921
ID ABR10645 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 922
ID ABR76644 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 923
ID ABR9348 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 924
ID ABR12475 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 925
ID ABO05765 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 926
ID ABO34890 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 927
ID ABO02966 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 928
ID ABR18944 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 929
ID ABR19249 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;

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Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 930
ID ABO46460 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 931
ID ABO48961 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 932
ID ADA41970 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 933
ID ABR69004 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 934
ID ABR89043 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 935
ID ABR72416 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 936
ID ABR74246 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 937
ID ABO18514 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 938
ID ADA17317 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 939
ID ABR80220 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049739-A1.

PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 940
ID ABM01441 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 941
ID ABM02051 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 942
ID ABR87213 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 943
ID ABM12780 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 944
ID ABM30534 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 945
ID ABM24434 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 946
ID ABO29348 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 947
ID ABO31178 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 948
ID ABM14305 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068686-A1.
PD 10-APR-2003.
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PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 949
 ID ABM09730 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003073178-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 950
 ID ABO38855 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068774-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 951
 ID ABM34620 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003104538-A1.
 PD 05-JUN-2003.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 952
 ID ABO31096 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003049781-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 953
 ID ADA42820 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein, #42.
 PN US2003054351-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 954
 ID ABO03922 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003036158-A1.
 PD 20-FEB-2003.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 955
 ID ABO10392 standard; protein; 360 AA.
 DE Human PRO polypeptide #14.
 PN US2003036151-A1.
 PD 20-FEB-2003.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 956
 ID ABR77635 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003040067-A1.
 PD 27-FEB-2003.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 957
 ID ABR78845 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003054456-A1.
 PD 20-MAR-2003.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 958
 ID ABO23939 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.

PN US2003054482-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 959
 ID ABR93703 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003054457-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 960
 ID ABM01746 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003059883-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 961
 ID ABM78169 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003049764-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 962
 ID ABR89958 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003073177-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 963
 ID ABM27484 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003064442-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 964
 ID ABM13085 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003064450-A1.
 PD 03-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 965
 ID ABO31788 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein (PRO) #14.
 PN US2003068731-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 966
 ID ABM14000 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068683-A1.
 PD 10-APR-2003.
 Query Match 7.3%; Score 121.5; DB 7; Length 360;
 Best Local Similarity 34.9%; Pred. No. 0.015;
 RESULT 967
 ID ABM08205 standard; protein; 360 AA.
 DE Human secreted polypeptide PRO271, SEQ ID NO:28.
 PN US2003068754-A1.
 PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 968
ID ABO40075 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US200308681-A1.
PD 10-APR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 969
ID ABO74510 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096351-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 970
ID ABO33705 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096358-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 971
ID ABO20164 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104556-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 972
ID ABO48656 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049756-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 973
ID ABR72721 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 974
ID ABO15363 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003036121-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 975
ID ABR85078 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003040065-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 976
ID ABO15058 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 977
ID ABO17193 standard; protein; 360 AA.

DE Human secreted/transmembrane protein (PRO) #14.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 978
ID ABO17482 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 979
ID ABR85383 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003049746-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 980
ID ABO17592 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 981
ID ABO76949 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003054464-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 982
ID ABO28128 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003064459-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 983
ID ABO22909 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068757-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 984
ID ABO30229 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068723-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 985
ID ABO21689 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068741-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 986
ID ABO21384 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068744-A1.
PD 10-APR-2003.

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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 987
ID ABM14915 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 988
ID ABO40990 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 989
ID ABO36720 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 990
ID ABO37330 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 991
ID ABM75120 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 992
ID ABM33400 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 993
ID ABO46155 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 994
ID ADA82463 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 995
ID ABM31754 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068680-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 996
ID ABM31144 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 997
ID ADB77739 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 998
ID ADB74875 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 999
ID ADB85771 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1000
ID ABM32059 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1001
ID ABM32364 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1002
ID ABM31449 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1003
ID ABM30839 standard; protein; 360 AA.
DE Human secreted polypeptide PRO271, SEQ ID NO:28.
PN US2003068771-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1004
ID ADC28521 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
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RESULT 1005
ID ADC39721 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1006
ID ADC40235 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1007
ID ADC19059 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1008
ID ADC34359 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1009
ID ADC29414 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1010
ID ADC28945 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1011
ID ADC40830 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1012
ID ADC19487 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1013
ID ADC33935 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1014

ID ADC13005 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1015
ID ADC12457 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1016
ID ADD05501 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1017
ID ADD05012 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1018
ID ADD04018 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1019
ID ADD03594 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1020
ID ADE34846 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1021
ID ADG02496 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1022
ID ADG01203 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
RESULT 1023
ID ADF95378 standard; protein; 360 AA.

DE Novel human secreted and transmembrane protein PRO271.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1024
ID ADG12193 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1025
ID ADH08853 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1026
ID ADH59329 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1027
ID ADI38108 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1028
ID ADJ26376 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1029
ID ADL32634 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1030
ID ADM30168 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 7; Length 360;
Pred. No. 0.015;
RESULT 1031
ID ADE79291 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1032
ID ADE79715 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003130489-A1.

PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1033
ID ADE73391 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1034
ID ADE74165 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1035
ID ADE73926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1036
ID ADE74777 standard; protein; 360 AA.
DE Human secreted/transmembrane protein (PRO) #14.
PN US2003211574-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1037
ID ADE99480 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1038
ID ADE98599 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1039
ID ADE99026 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1040
ID ADG40496 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GUEN/) GURNEY A L.
PA (MATH/) MATHER J P M.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1041

ID ADF73890 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1042
ID ADF95990 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215909-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1043
ID ADF73466 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1044
ID ADG04261 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215912-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1045
ID ADG00421 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003215911-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1046
ID ADG82677 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2003215910-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1047
ID ADG92309 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1048
ID ADG92736 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1049
ID ADH25958 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2003068770-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1050
ID ADH32927 standard; protein; 360 AA.
DE Human PRO polypeptide #14.

PN US2003068768-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1051
ID ADH20525 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1052
ID ADH07380 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1053
ID ADH59925 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1054
ID ADH06953 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1055
ID ADI18695 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1056
ID ADI65415 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148419-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;
RESULT 1057
ID ADI37678 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 7.3%; Score 121.5; DB 8; Length 360;
Best Local Similarity 34.9%; Pred. No. 0.015;

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RESULT 1058
ID ADH97474 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190610-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1059
ID ADI5842 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003148371-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1060
ID ADH60585 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004023331-A1.
PA (DESN/) DESNOYERS L.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (MATH/) MATHER J P.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1061
ID ADJ99642 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003187238-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1062
ID ADL08835 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003186358-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1063
ID ADJ54666 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004023321-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1064
ID ADP25176 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003096233-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1065
ID ADM29926 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2003190611-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1066
ID ADJ64437 standard; protein; 360 AA.
DE Human PRO polypeptide #14.
PN US2004038337-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1067
ID ADM31333 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048334-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1068
ID ADM36380 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004053358-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1069
ID ADM40185 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004048335-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1070
ID ADL91793 standard; protein; 360 AA.
DE Human PRO271 protein SEQ ID NO:14.
PN WO2004024076-A2.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1071
ID ADO06248 standard; protein; 360 AA.
DE Human PRO polypeptide #38.
PN US6686451-B1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1072
ID ADN37793 standard; protein; 360 AA.
DE Novel human secreted and transmembrane protein PRO271.
PN US2004091959-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1073
ID ADRI1100 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004137561-A1.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 7.3%; Score 121.5; DB 8; Length 360;
Pred. No. 0.015;
RESULT 1074
ID ADRI8009 standard; protein; 360 AA.
DE Human secreted/transmembrane protein, #42.
PN US2004147017-A1.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
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PA (GAOW/) GAO W. 7.3%; Score 121.5; DB 8; Length 360;
 PA (GERB/) GERBER H. 34.9%; Pred. No. 0.015;
 PA (GERR/) GERRITSEN M E. 360 AA.
 PA (GODD/) GODDARD A. 360 AA.
 PA (GODO/) GODOWSKI P J. 360 AA.
 PA (GRIM/) GRIMALDI C J. 360 AA.
 PA (GURN/) GURNEY A L. 360 AA.
 PA (HILL/) HILLAN K J. 360 AA.
 PA (KLJA/) KLJAVIN I J. 360 AA.
 PA (MATH/) MATHJER J P. 360 AA.
 PA (PAOJ/) PAO J. 360 AA.
 PA (PAON/) PAONI N F. 360 AA.
 PA (ROYM/) ROY M A. 360 AA.
 PA (STEW/) STEWART T A. 360 AA.
 PA (TUMA/) TUMAS D. 360 AA.
 PA (WILL/) WILLIAMS P M. 360 AA.
 PA (WOOD/) WOOD W I. 360 AA.
 Query Match
 Best Local Similarity 34.9%; Score 121.5; DB 8; Length 360;
 RESULT 1075
 ID ADT03685 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein, #42.
 PN US2003152922-A1.
 PD 14-AUG-2003.
 PA (GETH) GENENTECH INC.
 Query Match
 Best Local Similarity 34.9%; Score 121.5; DB 8; Length 360;
 RESULT 1076
 ID ADS74648 standard; protein; 360 AA.
 DE Human secreted/transmembrane protein #42.
 PN US2004185531-A1.
 PD 23-SEP-2004.
 PA (ASHK/) ASHKENAZI A.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOVERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GRIM/) GRIMALDI C J.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (MATH/) MATHJER J P.
 PA (PAOJ/) PAO J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (STEW/) STEWART T A.
 PA (TUMA/) TUMAS D.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 Query Match
 Best Local Similarity 34.9%; Score 121.5; DB 8; Length 360;
 RESULT 1077
 ID AAW5982 standard; protein; 528 AA.
 DE Amino acid sequence of the cDNA clone BEF (HSXCK41).
 PN WO9831800-A2.
 PD 23-JUL-1998.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (AUCK-) AUCKLAND UNISERVICES LTD.
 Query Match
 Best Local Similarity 24.1%; Score 121; DB 2; Length 528;
 RESULT 1078
 ID AAB61241 standard; protein; 528 AA.
 DE Human BEF protein.
 PN WO200100638-A2.
 PD 04-JAN-2001.
 PA (MILL-) MILLENNIUM PHARM INC.

Query Match
 Best Local Similarity 7.3%; Score 121; DB 4; Length 528;
 RESULT 1079
 ID ABO32677 standard; protein; 528 AA.
 DE Secreted polypeptide-related protein #75.
 PN US2003022279-A1.
 PD 30-JAN-2003.
 PA (FRAS/) FRASER C C.
 PA (BARN/) BARNES T M.
 PA (SHAR/) SHARP J D.
 PA (KIRS/) KIRST S J.
 PA (MYER/) MYERS P S.
 PA (LEIB/) LEIBY K R.
 PA (HOLT/) HOLTZMAN D A.
 PA (MCCA/) MCCARTHY S A.
 PA (WRIG/) WRIGHTON N.
 PA (MACK/) MACKAY C R.
 PA (GOOD/) GOODEARL A D J.
 Query Match
 Best Local Similarity 7.3%; Score 121; DB 6; Length 528;
 RESULT 1080
 ID ADB90786 standard; protein; 528 AA.
 DE Human BEF protein.
 PN US2003082586-A1.
 PD 01-MAY-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 7.3%; Score 121; DB 7; Length 528;
 RESULT 1081
 ID ADF71521 standard; protein; 528 AA.
 DE Human BEF protein.
 PN US2003175733-A1.
 PD 18-SEP-2003.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 7.3%; Score 121; DB 7; Length 528;
 RESULT 1082
 ID ADQ10337 standard; protein; 528 AA.
 DE Human polypeptide #171.
 PN US2004121396-A1.
 PD 24-JUN-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match
 Best Local Similarity 7.3%; Score 121; DB 8; Length 528;
 RESULT 1083
 ID AAR46627 standard; protein; 1257 AA.
 DE Neurocan core protein.
 PN WO9403601-A2.
 PD 17-FEB-1994.
 PA (UYNY) UNIV NEW YORK STATE.
 Query Match
 Best Local Similarity 7.3%; Score 120.5; DB 2; Length 1257;
 RESULT 1084
 ID ADQ39513 standard; protein; 1642 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1176.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match
 Best Local Similarity 7.2%; Score 118.5; DB 8; Length 1642;
 RESULT 1085
 ID ADQ39515 standard; protein; 1642 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1178.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 Query Match
 Best Local Similarity 7.2%; Score 118.5; DB 8; Length 1642;
 RESULT 1086
 ID ADN04531 standard; protein; 2000 AA.
 DE Antipsoriatic protein sequence #458.
 PN WO2004028479-A2.
 PD 08-APR-2004.

PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.31;
RESULT 1087
ID ADP21378 standard; protein; 2000 AA.
DE PRO polypeptide SEQ ID NO:916.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 7.2%; Score 118.5; DB 8; Length 2000;
Best Local Similarity 25.5%; Pred. No. 0.31;
RESULT 1088
ID ADD48597 standard; protein; 3396 AA.
DE Human Protein P13611, SEQ ID NO 14303.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 7.2%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1089
ID ADN95526 standard; protein; 3396 AA.
DE Human BEC/LEC-related protein sequence SeqID449.
PN WO2003080640-A1.
PD 02-OCT-2003.
PA (LUDW-) LUDWIG INST CANCER RES.
PA (LICN) LICENTIA LTD.
Query Match 7.2%; Score 118.5; DB 7; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1090
ID ADJ75521 standard; protein; 3396 AA.
DE Marker gene related amino acid sequence SEQ ID NO:773.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1091
ID ADQ39509 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1172.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1092
ID ADQ39510 standard; protein; 3396 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1173.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1093
ID ADR99164 standard; protein; 3396 AA.
DE Chondroitin sulfate proteoglycan 2 (versican), CSPG2, SEQ ID 170.
PN WO2004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 7.2%; Score 118.5; DB 8; Length 3396;
Best Local Similarity 25.5%; Pred. No. 0.63;
RESULT 1094
ID ADP71273 standard; protein; 191 AA.
DE Human Lf2 protein B-B' domain SeqID8.
PN JF2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 7.1%; Score 117; DB 8; Length 191;
Best Local Similarity 26.5%; Pred. No. 0.017;
RESULT 1095
ID ADM87304 standard; protein; 340 AA.
DE Human protein SEQ ID NO:397.
PN WO2004009834-A2.

PD 29-JAN-2004.
PA (NUVE-) NUVELO INC.
Query Match 7.1%; Score 117; DB 8; Length 340;
Best Local Similarity 26.5%; Pred. No. 0.037;
RESULT 1096
ID ABU11635 standard; protein; 343 AA.
DE Human MDDT polypeptide SEQ ID 582.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.1%; Score 117; DB 6; Length 343;
Best Local Similarity 26.5%; Pred. No. 0.038;
RESULT 1097
ID ADJ76266 standard; protein; 2397 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1518.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match 7.0%; Score 116; DB 8; Length 2397;
Best Local Similarity 28.4%; Pred. No. 0.68;
RESULT 1098
ID AAR85443 standard; protein; 908 AA.
DE Rat brevican core protein.
PN WO9526201-A1.
PD 05-OCT-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match 6.9%; Score 115; DB 2; Length 908;
Best Local Similarity 22.2%; Pred. No. 0.22;
RESULT 1099
ID ADO31200 standard; protein; 1257 AA.
DE Rat neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.9%; Score 114.5; DB 8; Length 1257;
Best Local Similarity 23.1%; Pred. No. 0.39;
RESULT 1100
ID ADD48595 standard; protein; 656 AA.
DE Rat Protein AF072892, SEQ ID NO 14301.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.9%; Score 114; DB 7; Length 656;
Best Local Similarity 28.4%; Pred. No. 0.18;
RESULT 1101
ID ABB10268 standard; protein; 287 AA.
DE Human cDNA SEQ ID NO: 576.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.8%; Score 112.5; DB 4; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.079;
RESULT 1102
ID ABP66855 standard; protein; 287 AA.
DE Human polypeptide SEQ ID NO 576.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 6.8%; Score 112.5; DB 5; Length 287;
Best Local Similarity 25.7%; Pred. No. 0.079;
RESULT 1103
ID ABU36285 standard; protein; 402 AA.
DE Protein encoded by Prokaryotic essential gene #21812.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 111.5; DB 6; Length 402;
Best Local Similarity 22.5%; Pred. No. 0.16;
RESULT 1104
ID ADP71271 standard; protein; 200 AA.

DE Human aggrecan protein B-B' domain SeqID6.
PN JF2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 6.7%; Score 111; DB 8; Length 200;
Best Local Similarity 37.4%; Pred. No. 0.066;
RESULT 1105
ID AAM52242 standard; protein; 655 AA.
DE Human versican isoform V3 Seq ID NO 2.
PN WO200179284-A2.
PD 25-OCT-2001.
PA (WIGH/) WIGHT T N.
PA (WERR/) MERRILEES M.
Query Match
Best Local Similarity 6.7%; Score 111; DB 5; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.34;
RESULT 1106
ID ADQ39511 standard; protein; 655 AA.
DE Human myocardial infarction-associated gene derived protein, Seq ID 1174.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 6.7%; Score 111; DB 8; Length 655;
Best Local Similarity 29.4%; Pred. No. 0.34;
RESULT 1107
ID AAR12609 standard; protein; 2409 AA.
DE Versican.
PN WO9108230-A.
PD 13-JUN-1991.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Query Match
Best Local Similarity 6.7%; Score 111; DB 2; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1108
ID ABR47429 standard; protein; 2409 AA.
DE Breast cancer associated protein sequence Seq ID NO:90.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match
Best Local Similarity 6.7%; Score 111; DB 6; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1109
ID ADQ39514 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, Seq ID 1177.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 6.7%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1110
ID ADQ39512 standard; protein; 2409 AA.
DE Human myocardial infarction-associated gene derived protein, Seq ID 1175.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 6.7%; Score 111; DB 8; Length 2409;
Best Local Similarity 29.4%; Pred. No. 2;
RESULT 1111
ID AAB12304 standard; protein; 341 AA.
DE Human secreted protein encoded by gene 4 clone HPXHC41.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.6%; Score 110; DB 3; Length 341;
Best Local Similarity 28.5%; Pred. No. 0.17;
RESULT 1112
ID AAY93913 standard; protein; 353 AA.
DE A human hyaluronan-binding protein, designated BM-HABP.
PN WO200039166-A1.
PD 06-JUL-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (AMNA-) AMERICAN NAT RED CROSS.
Query Match
Best Local Similarity 6.6%; Score 109; DB 3; Length 353;
Best Local Similarity 24.3%; Pred. No. 0.22;

RESULT 1113
ID ABP97200 standard; protein; 1321 AA.
DE Tumour-associated antigenic target protein TAT185 Seq ID NO:82.
PN WO2003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 6.6%; Score 109; DB 6; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1114
ID ADJ69615 standard; protein; 1321 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1421.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 6.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1115
ID ADN38944 standard; protein; 1321 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, Seq ID NO:262.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 6.6%; Score 109; DB 7; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1116
ID ADO31196 standard; protein; 1321 AA.
DE Human neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match
Best Local Similarity 6.6%; Score 109; DB 8; Length 1321;
Best Local Similarity 21.4%; Pred. No. 1.4;
RESULT 1117
ID ABJ56909 standard; protein; 322 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.25;
RESULT 1118
ID ABJ56908 standard; protein; 322 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 322;
Best Local Similarity 28.6%; Pred. No. 0.25;
RESULT 1119
ID ABJ56918 standard; protein; 353 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match
Best Local Similarity 6.5%; Score 108; DB 6; Length 353;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1120
ID AAY57081 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor amino acid sequence.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 6.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1121
ID AAY57084 standard; protein; 354 AA.
DE Human proteoglycan link protein precursor #2.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 6.5%; Score 108; DB 3; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;

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RESULT 1122
ID ABJ56902 standard; protein; 354 AA.
DE 151P3D4 v-1 354aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1123
ID ABJ56906 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1124
ID ABJ56914 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1125
ID ABJ56898 standard; protein; 354 AA.
DE 151P3D4 v-8 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1126
ID ABJ56895 standard; protein; 354 AA.
DE 151P3D4 v-5 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1127
ID ABJ56897 standard; protein; 354 AA.
DE 151P3D4 v-7 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1128
ID ABJ56901 standard; protein; 354 AA.
DE 151P3D4 v-11 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1129
ID ABJ56894 standard; protein; 354 AA.
DE 151P3D4 v-4 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1130
ID ABJ56905 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1131
ID AAR77034 standard; protein; 355 AA.
DE 151P3D4 v-9 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1132
ID ABJ56912 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1133
ID ABJ56893 standard; protein; 354 AA.
DE 151P3D4 v-3 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1134
ID ABJ56891 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1135
ID ABJ56896 standard; protein; 354 AA.
DE 151P3D4 v-6 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1136
ID ABJ56900 standard; protein; 354 AA.
DE 151P3D4 v-10 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1137
ID ABJ56889 standard; protein; 354 AA.
DE Transcript variant 121PIF1 v-1.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1138
ID ABJ56904 standard; protein; 354 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1139
ID ADP07795 standard; protein; 354 AA.
DE Human secreted protein, seq id 278.
PN WO2004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.5%; Score 108; DB 8; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.28;
RESULT 1140
ID AAR77034 standard; protein; 355 AA.
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DE Rat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYUA) UNIV YALE.
Query Match 6.5%; Score 108; DB 2; Length 355;
Best Local Similarity 28.9%; Pred. No. 0.28;
RESULT 1141
ID ADH71348 standard; protein; 552 AA.
DE Human protein of the invention NOV9s SEQ ID NO:244.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 108; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.51;
RESULT 1142
ID ABJ56890 standard; protein; 721 AA.
DE Transcript variant 151P3D4 v-2.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.74;
RESULT 1143
ID ABJ56892 standard; protein; 721 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.8%; Pred. No. 0.74;
RESULT 1144
ID ABJ56903 standard; protein; 721 AA.
DE 151P3D4 v-1 721aa protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 108; DB 6; Length 721;
Best Local Similarity 28.6%; Pred. No. 0.74;
RESULT 1145
ID ABG72500 standard; protein; 93 AA.
DE Human 190kDa Hyaluronan receptor for endocytosis (HARE) LINK domain.
PN WO200286093-A2.
PD 31-OCT-2002.
PA (WEIG/) WEIGEL P H.
PA (WEIG/) WEIGEL J A.
Query Match 6.5%; Score 107; DB 6; Length 93;
Best Local Similarity 29.2%; Pred. No. 0.055;
RESULT 1146
ID AAB83358 standard; protein; 315 AA.
DE NOV2 protein sequence.
PN WO200136638-A2.
PD 25-MAY-2001.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 4; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.3;
RESULT 1147
ID ADH71316 standard; protein; 315 AA.
DE Human protein of the invention NOV9c SEQ ID NO:212.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 315;
Best Local Similarity 29.2%; Pred. No. 0.3;
RESULT 1148
ID AAY57083 standard; protein; 339 AA.
DE Rat proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 107; DB 3; Length 339;
Best Local Similarity 28.8%; Pred. No. 0.33;
RESULT 1149
ID ABJ56915 standard; protein; 354 AA.

DE Rat cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 107; DB 6; Length 354;
Best Local Similarity 28.6%; Pred. No. 0.35;
RESULT 1150
ID AAY57082 standard; protein; 355 AA.
DE Chicken proteoglycan link protein precursor.
PN WO9956763-A1.
PD 11-NOV-1999.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.5%; Score 107; DB 3; Length 355;
Best Local Similarity 34.9%; Pred. No. 0.35;
RESULT 1151
ID ABJ56907 standard; protein; 355 AA.
DE Mouse cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.5%; Score 107; DB 6; Length 355;
Best Local Similarity 28.6%; Pred. No. 0.35;
RESULT 1152
ID ADH71336 standard; protein; 533 AA.
DE Human protein of the invention NOV9m SEQ ID NO:232.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.61;
RESULT 1153
ID ADH71334 standard; protein; 533 AA.
DE Human protein of the invention NOV9l SEQ ID NO:230.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 533;
Best Local Similarity 29.2%; Pred. No. 0.61;
RESULT 1154
ID ADH71340 standard; protein; 552 AA.
DE Human protein of the invention NOV9o SEQ ID NO:236.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1155
ID ADH71346 standard; protein; 552 AA.
DE Human protein of the invention NOV9r SEQ ID NO:242.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1156
ID ADH71354 standard; protein; 552 AA.
DE Human protein of the invention NOV9v SEQ ID NO:250.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1157
ID ADH71344 standard; protein; 552 AA.
DE Human protein of the invention NOV9q SEQ ID NO:240.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1158
ID ADH71342 standard; protein; 552 AA.
DE Human protein of the invention NOV9p SEQ ID NO:238.

PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1159
ID ADH71350 standard; protein; 552 AA.
DE Human protein of the invention NOV9t SEQ ID NO:246.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1160
ID ADH71314 standard; protein; 556 AA.
DE Human protein of the invention NOV9b SEQ ID NO:210.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 556;
Best Local Similarity 29.2%; Pred. No. 0.64;
RESULT 1161
ID ABM83433 standard; protein; 774 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3682.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.5%; Score 107; DB 8; Length 774;
Best Local Similarity 21.5%; Pred. No. 1;
RESULT 1162
ID ABM83432 standard; protein; 822 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:3681.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.5%; Score 107; DB 8; Length 822;
Best Local Similarity 21.5%; Pred. No. 1.1;
RESULT 1163
ID ADO31202 standard; protein; 1288 AA.
DE Mouse neurocan protein for glucosaminoglycan reduction in glial scars.
PN WO2004041197-A2.
PD 21-MAY-2004.
PA (UYCA-) UNIV CASE WESTERN RESERVE.
Query Match 6.5%; Score 107; DB 8; Length 1268;
Best Local Similarity 26.2%; Pred. No. 2;
RESULT 1164
ID ABB69806 standard; protein; 1795 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36210.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE-) PE CORP NY.
Query Match 6.5%; Score 107; DB 4; Length 1795;
Best Local Similarity 24.1%; Pred. No. 3.2;
RESULT 1165
ID ADH71332 standard; protein; 2417 AA.
DE Human protein of the invention NOV9k SEQ ID NO:228.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 8; Length 2417;
Best Local Similarity 29.2%; Pred. No. 4.8;
RESULT 1166
ID ABJ10587 standard; protein; 2420 AA.
DE Human novel protein NOV1b SEQ ID NO: 4.
PN WO200259315-A2.
PD 01-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 6.5%; Score 107; DB 5; Length 2420;
Best Local Similarity 29.2%; Pred. No. 4.9;
RESULT 1167
ID ADO09838 standard; protein; 2420 AA.
DE Human NOV1b.
PN US2004018970-A1.

PD 29-JAN-2004.
PA (SHIM/) SHIMKETS R A.
PA (PATT/) PATTURAJAN M.
PA (VERN/) VERNET C A M.
PA (CASM/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (GANG/) GANGOLLI E A.
PA (MILL/) MILLER C E.
PA (BOLD/) BOLDOG F L.
PA (LILL/) LI L.
PA (TAUP/) TAUPIER R J.
PA (KEKU/) KEKUDA R.
PA (SMIT/) SMITHSON G.
PA (ZERR/) ZERHUSEN B D.
PA (LIUX/) LIU X.
PA (COLM/) COLMAN S D.
PA (TCH/) TCHERNEV V T.
PA (SIJ/) SI J.
PA (EDIN/) EDINGER S R.
PA (STON/) STONE D J.
PA (SCIO/) SCIORE P.
PA (MILL/) MILLET I.
PA (ROTH/) ROTHENBERG M E.
Query Match 6.5%; Score 107; DB 8; Length 2420;
Best Local Similarity 29.2%; Pred. No. 4.9;
RESULT 1168
ID ADH71338 standard; protein; 552 AA.
DE Human protein of the invention NOV9n SEQ ID NO:234.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.4%; Score 106; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 0.79;
RESULT 1169
ID AAY57080 standard; protein; 354 AA.
DE Human link protein precursor amino acid sequence.
PN WO9556763-A1.
PD 11-NOV-1999.
PA (REGC-) UNIV CALIFORNIA.
Query Match 6.3%; Score 105; DB 3; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.54;
RESULT 1170
ID ABJ56913 standard; protein; 354 AA.
DE Bovine cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.3%; Score 105; DB 6; Length 354;
Best Local Similarity 33.7%; Pred. No. 0.54;
RESULT 1171
ID AAB42164 standard; protein; 330 AA.
DE Human ORFX ORF1928 polypeptide sequence SEQ ID NO:3856.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 104.5; DB 3; Length 330;
Best Local Similarity 18.7%; Pred. No. 0.54;
RESULT 1172
ID ABU07339 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2040.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.
Query Match 6.3%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.18;
RESULT 1173
ID ABU07336 standard; protein; 139 AA.
DE Human expressed protein tag (EPT) #2037.
PN WO200278524-A2.
PD 10-OCT-2002.
PA (ZYCO-) ZYCOS INC.

Query Match 6.3%; Score 104; DB 6; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.18;
RESULT 1174
ID ADQ39387 standard; protein; 139 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1050.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.3%; Score 104; DB 8; Length 139;
Best Local Similarity 20.7%; Pred. No. 0.18;
RESULT 1175
ID ADP71269 standard; protein; 195 AA.
DE Human LPI protein B-B' domain SeqID4.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 6.3%; Score 104; DB 8; Length 195;
Best Local Similarity 33.7%; Pred. No. 0.29;
RESULT 1176
ID ADP71267 standard; protein; 200 AA.
DE Human versican protein B-B' domain SeqID2.
PN JP2004154038-A.
PD 03-JUN-2004.
PA (SEKG) SEIKAGAKU KOGYO CO LTD.
Query Match 6.3%; Score 104; DB 8; Length 200;
Best Local Similarity 32.5%; Pred. No. 0.3;
RESULT 1177
ID ADH71352 standard; protein; 552 AA.
DE Human protein of the invention NOV9u SEQ ID NO:248.
PN WO200171042-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 6.3%; Score 104; DB 8; Length 552;
Best Local Similarity 29.2%; Pred. No. 1.2;
RESULT 1178
ID ABB60536 standard; protein; 1712 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8400.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 104; DB 4; Length 1712;
Best Local Similarity 22.7%; Pred. No. 5.8;
RESULT 1179
ID ABB65987 standard; protein; 183 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24753.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 102.5; DB 4; Length 183;
Best Local Similarity 29.7%; Pred. No. 0.37;
RESULT 1180
ID ADN23553 standard; protein; 380 AA.
DE Bacterial polypeptide #6206.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 101.5; DB 8; Length 380;
Best Local Similarity 25.5%; Pred. No. 1.3;
RESULT 1181
ID AAB23034 standard; protein; 590 AA.
DE Human SLIT protein-like splice variant, SECX 3352358-2.
PN WO200053742-A2.
PD 14-SEP-2000.
PA (CURA-) CURAGEN CORP.
Query Match 6.1%; Score 101.5; DB 3; Length 590;
Best Local Similarity 20.6%; Pred. No. 2.3;
RESULT 1182
ID ADA23289 standard; protein; 590 AA.
DE Human SECX polypeptide, SEC6.

PN US2003054514-A1.
PD 20-MAR-2003.
PA (SHIM/) SHIMKETS R A.
PA (IARO/) LAROCHELLE W J.
Query Match 6.1%; Score 101.5; DB 6; Length 590;
Best Local Similarity 20.8%; Pred. No. 2.3;
RESULT 1183
ID AAU76528 standard; protein; 402 AA.
DE Human LP polypeptide #1.
PN WO200216578-A2.
PD 28-FEB-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 6.1%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1184
ID AAU09883 standard; protein; 402 AA.
DE Novel human secreted protein #23.
PN WO200179454-A1.
PD 25-OCT-2001.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match 6.1%; Score 100.5; DB 5; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1185
ID ADF59259 standard; protein; 402 AA.
DE Human polypeptide sequence SEQ ID NO:1667.
PN WO2003080795-A2.
PD 02-OCT-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 100.5; DB 7; Length 402;
Best Local Similarity 30.9%; Pred. No. 1.7;
RESULT 1186
ID ADF74155 standard; protein; 412 AA.
DE Human novel brain/hippocampus protein #43.
PN JP2003009886-A.
PD 14-JAN-2003.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
PA (PROT-) PROTEIN EXPRESS KK.
Query Match 6.1%; Score 100.5; DB 7; Length 412;
Best Local Similarity 30.9%; Pred. No. 1.8;
RESULT 1187
ID ABB68940 standard; protein; 1379 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 33612.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.1%; Score 100.5; DB 4; Length 1379;
Best Local Similarity 20.2%; Pred. No. 9.2;
RESULT 1188
ID AAR77035 standard; protein; 378 AA.
DE Cat brain-enriched hyaluronan binding protein.
PN WO9527785-A1.
PD 19-OCT-1995.
PA (UYVA) UNIV VALE.
Query Match 6.0%; Score 100; DB 2; Length 378;
Best Local Similarity 24.1%; Pred. No. 1.7;
RESULT 1189
ID ABP57346 standard; protein; 402 AA.
DE Human secreted protein SECP-17 SEQ ID NO:17.
PN WO2003004615-A2.
PD 16-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
PA (LUVY/) LU Y.
Query Match 6.0%; Score 99.5; DB 6; Length 402;
Best Local Similarity 30.9%; Pred. No. 2.1;
RESULT 1190
ID ABJ56917 standard; protein; 201 AA.
DE Human cartilage link protein.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.91;

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RESULT 1191
ID ABJ56916 standard; protein; 201 AA.
DE 151P3D4 v-1 protein clone-1 from placenta.
PN WO200283860-A2.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 201;
Best Local Similarity 28.0%; Pred. No. 0.91;
RESULT 1192
ID ADO29463 standard; protein; 410 AA.
DE Mouse GPCR GPRC5B, SEQ ID NO:565.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.0%; Score 99; DB 8; Length 410;
Best Local Similarity 22.0%; Pred. No. 2.4;
RESULT 1193
ID ABJ56919 standard; protein; 600 AA.
DE 151P3D4 v-2 protein clone-1 from placenta.
PN WO200283860-A2.
PD 24-OCT-2002.
PA (AGEN-) AGENSYS INC.
Query Match 6.0%; Score 99; DB 6; Length 600;
Best Local Similarity 28.0%; Pred. No. 4.1;
RESULT 1194
ID ABB70377 standard; protein; 1428 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 37923.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 6.0%; Score 99; DB 4; Length 1428;
Best Local Similarity 28.4%; Pred. No. 13;
RESULT 1195
ID ABB69720 standard; protein; 1126 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35952.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.9%; Score 98.5; DB 4; Length 1126;
Best Local Similarity 25.0%; Pred. No. 11;
RESULT 1196
ID AAY95559 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV-1 deletion allele lov-1(sy582del).
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 3; Length 2870;
Best Local Similarity 23.1%; Pred. No. 39;
RESULT 1197
ID ADN07634 standard; protein; 2870 AA.
DE Caenorhabditis elegans LOV -1 deletion mutant protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 8; Length 2870;
Best Local Similarity 23.1%; Pred. No. 39;
RESULT 1198
ID AAY95556 standard; protein; 3178 AA.
DE Caenorhabditis elegans LOV-1 (location of vulva) protein.
PN WO200040711-A2.
PD 13-JUL-2000.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 3; Length 3178;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1199
ID ADN07623 standard; protein; 3178 AA.
DE Caenorhabditis elegans location of vulva (LOV) -1 protein.
PN US6723557-B1.
PD 20-APR-2004.
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.
Query Match 5.9%; Score 98.5; DB 8; Length 3178;
Best Local Similarity 23.1%; Pred. No. 45;
RESULT 1200
ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.

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ID ABB60403 standard; protein; 2112 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8001.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.9%; Score 98; DB 4; Length 2112;
Best Local Similarity 25.9%; Pred. No. 29;
RESULT 1201
ID AAB75555 standard; protein; 298 AA.
DE Gene 1 human secreted protein homologous amino acid sequence #109.
PN WO200077026-A1.
PD 21-DEC-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
Query Match 5.9%; Score 97.5; DB 4; Length 298;
Best Local Similarity 19.8%; Pred. No. 2.2;
RESULT 1202
ID ADE58456 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4331.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1203
ID ADE58468 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4343.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1204
ID ADE58460 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4335.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1205
ID ADE58464 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4339.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1206
ID ADE58472 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4347.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1207
ID ADE58476 standard; protein; 1031 AA.
DE Rat Protein AAK52670, SEQ ID NO 4351.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.8%; Score 96.5; DB 7; Length 1031;
Best Local Similarity 21.3%; Pred. No. 15;
RESULT 1208
ID ADO41972 standard; protein; 231 AA.
DE Human cell adhesion and extracellular matrix protein 1 SeqID1.

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PN WO2004048529-A2.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 95.5; DB 8; Length 231;
Best Local Similarity 30.2%; Pred. No. 2.4;
RESULT 1209
ID ADO67145 standard; protein; 803 AA.
DE Novel human protein sequence #2118.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.7%; Score 94; DB 8; Length 803;
Best Local Similarity 21.9%; Pred. No. 18;
RESULT 1210
ID AAU18060 standard; protein; 258 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 205.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1211
ID ABB10532 standard; protein; 258 AA.
DE Human cDNA SEQ ID NO: 840.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1212
ID ABP67119 standard; protein; 258 AA.
DE Human polypeptide SEQ ID NO 840.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.6%; Score 93.5; DB 5; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1213
ID ADB31684 standard; protein; 258 AA.
DE Human novel protein SEQ ID NO 205.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 7; Length 258;
Best Local Similarity 24.6%; Pred. No. 4.2;
RESULT 1214
ID AAU17999 standard; protein; 261 AA.
DE Human immunoglobulin polypeptide SEQ ID NO 144.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1215
ID ABB10361 standard; protein; 261 AA.
DE Human cDNA SEQ ID NO: 669.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 4; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1216
ID ABP66948 standard; protein; 261 AA.
DE Human polypeptide SEQ ID NO 669.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.6%; Score 93.5; DB 5; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1217
ID ADB31623 standard; protein; 261 AA.
DE Human novel protein SEQ ID NO 144.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.6%; Score 93.5; DB 7; Length 261;
Best Local Similarity 24.6%; Pred. No. 4.3;
RESULT 1218
ID ABG01510 standard; protein; 320 AA.
DE Novel human diagnostic protein #1501.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 93.5; DB 4; Length 320;
Best Local Similarity 23.2%; Pred. No. 5.7;
RESULT 1219
ID ADE36618 standard; protein; 339 AA.
DE Plasmid PCR2.1-CG57008-03-S843 15B protein insert SEQ ID NO:28.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 6.2;
RESULT 1220
ID ADE36592 standard; protein; 339 AA.
DE Human NOV1a protein SEQ ID NO:2.
PN WO2003080856-A2.
PD 02-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.6%; Score 93.5; DB 7; Length 339;
Best Local Similarity 23.1%; Pred. No. 6.2;
RESULT 1221
ID ABR58582 standard; protein; 359 AA.
DE Human cancer related protein SEQ ID NO:239.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1222
ID ABP70439 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1223
ID ABP70441 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 4.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1224
ID ABP70438 standard; protein; 359 AA.
DE Amino acid sequence of human TIM-1 allele 1.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1225
ID ABR48174 standard; protein; 359 AA.
DE Human bladder cancer associated protein sequence SEQ ID NO:64.
PN WO2003003906-A2.
PD 16-JAN-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 5.6%; Score 93.5; DB 6; Length 359;
Best Local Similarity 23.1%; Pred. No. 6.7;
RESULT 1226
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ID AAO26680 standard; protein; 359 AA.
 DE KIM-1 related protein, SEQ ID NO 8.
 PN WO200298920-A1.
 PD 12-DEC-2002.
 PA (BIOJ) BIOGEN INC.
 PA (GEO) GEN HOSPITAL CORP.
 Query Match 5.6%; Score 93.5; DB 6; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1227
 ID ADE36594 standard; protein; 359 AA.
 DE Human NOV1B protein SEQ ID NO:4.
 PN WO2003080856-A2.
 PD 02-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.6%; Score 93.5; DB 7; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1228
 ID ADN38984 standard; protein; 359 AA.
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:302.
 PN WO2003042661-A2.
 PD 22-MAY-2003.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 Query Match 5.6%; Score 93.5; DB 7; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1229
 ID ADQ76690 standard; protein; 359 AA.
 DE Human kidney injury molecule-1 (KIM-1).
 PN WO2004060041-A2.
 PD 22-JUL-2004.
 PA (BIOG-) BIOGEN IDEC MA INC.
 Query Match 5.6%; Score 93.5; DB 8; Length 359;
 Best Local Similarity 23.1%; Pred. No. 6.7;
 RESULT 1230
 ID ABG07923 standard; protein; 366 AA.
 DE Novel human diagnostic protein #7914.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.6%; Score 93.5; DB 4; Length 366;
 Best Local Similarity 23.2%; Pred. No. 6.9;
 RESULT 1231
 ID ADP04445 standard; protein; 1381 AA.
 DE Sea squirt protein with tissue specific expression in development Seq40.
 PN JP2004057129-A.
 PD 26-FEB-2004.
 PA (KAGA-) KAGAKU GIUTSU SHINKO JIGYODAN.
 Query Match 5.6%; Score 93.5; DB 8; Length 1381;
 Best Local Similarity 22.9%; Pred. No. 42;
 RESULT 1232
 ID ABR63235 standard; protein; 2055 AA.
 DE Glucanase sequence from strain KG15.
 PN WO2003008618-A2.
 PD 30-JAN-2003.
 PA (NEDE-) NEDERLANDSE ORG TOEGEPAST.
 Query Match 5.6%; Score 93.5; DB 6; Length 2055;
 Best Local Similarity 23.3%; Pred. No. 73;
 RESULT 1233
 ID AAR88466 standard; protein; 629 AA.
 DE Drosophila scavenger receptor class CI.
 PN WO9600288-A2.
 PD 04-JAN-1996.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 5.6%; Score 93; DB 2; Length 629;
 Best Local Similarity 19.9%; Pred. No. 16;
 RESULT 1234
 ID ABG33057 standard; protein; 629 AA.
 DE Fruit fly scavenger receptor type CI (dsr-CI).
 PN US6429289-B1.
 PD 06-AUG-2002.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 5.6%; Score 93; DB 5; Length 629;
 Best Local Similarity 19.9%; Pred. No. 16;
 RESULT 1235

ID AAE21524 standard; protein; 629 AA.
 DE Drosophila melanogaster scavenger receptor class CI (dsr-CI).
 PN US6350859-B1.
 PD 26-FEB-2002.
 PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
 Query Match 5.6%; Score 93; DB 5; Length 629;
 Best Local Similarity 19.9%; Pred. No. 16;
 RESULT 1236
 ID ABP73157 standard; protein; 40 AA.
 DE Deletion mutant of a CD44-hyaluronic acid binding domain.
 PN WO2003018044-A1.
 PD 06-MAR-2003.
 PA (STRO/) STROEMBLAD S.
 PA (KOGE/) KOGERMAN P.
 PA (PAEL/) PAELL T.
 Query Match 5.6%; Score 92.5; DB 6; Length 40;
 Best Local Similarity 54.1%; Pred. No. 0.41;
 RESULT 1237
 ID AAW61380 standard; protein; 300 AA.
 DE Mouse junctional adhesion molecule protein.
 PN WO9824897-A1.
 PD 11-JUN-1998.
 PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
 Query Match 5.6%; Score 92.5; DB 2; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1238
 ID AAY23325 standard; protein; 300 AA.
 DE A33 related antigen JAM.
 PN WO9927098-A2.
 PD 03-JUN-1999.
 PA (GETH) GENENTECH INC.
 Query Match 5.6%; Score 92.5; DB 2; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1239
 ID ADH62537 standard; protein; 300 AA.
 DE Murine JAM protein used in the exemplification of the invention.
 PN US2003171568-A1.
 PD 11-SEP-2003.
 PA (ASHK/) ASHKENAZI A.
 PA (FONG/) FONG S.
 PA (GODD/) GODDARD A.
 PA (GURN/) GURNEY A L.
 PA (NAPI/) NAPIER M A.
 PA (TUMA/) TUMAS D.
 PA (WOOD/) WOOD W I.
 Query Match 5.6%; Score 92.5; DB 7; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1240
 ID ADK40853 standard; protein; 300 AA.
 DE Mouse junction adhesion molecule (JAM).
 PN US6699688-B1.
 PD 02-MAR-2004.
 PA (UYNY) UNIV NEW YORK STATE RES FOUND.
 Query Match 5.6%; Score 92.5; DB 8; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1241
 ID ADN35293 standard; protein; 300 AA.
 DE Human JAM protein.
 PN WO2004031105-A2.
 PD 15-APR-2004.
 PA (GETH) GENENTECH INC.
 Query Match 5.6%; Score 92.5; DB 8; Length 300;
 Best Local Similarity 23.4%; Pred. No. 6.5;
 RESULT 1242
 ID ABP70440 standard; protein; 365 AA.
 DE Amino acid sequence of human TIM-1 allele 3.
 PN WO2003002722-A2.
 PD 09-JAN-2003.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 Query Match 5.6%; Score 92.5; DB 6; Length 365;
 Best Local Similarity 22.6%; Pred. No. 8.5;
 RESULT 1243
 ID ABB50001 standard; protein; 569 AA.

DE Listeria monocytogenes protein #2705.
PN WO200177335-A2.
PA (INSP) INST PASTEUR.
Query Match 5.6%; Score 92.5; DB 5; Length 569;
Best Local Similarity 21.4%; Pred. No. 16;
RESULT 1244
ID ABU32518 standard; protein; 569 AA.
DE Protein encoded by Prokaryotic essential gene #18045.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.6%; Score 92.5; DB 6; Length 569;
Best Local Similarity 21.4%; Pred. No. 16;
RESULT 1245
ID AAU48553 standard; protein; 706 AA.
DE Propionibacterium acnes immunogenic protein #9449.
PN WO200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.6%; Score 92.5; DB 4; Length 706;
Best Local Similarity 25.4%; Pred. No. 21;
RESULT 1246
ID ABM45072 standard; protein; 706 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #9748.
PN WO2003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.6%; Score 92.5; DB 6; Length 706;
Best Local Similarity 25.4%; Pred. No. 21;
RESULT 1247
ID ADN18863 standard; protein; 994 AA.
DE Bacterial polypeptide #1516.
PN US2003233675-A1.
PD 18-DEC-2003
PA (CAOV/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.6%; Score 92.5; DB 8; Length 994;
Best Local Similarity 19.7%; Pred. No. 34;
RESULT 1248
ID ABR53566 standard; protein; 1636 AA.
DE Protein sequence #SEQ ID 1997.
PN EP1258494-A1.
PD 20-NOV-2002.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 92.5; DB 6; Length 1636;
Best Local Similarity 19.7%; Pred. No. 67;
RESULT 1249
ID ADK64364 standard; protein; 1636 AA.
DE Disease treating protein complex-derived protein #1193.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Query Match 5.6%; Score 92.5; DB 7; Length 1636;
Best Local Similarity 19.7%; Pred. No. 67;
RESULT 1250
ID ABP70442 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 5.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.6%; Score 92; DB 6; Length 364;
Best Local Similarity 21.8%; Pred. No. 9.4;
RESULT 1251
ID ABG93047 standard; protein; 966 AA.
DE S. cerevisiae BAX-associated protein fragment SEQ ID 52.
PN WO200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.6%; Score 92; DB 5; Length 966;
Best Local Similarity 21.8%; Pred. No. 9.4;
RESULT 1252
ID ADL72180 standard; protein; 2829 AA.
DE X. laevis mutated adenomatous polyposis coli (APC) protein.
PN WO2004018677-A1.
PD 04-MAR-2004.
PA (EISA) EISAI CO LTD.
Query Match 5.6%; Score 92; DB 8; Length 2829;
Best Local Similarity 20.7%; Pred. No. 1.6e+02;
RESULT 1253
ID AAU18036 standard; protein; 166 AA.
DE Human immunoglobulin polypeptide SEQ ID No 181.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1254
ID ABB10469 standard; protein; 166 AA.
DE Human cDNA SEQ ID NO: 777.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 4; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1255
ID ABP67056 standard; protein; 166 AA.
DE Human polypeptide SEQ ID NO 777.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.5%; Score 91.5; DB 5; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1256
ID ADB31660 standard; protein; 166 AA.
DE Human novel protein SEQ ID NO 181.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.5%; Score 91.5; DB 7; Length 166;
Best Local Similarity 31.9%; Pred. No. 3.6;
RESULT 1257
ID ADR46581 standard; protein; 300 AA.
DE Mouse junctional adhesion molecule-1, SEQ ID 12.
PN JP2004242513-A.
PD 02-SEP-2004.
PA (DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
Query Match 5.5%; Score 91.5; DB 8; Length 300;
Best Local Similarity 23.4%; Pred. No. 8.1;
RESULT 1258
ID AAM52302 standard; protein; 350 AA.
DE ActA protein fragment #2.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 350;
Best Local Similarity 22.0%; Pred. No. 10;
RESULT 1259
ID AAM52301 standard; protein; 376 AA.
DE ActA protein fragment #1.
PN WO200171356-A2.
PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURI-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 376;
Best Local Similarity 22.0%; Pred. No. 11;
RESULT 1260
ID AAM52300 standard; protein; 610 AA.
DE ActA protein.
PN WO200171356-A2.

PD 27-SEP-2001.
PA (CNRS) CENT NAT RECH SCI.
PA (CURT-) INST CURIE.
Query Match 5.5%; Score 91.5; DB 4; Length 610;
Best Local Similarity 22.0%; Pred. No. 21;
RESULT 1261
ID AAG79171 standard; protein; 639 AA.
DE Amino acid sequence of an ActA fragment.
PN WO200174858-A2.
PD 11-OCT-2001.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match 5.5%; Score 91.5; DB 4; Length 639;
Best Local Similarity 22.0%; Pred. No. 23;
RESULT 1262
ID AAU09142 standard; protein; 639 AA.
DE Lysteria monocytogenes ActA.
PN WO200174853-A2.
PD 11-OCT-2001.
PA (MASI) MASSACHUSETTS INST TECHNOLOGY.
PA (GBFB) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
Query Match 5.5%; Score 91.5; DB 4; Length 639;
Best Local Similarity 22.0%; Pred. No. 23;
RESULT 1263
ID ABB47677 standard; protein; 639 AA.
DE Listeria monocytogenes protein #381.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.5%; Score 91.5; DB 5; Length 639;
Best Local Similarity 22.0%; Pred. No. 23;
RESULT 1264
ID ADM48341 standard; protein; 681 AA.
DE Marburg virus glycoprotein, GP.
PN US2003215794-A1.
PD 20-NOV-2003.
PA (KAWA/) KAWAOKA Y.
PA (JASE/) JASENOSKY L D.
PA (NEUM/) NEUMANN G.
Query Match 5.5%; Score 91.5; DB 8; Length 681;
Best Local Similarity 19.2%; Pred. No. 25;
RESULT 1265
ID ADN20575 standard; protein; 1103 AA.
DE Bacterial polypeptide #3228.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.5%; Score 91.5; DB 8; Length 1103;
Best Local Similarity 24.3%; Pred. No. 48;
RESULT 1266
ID ABP60839 standard; protein; 246 AA.
DE Caenorhabditis elegans thioredoxin-like protein SEQ ID NO:188.
PN WO200250289-A1.
PD 27-JUN-2002.
PA (SEMB-) SEMBIOSYS GENETICS INC.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.5%; Score 91; DB 5; Length 246;
Best Local Similarity 27.0%; Pred. No. 6.9;
RESULT 1267
ID ADG73740 standard; protein; 505 AA.
DE Aspergillus niger Brea-109.
PN US2003215950-A1.
PD 20-NOV-2003.
PA (LASU/) LASURE L L.
PA (DAIZ/) DAI Z.
Query Match 5.5%; Score 90.5; DB 8; Length 505;
Best Local Similarity 27.0%; Pred. No. 21;
RESULT 1268
ID ABB60186 standard; protein; 1714 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 7350.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 90.5; DB 4; Length 1714;
Best Local Similarity 26.7%; Pred. No. 1.1e+02;
RESULT 1269
ID ABB69419 standard; protein; 1976 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35049.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.5%; Score 90.5; DB 4; Length 1976;
Best Local Similarity 38.5%; Pred. No. 1.3e+02;
RESULT 1270
ID ABP70443 standard; protein; 364 AA.
DE Amino acid sequence of human TIM-1 allele 6.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STED) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 90; DB 6; Length 364;
Best Local Similarity 21.6%; Pred. No. 15;
RESULT 1271
ID ABB59507 standard; protein; 629 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5313.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 90; DB 4; Length 629;
Best Local Similarity 20.7%; Pred. No. 31;
RESULT 1272
ID ADD47260 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12954.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 55;
RESULT 1273
ID ADE58049 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3917.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 55;
RESULT 1274
ID ADD47264 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 12958.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 55;
RESULT 1275
ID ADE58045 standard; protein; 957 AA.
DE Human Protein AAC02272, SEQ ID NO 3913.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.4%; Score 90; DB 7; Length 957;
Best Local Similarity 18.3%; Pred. No. 55;
RESULT 1276
ID ADO29696 standard; protein; 1217 AA.
DE Human colorectal cancer-associated protein #51.
PN EP1439393-A2.
PD 21-JUL-2004.
PA (FARB) BAYER HEALTHCARE LLC.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

Query Match 5.4%; Score 90; DB 8; Length 1217;
Best Local Similarity 18.3%; Pred. No. 76;
RESULT 1277
ID ABG66756 standard; protein; 1296 AA.
DE Human novel polypeptide #91.
PN WO20024340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 83;
RESULT 1278
ID ABG66702 standard; protein; 1296 AA.
DE Human novel polypeptide #37.
PN WO20024340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.4%; Score 90; DB 5; Length 1296;
Best Local Similarity 18.3%; Pred. No. 83;
RESULT 1279
ID ABP70432 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 BALB/c allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1280
ID ABP70433 standard; protein; 305 AA.
DE Amino acid sequence of murine TIM-2 ES-HBA and DBA/2J allele.
PN WO2003002722-A2.
PD 09-JAN-2003.
PA (STRD) UNIV LELAND STANFORD JUNIOR.
Query Match 5.4%; Score 89.5; DB 6; Length 305;
Best Local Similarity 24.3%; Pred. No. 13;
RESULT 1281
ID AAR69555 standard; protein; 410 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-2.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.4%; Score 89.5; DB 2; Length 410;
Best Local Similarity 21.0%; Pred. No. 19;
RESULT 1282
ID AAR85213 standard; protein; 480 AA.
DE Blowfly larvae PM95 antigen.
PN AU9517609-A.
PD 02-NOV-1995.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match 5.4%; Score 89.5; DB 2; Length 480;
Best Local Similarity 22.1%; Pred. No. 24;
RESULT 1283
ID ABO48994 standard; protein; 917 AA.
DE Murine cancer-associated protein (CAP) MP07-101.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 5.4%; Score 89.5; DB 8; Length 917;
Best Local Similarity 21.4%; Pred. No. 58;
RESULT 1284
ID ABB65879 standard; protein; 307 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24429.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 307;
Best Local Similarity 31.6%; Pred. No. 14;
RESULT 1285
ID ABP69313 standard; protein; 343 AA.
DE Human polypeptide SEQ ID NO 1360.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.

Query Match 5.4%; Score 89; DB 5; Length 343;
Best Local Similarity 27.7%; Pred. No. 17;
RESULT 1286
ID AAR69554 standard; protein; 416 AA.
DE Human lysosomal membrane sialoglycoprotein lamp-1.
PN WO9429342-A1.
PD 22-DEC-1994.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
PA (UNMI) UNIV MICHIGAN.
Query Match 5.4%; Score 89; DB 2; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1287
ID AAY52550 standard; protein; 416 AA.
DE Human lysosomal membrane glycoprotein-1 (LAMP-1).
PN WO9958658-A2.
PD 18-NOV-1999.
PA (EPIM-) EPIMUNE INC.
Query Match 5.4%; Score 89; DB 3; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1288
ID ADP65283 standard; protein; 416 AA.
DE Human lysosomal-associated membrane protein 1.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 5.4%; Score 89; DB 7; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1289
ID ADN03755 standard; protein; 416 AA.
DE Antipsoriatic protein sequence #74.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1290
ID ADP49321 standard; protein; 416 AA.
DE Human lysosomal associated membrane protein LAMP #1.
PN WO2004048537-A2.
PD 10-JUN-2004.
PA (EXSL-) EXELIXIS INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1291
ID ADP3231 standard; protein; 416 AA.
DE PRO polypeptide SEQ ID NO:325.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.4%; Score 89; DB 8; Length 416;
Best Local Similarity 23.6%; Pred. No. 22;
RESULT 1292
ID ADR86408 standard; protein; 832 AA.
DE Aspergillus fumigatus essential gene protein #458.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 5.4%; Score 89; DB 8; Length 832;
Best Local Similarity 19.8%; Pred. No. 56;
RESULT 1293
ID ABB70039 standard; protein; 846 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 16909.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 846;
Best Local Similarity 22.5%; Pred. No. 58;
RESULT 1294
ID ABB67102 standard; protein; 882 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 28098.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Query Match 5.4%; Score 89; DB 4; Length 882;
Best Local Similarity 22.5%; Pred. No. 61;
RESULT 1295
ID ADQ37103 standard; protein; 951 AA.
DE Cell proliferation-related polypeptide #118.
PN WO2004061122-A2.
PD 22-JUL-2004.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 5.4%; Score 89; DB 8; Length 951;
Best Local Similarity 22.1%; Pred. No. 68;
RESULT 1296
ID ADI19804 standard; protein; 1076 AA.
DE Protein encoded by novel human channel/transporter gene #122.
PN WO200154472-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.4%; Score 89; DB 4; Length 1076;
Best Local Similarity 21.1%; Pred. No. 80;
RESULT 1297
ID AAG39194 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48458.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 88.5; DB 3; Length 193;
Best Local Similarity 21.4%; Pred. No. 8.5;
RESULT 1298
ID AAG39193 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48457.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.3%; Score 88.5; DB 3; Length 199;
Best Local Similarity 21.4%; Pred. No. 8.8;
RESULT 1299
ID AAG15314 standard; protein; 358 AA.
DE Novel human diagnostic protein #15305.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 88.5; DB 4; Length 358;
Best Local Similarity 20.2%; Pred. No. 20;
RESULT 1300
ID AAR11605 standard; protein; 392 AA.
DE Human 75kD TNF-binding protein.
PN EP417563-A.
PD 20-MAR-1991.
PA (HOFF) HOFFMANN-LA ROCHE AG.
Query Match 5.3%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 22;
RESULT 1301
ID AAY10935 standard; protein; 392 AA.
DE Human tumour necrosis factor binding protein fragment.
PN EP939121-A2.
PD 01-SEP-1999.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.3%; Score 88.5; DB 2; Length 392;
Best Local Similarity 21.8%; Pred. No. 22;
RESULT 1302
ID AAB86818 standard; protein; 392 AA.
DE Human TNF β -associated protein #2.
PN EP132471-A2.
PD 12-SEP-2001.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 5.3%; Score 88.5; DB 4; Length 392;
Best Local Similarity 21.8%; Pred. No. 22;
RESULT 1303
ID ABO68455 standard; protein; 451 AA.
DE Pseudomonas aeruginosa polypeptide #630.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.3%; Score 88.5; DB 7; Length 451;
Best Local Similarity 20.7%; Pred. No. 27;
RESULT 1304
ID ABB63417 standard; protein; 481 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 17043.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 88.5; DB 4; Length 481;
Best Local Similarity 21.2%; Pred. No. 30;
RESULT 1305
ID AAG64210 standard; protein; 596 AA.
DE Murine HSP47 interacting protein, M4.
PN JP2001145493-A.
PD 29-MAY-2001.
PA (KACA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.3%; Score 88.5; DB 4; Length 596;
Best Local Similarity 21.3%; Pred. No. 40;
RESULT 1306
ID AAY37234 standard; protein; 708 AA.
DE Chlamydia trachomatis cellular envelope protein.
PN WO9928475-A2.
PD 10-JUN-1999.
PA (GEST) GENSET.
Query Match 5.3%; Score 88.5; DB 2; Length 708;
Best Local Similarity 23.6%; Pred. No. 50;
RESULT 1307
ID AAR63068 standard; protein; 905 AA.
DE Human EAA3b excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAMB/) KAMBOJ R.
Query Match 5.3%; Score 88; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 79;
RESULT 1308
ID ADB86597 standard; protein; 995 AA.
DE Frog tail resorption protein.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Query Match 5.3%; Score 88; DB 8; Length 995;
Best Local Similarity 19.9%; Pred. No. 90;
RESULT 1309
ID ADN23131 standard; protein; 3507 AA.
DE Bacterial polypeptide #5784.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 88; DB 8; Length 3507;
Best Local Similarity 20.1%; Pred. No. 5.1e+02;
RESULT 1310
ID ABP43908 standard; protein; 4315 AA.
DE MUC5B partial gene protein.
PN WO200231111-A2.
PD 18-APR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.3%; Score 88; DB 5; Length 4315;
Best Local Similarity 23.8%; Pred. No. 6.7e+02;
RESULT 1311
ID ADL23265 standard; protein; 5703 AA.
DE Human WOC5B.
PN WO2004019041-A1.
PD 04-MAR-2004.
PA (PROT-) PROTEOME SYSTEMS INTELLECTUAL PROPERTY P.

PA (PACK/) PACKER N H.
 PA (KARL/) KARLSSON N.
 PA (SCHU/) SCHULZ B L.
 Query Match 5.3%; Score 88; DB 8; Length 5703;
 Best Local Similarity 23.8%; Pred. No. 9.9e+02;
 RESULT 1312
 ID AAG13468 standard; protein; 310 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 12974.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 5.3%; Score 87.5; DB 3; Length 310;
 Best Local Similarity 23.2%; Pred. No. 20;
 RESULT 1313
 ID AAG13467 standard; protein; 331 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 12973.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 5.3%; Score 87.5; DB 3; Length 331;
 Best Local Similarity 23.2%; Pred. No. 22;
 RESULT 1314
 ID AAY52525 standard; protein; 536 AA.
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-536.
 PN WO9954349-A2.
 PD 28-OCT-1999.
 PA (HESK-) HESKA CORP.
 Query Match 5.3%; Score 87.5; DB 3; Length 536;
 Best Local Similarity 23.9%; Pred. No. 43;
 RESULT 1315
 ID AAU96329 standard; protein; 536 AA.
 DE Der HMW-map polypeptide #16.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match 5.3%; Score 87.5; DB 5; Length 536;
 Best Local Similarity 23.9%; Pred. No. 43;
 RESULT 1316
 ID AAY52523 standard; protein; 555 AA.
 DE House dust mite (D. farinae) mite allergen protein (map) PDerf98-555.
 PN WO9954349-A2.
 PD 28-OCT-1999.
 PA (HESK-) HESKA CORP.
 Query Match 5.3%; Score 87.5; DB 3; Length 555;
 Best Local Similarity 23.9%; Pred. No. 45;
 RESULT 1317
 ID AAU96327 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #14.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match 5.3%; Score 87.5; DB 5; Length 555;
 Best Local Similarity 23.9%; Pred. No. 45;
 RESULT 1318
 ID AAU96328 standard; protein; 555 AA.
 DE Der HMW-map polypeptide #15.
 PN WO200222807-A2.
 PD 21-MAR-2002.
 PA (HESK-) HESKA CORP.
 Query Match 5.3%; Score 87.5; DB 5; Length 555;
 Best Local Similarity 23.9%; Pred. No. 45;
 RESULT 1319
 ID ADB64946 standard; protein; 717 AA.
 DE Human protein encoded by clone PROST20036350.
 PN EP1308459-A2.
 PD 07-MAY-2003.
 PA (HELI-) HELIX RES INST.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 5.3%; Score 87.5; DB 7; Length 717;
 Best Local Similarity 17.8%; Pred. No. 64;
 RESULT 1320
 ID ADH71768 standard; protein; 904 AA.
 DE Human protein of the invention NOV28n SEQ ID NO:664.
 PN WO2003102155-A2.
 PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.
 Query Match 5.3%; Score 87.5; DB 8; Length 904;
 Best Local Similarity 23.8%; Pred. No. 88;
 RESULT 1321
 ID AAW16313 standard; protein; 906 AA.
 DE Yeast alpha factor-G-alpha protein fusion.
 PN WO9711159-A1.
 PD 27-MAR-1997.
 PA (HEAR-) HEARTLAND BIOTECHNOLOGIES LLC.
 Query Match 5.3%; Score 87.5; DB 2; Length 906;
 Best Local Similarity 19.7%; Pred. No. 88;
 RESULT 1322
 ID AAW54844 standard; protein; 1085 AA.
 DE Bovine parathyroid calcium receptor 1 protein 5kb fragment.
 PN US5763569-A.
 PD 09-JUN-1998.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match 5.3%; Score 87.5; DB 2; Length 1085;
 Best Local Similarity 22.7%; Pred. No. 1.1e+02;
 RESULT 1323
 ID AAY41778 standard; protein; 1085 AA.
 DE Bovine parathyroid calcium receptor 1 protein sequence.
 PN US5962314-A.
 PD 05-OCT-1999.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match 5.3%; Score 87.5; DB 2; Length 1085;
 Best Local Similarity 22.7%; Pred. No. 1.1e+02;
 RESULT 1324
 ID AAW89563 standard; protein; 1085 AA.
 DE Bovine parathyroid calcium receptor BopCar 1.
 PN US5858684-A.
 PD 12-JAN-1999.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match 5.3%; Score 87.5; DB 2; Length 1085;
 Best Local Similarity 22.7%; Pred. No. 1.1e+02;
 RESULT 1325
 ID AAY51825 standard; protein; 1085 AA.
 DE Bovine calcium receptor BopCar1 protein.
 PN US6031003-A.
 PD 29-FEB-2000.
 PA (NPSP-) NPS PHARM INC.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL.
 Query Match 5.3%; Score 87.5; DB 3; Length 1085;
 Best Local Similarity 22.7%; Pred. No. 1.1e+02;
 RESULT 1326
 ID AAB47820 standard; protein; 1085 AA.
 DE BopCar1.
 PN US6313146-B1.
 PD 06-NOV-2001.
 PA (NPSP-) NPS PHARM INC.
 Query Match 5.3%; Score 87.5; DB 5; Length 1085;
 Best Local Similarity 22.7%; Pred. No. 1.1e+02;
 RESULT 1327
 ID ADJ93194 standard; protein; 1085 AA.
 DE Bovine extracellular Ca-sensing receptor.
 PN WO200296946-A1.
 PD 05-DEC-2002.
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 Query Match 5.3%; Score 87.5; DB 7; Length 1085;
 Best Local Similarity 22.7%; Pred. No. 1.1e+02;
 RESULT 1328
 ID ADI40961 standard; protein; 1085 AA.
 DE Bovine GPCR CASR.
 PN US2004018976-A1.
 PD 29-JAN-2004.
 PA (FEDE/) FEDER J N.
 PA (MINT/) MINTIER G.
 PA (RAMA/) RAMANATHAN C S.
 Query Match 5.3%; Score 87.5; DB 8; Length 1085;
 Best Local Similarity 22.7%; Pred. No. 1.1e+02;

RESULT 1329
ID ADI41015 standard; protein; 1085 AA.
DE Bovine GPCR CASR #2.
PN US2004018976-A1.
PA (MILH/) MILHAUSEN M J. 5.3%; Score 87; DB 8; Length 1085;
PD 29-JAN-2004.
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
Query Match 5.3%; Score 87.5; DB 8; Length 1085;
Best Local Similarity 22.7%; Pred. No. 1.1e+02;
RESULT 1330
ID ADS24007 standard; protein; 1322 AA.
DE Bacterial polypeptide #13040.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 87.5; DB 8; Length 1322;
Best Local Similarity 22.9%; Pred. No. 1.5e+02;
RESULT 1331
ID ADD44997 standard; protein; 235 AA.
DE Rat Protein CAA82313, SEQ ID NO 10428.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.3%; Score 87; DB 7; Length 235;
Best Local Similarity 27.8%; Pred. No. 15;
RESULT 1332
ID AAY29082 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1333
ID AAY29081 standard; protein; 288 AA.
DE T. gondii immunogenic protein.
PN WO9932633-A1.
PD 01-JUL-1999.
PA (HESK-) HESKA CORP.
Query Match 5.3%; Score 87; DB 2; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1334
ID AAU25553 standard; protein; 288 AA.
DE T. gondii immunogenic protein Ptg1397.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J. 5.3%; Score 87; DB 4; Length 288;
Query Match 5.3%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1335
ID RAU25552 standard; protein; 288 AA.
DE T. gondii immunogenic protein Ptg288.
PN US2001014447-A1.
PD 16-AUG-2001.
PA (MILH/) MILHAUSEN M J. 5.3%; Score 87; DB 4; Length 288;
Query Match 5.3%; Score 87; DB 4; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1336
ID ADG17391 standard; protein; 288 AA.
DE T. gondii protein #79.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J. 5.3%; Score 87; DB 7; Length 288;
Query Match 5.3%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1337
ID ADG17394 standard; protein; 288 AA.

DE T. gondii protein #82.
PN US2003194393-A1.
PD 16-OCT-2003.
PA (MILH/) MILHAUSEN M J. 5.3%; Score 87; DB 7; Length 288;
Query Match 5.3%; Score 87; DB 7; Length 288;
Best Local Similarity 29.7%; Pred. No. 20;
RESULT 1338
ID ADJ76313 standard; protein; 363 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1565.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC. 5.3%; Score 87; DB 8; Length 363;
Query Match 5.3%; Score 87; DB 8; Length 363;
Best Local Similarity 25.3%; Pred. No. 28;
RESULT 1339
ID AAR01940 standard; protein; 417 AA.
DE Tumour necrosis factor.
PN JP01285191-A.
PD 16-NOV-1989.
PA (GREC) GREEN CROSS CORP.
Query Match 5.3%; Score 87; DB 2; Length 417;
Best Local Similarity 23.6%; Pred. No. 34;
RESULT 1340
ID AAG83274 standard; protein; 631 AA.
DE Chlamydia trachomatis PmpH(N-term) fusion protein.
PN WO200140474-A2.
PD 07-JUN-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 4; Length 631;
Best Local Similarity 28.1%; Pred. No. 60;
RESULT 1341
ID ABB94245 standard; protein; 631 AA.
DE Chlamydia trachomatis protein sequence SEQ ID NO:325.
PN WO200208267-A2.
PD 31-JAN-2002.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 5; Length 631;
Best Local Similarity 28.1%; Pred. No. 60;
RESULT 1342
ID ADA2755 standard; protein; 664 AA.
DE Chlamydia pmpH passenger domain protein SEQ ID NO:168.
PN WO2003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 7; Length 664;
Best Local Similarity 28.1%; Pred. No. 64;
RESULT 1343
ID AAR63070 standard; protein; 849 AA.
DE Human EAA3d excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAME/) KAMBOJ R. 5.3%; Score 87; DB 2; Length 849;
Query Match 5.3%; Score 87; DB 2; Length 849;
Best Local Similarity 22.4%; Pred. No. 90;
RESULT 1344
ID AAR60563 standard; protein; 862 AA.
DE Yeast 2.6 kb agglutination gene FLO1S.
PN WO9419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.3%; Score 87; DB 2; Length 862;
Best Local Similarity 19.1%; Pred. No. 92;
RESULT 1345
ID AAR58754 standard; protein; 894 AA.
DE S. cerevisiae FLO1.
PN WO9418330-A1.
PD 18-AUG-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.3%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 96;
RESULT 1346

ID AAR47578 standard; protein; 894 AA.
DE Flocculation protein of *Saccharomyces cerevisiae*.
PN W09401567-A1.
PD 20-JAN-1994.
PA (UNIL) UNILEVER PLC.
PA (UNIL) UNILEVER NV.
Query Match 5.3%; Score 87; DB 2; Length 894;
Best Local Similarity 19.1%; Pred. No. 96;
RESULT 1347
ID AAR60112 standard; protein; 905 AA.
DE Human EAA3a excitatory amino acid receptor.
PN CA2110933-A.
PD 12-JUN-1994.
PA (KAMB/) KAMBOJ R.
Query Match 5.3%; Score 87; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 98;
RESULT 1348
ID AAR75883 standard; protein; 905 AA.
DE Human EAA3 receptor (Q-591).
PN W09517508-A2.
PD 29-JUN-1995.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.3%; Score 87; DB 2; Length 905;
Best Local Similarity 22.4%; Pred. No. 98;
RESULT 1349
ID AAB19496 standard; protein; 905 AA.
DE The Q591 form of the human EAA3 receptor.
PN US6136544-A.
PD 24-OCT-2000.
PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
Query Match 5.3%; Score 87; DB 4; Length 905;
Best Local Similarity 22.4%; Pred. No. 98;
RESULT 1350
ID AAU38901 standard; protein; 1016 AA.
DE C. trachomatis CT872 protein.
PN W0200181379-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 4; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1351
ID ABG91037 standard; protein; 1016 AA.
DE Chlamydia trachomatis outer membrane protein H protein.
PN W0200262380-A2.
PD 15-AUG-2002.
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
Query Match 5.3%; Score 87; DB 5; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1352
ID .ADD42682 standard; protein; 1016 AA.
DE Chlamydia trachomatis antigen protein SEQ ID NO:95.
PN W02003041560-A2.
PD 22-MAY-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.3%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1353
ID ADD43800 standard; protein; 1016 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID NO 95.
PN W02003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 5.3%; Score 87; DB 7; Length 1016;
Best Local Similarity 28.1%; Pred. No. 1.1e+02;
RESULT 1354
ID AAR60562 standard; protein; 1537 AA.
DE Yeast 4.7 kb agglutination gene FLO1L.
PN W09419475-A2.
PD 01-SEP-1994.
PA (SAPB) SAPORO BREWERIES.
PA (PANI-) PANIMOLABORATORIO BRYGGERILABORATORIUM.
Query Match 5.3%; Score 87; DB 2; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2e+02;

RESULT 1355
ID ADP87475 standard; protein; 1537 AA.
DE *S. cerevisiae* glucan synthase pathway protein YAR050W (FLO1) SeqID17.
PN W02004057033-A1.
PD 08-JUL-2004.
PA (ROSE-) ROSETTA INPHARMATICS LLC.
Query Match 5.3%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2e+02;
RESULT 1356
ID ADN18745 standard; protein; 1537 AA.
DE Bacterial polypeptide #1398.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.3%; Score 87; DB 8; Length 1537;
Best Local Similarity 19.1%; Pred. No. 2e+02;
RESULT 1357
ID ABB67362 standard; protein; 1575 AA.
DE *Drosophila melanogaster* polypeptide SEQ ID NO 28878.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.3%; Score 87; DB 4; Length 1575;
Best Local Similarity 20.5%; Pred. No. 2.1e+02;
RESULT 1358
ID AAU39177 standard; protein; 238 AA.
DE *Propionibacterium acnes* immunogenic protein #73.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 86.5; DB 4; Length 238;
Best Local Similarity 22.7%; Pred. No. 1.7;
RESULT 1359
ID ABM35696 standard; protein; 238 AA.
DE *Propionibacterium acnes* predicted ORF-encoded polypeptide #372.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 5.2%; Score 86.5; DB 6; Length 238;
Best Local Similarity 22.7%; Pred. No. 1.7;
RESULT 1360
ID AAP1941 standard; peptide; 400 AA.
DE Sequence of preprospasmolysin.
PN DE3808456-A.
PD 28-SEP-1989.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
Query Match 5.2%; Score 86.5; DB 1; Length 400;
Best Local Similarity 30.8%; Pred. No. 36;
RESULT 1361
ID ADN19290 standard; protein; 503 AA.
DE Bacterial polypeptide #1943.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.2%; Score 86.5; DB 8; Length 503;
Best Local Similarity 22.1%; Pred. No. 49;
RESULT 1362
ID ABU25742 standard; protein; 687 AA.
DE Protein encoded by *Prokaryotic essential gene #11369*.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 86.5; DB 6; Length 687;
Best Local Similarity 23.2%; Pred. No. 75;
RESULT 1363

ID ABG15647 standard; protein; 714 AA.
 DE Novel human diagnostic protein #15638.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.2%; Score 86.5; DB 4; Length 714;
 Best Local Similarity 18.2%; Pred. No. 79;
 RESULT 1364
 ID ABG15147 standard; protein; 714 AA.
 DE Novel human diagnostic protein #15138.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.2%; Score 86.5; DB 4; Length 714;
 Best Local Similarity 18.2%; Pred. No. 79;
 RESULT 1365
 ID AAY54466 standard; protein; 788 AA.
 DE Amino acid sequence of intestinal insect mucin isoform IIM14.
 PN WO9967373-A2.
 PD 29-DEC-1999.
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 Query Match 5.2%; Score 86.5; DB 3; Length 788;
 Best Local Similarity 27.2%; Pred. No. 90;
 RESULT 1366
 ID AAY54467 standard; protein; 807 AA.
 DE Amini acid sequence of intestinal insect mucin isoform IIM22.
 PN WO9967373-A2.
 PD 29-DEC-1999.
 PA (BOYC-) BOYCE THOMPSON INST PLANT RES.
 Query Match 5.2%; Score 86.5; DB 3; Length 807;
 Best Local Similarity 27.2%; Pred. No. 93;
 RESULT 1367
 ID ADA14416 standard; protein; 1579 AA.
 DE Mouse spermatogenesis related protein sequence SEQ ID NO:158.
 PN WO2003068969-A1.
 PD 21-AUG-2003.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 5.2%; Score 86.5; DB 6; Length 1579;
 Best Local Similarity 21.1%; Pred. No. 2.3e+02;
 RESULT 1368
 ID AAY57453 standard; protein; 2781 AA.
 DE Human transcriptional regulatory factor SEQ ID NO:10.
 PN WO9957143-A1.
 PD 11-NOV-1999.
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 Query Match 5.2%; Score 86.5; DB 3; Length 2781;
 Best Local Similarity 20.8%; Pred. No. 5.1e+02;
 RESULT 1369
 ID ADF42724 standard; protein; 2781 AA.
 DE Human BPTF amino acid sequence SEQ ID NO:30.
 PN WO2003102163-A2.
 PD 11-DEC-2003.
 PA (META-) METABOLEX INC.
 Query Match 5.2%; Score 86.5; DB 8; Length 2781;
 Best Local Similarity 20.8%; Pred. No. 5.1e+02;
 RESULT 1370
 ID ADO0984 standard; protein; 2781 AA.
 DE Human homologue of Fruit fly AD-related protein CG17135.
 PN US2004067535-A1.
 PD 08-APR-2004.
 PA (LIFE-) LIFE SCI DEV CORP.
 Query Match 5.2%; Score 86.5; DB 8; Length 2781;
 Best Local Similarity 20.8%; Pred. No. 5.1e+02;
 RESULT 1371
 ID ADQ18653 standard; protein; 2781 AA.
 DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1472.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 5.2%; Score 86.5; DB 8; Length 2781;
 Best Local Similarity 20.8%; Pred. No. 5.1e+02;
 RESULT 1372
 ID AAY57452 standard; protein; 2907 AA.
 DE Novel human diagnostic protein #5666.
 DE Human transcriptional regulatory factor SEQ ID NO:1.
 PN WO9957143-A1.
 PD 11-NOV-1999.
 PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
 Query Match 5.2%; Score 86.5; DB 3; Length 2907;
 Best Local Similarity 20.8%; Pred. No. 5.4e+02;
 RESULT 1373
 ID ABM82857 standard; protein; 476 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:3106.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 5.2%; Score 86; DB 8; Length 476;
 Best Local Similarity 32.1%; Pred. No. 50;
 RESULT 1374
 ID ABM83144 standard; protein; 476 AA.
 DE Human diagnostic and therapeutic pproteins SEQ ID NO:3393.
 PN WO2004023973-A2.
 PD 25-MAR-2004.
 PA (INCY-) INCYTE CORP.
 Query Match 5.2%; Score 86; DB 8; Length 476;
 Best Local Similarity 32.1%; Pred. No. 50;
 RESULT 1375
 ID AAB98978 standard; protein; 551 AA.
 DE Rabbit PC12P1.
 PN WO200134797-A1.
 PD 17-MAY-2001.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 5.2%; Score 86; DB 4; Length 551;
 Best Local Similarity 26.4%; Pred. No. 62;
 RESULT 1376
 ID ADD18594 standard; protein; 601 AA.
 DE Human disease related protein Seqid25.
 PN WO2003018621-A2.
 PD 06-MAR-2003.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 Query Match 5.2%; Score 86; DB 7; Length 601;
 Best Local Similarity 22.0%; Pred. No. 69;
 RESULT 1377
 ID AAY05477 standard; protein; 750 AA.
 DE C. albicans Rbt1 protein sequence.
 PN WO9918115-A1.
 PD 15-APR-1999.
 PA (REGC) UNIV CALIFORNIA.
 Query Match 5.2%; Score 86; DB 2; Length 750;
 Best Local Similarity 23.4%; Pred. No. 94;
 RESULT 1378
 ID AAB19499 standard; protein; 905 AA.
 DE Amino acid sequence of the R591 form of the human EAA3 receptor.
 PN US6136544-A.
 PD 24-OCT-2000.
 PA (ALIX) ALLELIX BIOPHARMACEUTICALS INC.
 Query Match 5.2%; Score 86; DB 4; Length 905;
 Best Local Similarity 22.4%; Pred. No. 1.2e+02;
 RESULT 1379
 ID ADB79822 standard; protein; 1080 AA.
 DE Mouse putative deubiquitinating enzyme 8, SEQ ID 62.
 PN EP1279744-A2.
 PD 29-JAN-2003.
 PA (WARN) WARNER LAMBERT CO.
 Query Match 5.2%; Score 86; DB 7; Length 1080;
 Best Local Similarity 20.2%; Pred. No. 1.6e+02;
 RESULT 1380
 ID ABG28388 standard; protein; 1086 AA.
 DE Novel human diagnostic protein #28379.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 5.2%; Score 86; DB 4; Length 1086;
 Best Local Similarity 19.8%; Pred. No. 1.6e+02;
 RESULT 1381
 ID ABG05675 standard; protein; 1190 AA.
 DE Novel human diagnostic protein #5666.

PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSE INC.
Query Match 5.2%; Score 86; DB 4; Length 1190;
Best Local Similarity 19.8%; Pred. No. 1.8e+02;
RESULT 1382
ID AAG23116 standard; protein; 193 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26303.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.2%; Score 85.5; DB 3; Length 193;
Best Local Similarity 20.9%; Pred. No. 16;
RESULT 1383
ID AAG23115 standard; protein; 199 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26302.
PN EPI033405-A2.
PD 06-SEP-2000.
Query Match 5.2%; Score 85.5; DB 3; Length 199;
Best Local Similarity 20.9%; Pred. No. 17;
RESULT 1384
ID AAB09826 standard; protein; 346 AA.
DE Endoglucanase protein sequence 6.
PN WO200024879-A1.
PD 04-MAY-2000.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 3; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1385
ID AAO15057 standard; protein; 346 AA.
DE Phycomyces nitens endoglucanase-related protein.
PN WO200242474-A1.
PD 30-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1386
ID ABB08065 standard; protein; 346 AA.
DE P. nitens CP99002 PCEI protein.
PN WO200238754-A1.
PD 16-MAY-2002.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 5; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1387
ID ADA37114 standard; protein; 346 AA.
DE Phycomyces nitens CP99002 PCEI protein SEQ ID NO: 6.
PN WO2003052105-A1.
PD 26-JUN-2003.
PA (MEIJ) MEIJI SEIKA KAISHA LTD.
Query Match 5.2%; Score 85.5; DB 6; Length 346;
Best Local Similarity 22.4%; Pred. No. 36;
RESULT 1388
ID AAR57350 standard; protein; 354 AA.
DE Human cartilage link protein.
PN WO9415627-A1.
PD 21-JUL-1994.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 2; Length 354;
Best Local Similarity 26.2%; Pred. No. 37;
RESULT 1389
ID ABB93134 standard; protein; 649 AA.
DE Herbicidally active polypeptide SEQ ID NO 2345.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 5; Length 649;
Best Local Similarity 23.4%; Pred. No. 86;
RESULT 1390
ID ABB78250 standard; protein; 652 AA.
DE Amino acid sequence of a human heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 652;
Best Local Similarity 22.4%; Pred. No. 87;
RESULT 1391
ID ABU15839 standard; protein; 686 AA.
DE Protein encoded by Prokaryotic essential gene #1366.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.2%; Score 85.5; DB 6; Length 686;
Best Local Similarity 24.2%; Pred. No. 93;
RESULT 1392
ID ADN47243 standard; protein; 695 AA.
DE Thermococcus kodakaraensis KOD1 protein sequence SeqID1121.
PN WO2004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.2%; Score 85.5; DB 8; Length 695;
Best Local Similarity 20.6%; Pred. No. 94;
RESULT 1393
ID ADD47689 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13385.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1394
ID ADD47692 standard; protein; 780 AA.
DE Human Protein XP_027074, SEQ ID NO 13388.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.2%; Score 85.5; DB 7; Length 780;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1395
ID AAB07743 standard; protein; 781 AA.
DE A snake venom protease (SVPH-4) polypeptide variant SVPH-4b.
PN WO200043525-A2.
PD 27-JUL-2000.
PA (IMMV) IMMUNEX CORP.
Query Match 5.2%; Score 85.5; DB 3; Length 781;
Best Local Similarity 17.9%; Pred. No. 1.1e+02;
RESULT 1396
ID ADE71292 standard; protein; 781 AA.
DE Novel human protein #46.
PN JP2002345493-A.
PD 03-DEC-2002.
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.
Query Match 5.2%; Score 85.5; DB 7; Length 781;
Best Local Similarity 23.2%; Pred. No. 1.1e+02;
RESULT 1397
ID ABB78248 standard; protein; 841 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 841;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1398
ID ABB71012 standard; protein; 843 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 19828.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.2%; Score 85.5; DB 4; Length 843;
Best Local Similarity 22.5%; Pred. No. 1.2e+02;
RESULT 1399
ID ABB78249 standard; protein; 977 AA.
DE Amino acid sequence of a zebrafish heart of glass polypeptide.
PN WO200262205-A2.
PD 15-AUG-2002.

PA (GEHO) GEN HOSPITAL CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 977;
Best Local Similarity 22.4%; Pred. No. 1.5e+02;
RESULT 1400
ID ABUS4710 standard; protein; 1784 AA.
DE Human CA125 protein amino terminal sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 1784;
Best Local Similarity 27.2%; Pred. No. 3.4e+02;
RESULT 1401
ID ABUS4858 standard; protein; 1794 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 1794;
Best Local Similarity 27.2%; Pred. No. 3.5e+02;
RESULT 1402
ID ABUS4707 standard; protein; 1821 AA.
DE Human CA125 amino terminal domain.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 1821;
Best Local Similarity 27.2%; Pred. No. 3.5e+02;
RESULT 1403
ID ADE40509 standard; protein; 2055 AA.
DE Human nuclear receptor coactivator ARAP3.
PN DE10135787-A1.
PD 13-FEB-2003.
PA (JENP) JENAPHARM GMBH & CO KG.
Query Match 5.2%; Score 85.5; DB 8; Length 2055;
Best Local Similarity 20.5%; Pred. No. 4.2e+02;
RESULT 1404
ID ABG95034 standard; protein; 2311 AA.
DE Human translocation (4; 11)(q21; q23) protein #1.
PN WO200265900-A2.
PD 12-SEP-2003.
PA (CONF-) CONFORMA THERAPEUTICS CORP.
Query Match 5.2%; Score 85.5; DB 5; Length 2311;
Best Local Similarity 24.3%; Pred. No. 4.9e+02;
RESULT 1405
ID ABG31317 standard; protein; 2586 AA.
DE Human S-3 Corrected OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 5; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1406
ID ABG32891 standard; protein; 2586 AA.
DE Human osteoclast protein (OCP) #1.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.2%; Score 85.5; DB 5; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1407
ID ADL02231 standard; protein; 2586 AA.
DE Human OCP protein #1.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1408
ID ADL02234 standard; protein; 2586 AA.

DE Human OCP protein #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2586;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1409
ID AAB47935 standard; protein; 2587 AA.
DE Human OCP.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.2%; Score 85.5; DB 5; Length 2587;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1410
ID ABG32896 standard; protein; 2587 AA.
DE Human osteoclast protein (OCP) #2.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Query Match 5.2%; Score 85.5; DB 5; Length 2587;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1411
ID ADL02236 standard; protein; 2587 AA.
DE Human OCP protein #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2587;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1412
ID ABG31323 standard; protein; 2589 AA.
DE Human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 5; Length 2589;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1413
ID ADL02244 standard; protein; 2589 AA.
DE Human OCP protein #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Query Match 5.2%; Score 85.5; DB 8; Length 2589;
Best Local Similarity 25.8%; Pred. No. 5.7e+02;
RESULT 1414
ID AAE34702 standard; protein; 5877 AA.
DE Human mucin (MUC-16B).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
Query Match 5.2%; Score 85.5; DB 6; Length 5877;
Best Local Similarity 27.2%; Pred. No. 1.8e+03;
RESULT 1415
ID ABUS4721 standard; protein; 11721 AA.
DE Human CA125 full length protein sequence.
PN WO200283866-A2.
PD 24-OCT-2002.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 6; Length 11721;
Best Local Similarity 27.2%; Pred. No. 4.6e+03;
RESULT 1416
ID ADP84155 standard; protein; 22157 AA.
DE Human CA125 protein sequence SeqID 5.

PN WO2004045553-A2.
PA (UYAR-) UNIV ARKANSAS.
Query Match 5.2%; Score 85.5; DB 8; Length 22157;
Best Local Similarity 27.2%; Pred. No. 1.1e+04;
RESULT 1417
ID AAB39253 standard; protein; 280 AA.
DE Gene 15 human secreted protein homologous amino acid sequence #133.
PN WO200056754-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.1%; Score 85; DB 3; Length 280;
Best Local Similarity 23.2%; Pred. No. 30;
RESULT 1418
ID ABB71546 standard; protein; 326 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 41430.
PN WO200171042-A2.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 85; DB 4; Length 326;
Best Local Similarity 22.8%; Pred. No. 37;
RESULT 1419
ID ADQ25899 standard; protein; 472 AA.
DE B amyloidofaciens dipeptide synthesising protein SEQ ID NO: 7.
PN EP143791-A2.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match 5.1%; Score 85; DB 8; Length 472;
Best Local Similarity 20.3%; Pred. No. 62;
RESULT 1420
ID ABR53289 standard; protein; 576 AA.
DE Protein sequence #SEQ ID 1443.
PN EP1258494-A1.
PA (CELL-) CELLZOME AG.
Query Match 5.1%; Score 85; DB 6; Length 576;
Best Local Similarity 21.0%; Pred. No. 81;
RESULT 1421
ID ADK63572 standard; protein; 576 AA.
DE Disease treating protein complex-derived protein #867.
PN EP1338608-A2.
PA (CELL-) CELLZOME AG.
Query Match 5.1%; Score 85; DB 7; Length 576;
Best Local Similarity 21.0%; Pred. No. 81;
RESULT 1422
ID ABB55236 standard; protein; 627 AA.
DE Lactococcus lactis protein yffc.
PN FR2807446-A1.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.1%; Score 85; DB 5; Length 627;
Best Local Similarity 21.5%; Pred. No. 91;
RESULT 1423
ID ADS29466 standard; protein; 627 AA.
DE Bacterial polypeptide #18499.
PN US2003233675-A1.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 85; DB 8; Length 627;
Best Local Similarity 21.5%; Pred. No. 91;
RESULT 1424
ID ADA55053 standard; protein; 637 AA.
DE Human protein, SEQ ID 2621.
PN EP1293569-A2.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 85; DB 6; Length 637;

Best Local Similarity 21.7%; Pred. No. 93;
RESULT 1425
ID AAB29654 standard; protein; 667 AA.
DE Human membrane-associated protein HUMAP-11.
PN WO200065054-A2.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.1%; Score 85; DB 3; Length 667;
Best Local Similarity 21.7%; Pred. No. 1e+02;
RESULT 1426
ID ABB60387 standard; protein; 1049 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 7953.
PN WO200171042-A2.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 85; DB 4; Length 1049;
Best Local Similarity 22.1%; Pred. No. 1.9e+02;
RESULT 1427
ID AAU14240 standard; protein; 1061 AA.
DE Human novel protein #111.
PN WO200155437-A2.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 85; DB 4; Length 1061;
Best Local Similarity 20.2%; Pred. No. 1.9e+02;
RESULT 1428
ID AAU14241 standard; protein; 1091 AA.
DE Human novel protein #112.
PN WO200155437-A2.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 85; DB 4; Length 1091;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1429
ID ABB69973 standard; protein; 1354 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 36711.
PN WO200171042-A2.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 85; DB 4; Length 1354;
Best Local Similarity 19.4%; Pred. No. 2.6e+02;
RESULT 1430
ID AAE17600 standard; protein; 1438 AA.
DE Human extracellular messenger (XMES)-2 protein.
PN WO200194587-A2.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.1%; Score 85; DB 5; Length 1438;
Best Local Similarity 20.2%; Pred. No. 2.9e+02;
RESULT 1431
ID ADM47185 standard; protein; 1671 AA.
DE Neurexin III-alpha membrane-bound type I precursor like NOVX 3a protein.
PN WO2003083039-A2.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 85; DB 7; Length 1671;
Best Local Similarity 21.7%; Pred. No. 3.5e+02;
RESULT 1432
ID ADO26854 standard; protein; 196 AA.
DE Human receptors and membrane-associated protein, REMAP-44.
PN WO2004044159-A2.
PA (INCY-) INCYTE CORP.
Query Match 5.1%; Score 84.5; DB 8; Length 196;
Best Local Similarity 23.1%; Pred. No. 21;
RESULT 1433
ID AAW25156 standard; protein; 562 AA.
DE HIV-1 Rev/HTLV-1 Rex activation domain binding protein.
PN WO9706257-A1.
PA (UYDU-) UNIV DUKE.
Query Match 5.1%; Score 84.5; DB 2; Length 562;
Best Local Similarity 23.4%; Pred. No. 88;

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RESULT 1434
ID AAW63285 standard; protein; 562 AA.
DE Human h-RAB.
PN WO9846744-A1.
PD 22-OCT-1998.
PA (EUON-) IST EURO DI ONCOLOGIA SRL.
Query Match 5.1%; Score 84.5; DB 2; Length 562;
Best Local Similarity 23.4%; Pred. No. 88;
RESULT 1435
ID ADM05676 standard; protein; 569 AA.
DE Human protein of the invention SEQ ID NO:4361.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 84.5; DB 7; Length 569;
Best Local Similarity 23.4%; Pred. No. 89;
RESULT 1436
ID ADS44145 standard; protein; 658 AA.
DE Bacterial polypeptide #22575.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 84.5; DB 8; Length 658;
Best Local Similarity 19.3%; Pred. No. 1.1e+02;
RESULT 1437
ID ABB60849 standard; protein; 826 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 9339.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.1%; Score 84.5; DB 4; Length 826;
Best Local Similarity 20.9%; Pred. No. 1.5e+02;
RESULT 1438
ID AAR99638 standard; protein; 1011 AA.
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit.
PN WO9614077-A1.
PD 17-MAY-1996.
PA (TROP-) TROPHIX PHARM INC.
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.
Query Match 5.1%; Score 84.5; DB 2; Length 1011;
Best Local Similarity 20.5%; Pred. No. 2e+02;
RESULT 1439
ID AAR99639 standard; protein; 1984 AA.
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit.
PN WO9614077-A1.
PD 17-MAY-1996.
PA (TROP-) TROPHIX PHARM INC.
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.
Query Match 5.1%; Score 84.5; DB 2; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1440
ID ADE54547 standard; protein; 1984 AA.
DE Rat Protein AAB50403, SEQ ID NO 350.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.1%; Score 84.5; DB 7; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1441
ID ADE54551 standard; protein; 1984 AA.
DE Rat Protein AAB50403, SEQ ID NO 354.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.1%; Score 84.5; DB 7; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1442
ID ADE63027 standard; protein; 1984 AA.
DE Rat Protein AAB50403, SEQ ID NO 8961.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
Query Match 5.1%; Score 84.5; DB 7; Length 1984;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1443
ID AAR92317 standard; protein; 1989 AA.
DE Peripheral nervous system sodium channel peptide-1 alpha-subunit.
PN WO9614077-A1.
PD 17-MAY-1996.
PA (TROP-) TROPHIX PHARM INC.
PA (UYNY ) UNIV NEW YORK STATE RES FOUND.
Query Match 5.1%; Score 84.5; DB 2; Length 1989;
Best Local Similarity 20.5%; Pred. No. 5e+02;
RESULT 1444
ID ABB65890 standard; protein; 2015 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 24462.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Query Match 5.1%; Score 84.5; DB 4; Length 2015;
Best Local Similarity 19.0%; Pred. No. 5.1e+02;
RESULT 1445
ID ADJ66747 standard; protein; 2234 AA.
DE Human Muc16 GST fusion protein amino acid sequence SeqID20.
PN WO2004005470-A2.
PD 15-JAN-2004.
PA (IMMU-) IMMUNOGEN INC.
Query Match 5.1%; Score 84.5; DB 8; Length 2234;
Best Local Similarity 27.2%; Pred. No. 5.8e+02;
RESULT 1446
ID ABM70225 standard; protein; 2466 AA.
DE Photorhabdus luminescens protein sequence #3322.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (CNRS ) CNRS CENT NAT RECH SCI.
Query Match 5.1%; Score 84.5; DB 6; Length 2466;
Best Local Similarity 23.7%; Pred. No. 6.7e+02;
RESULT 1447
ID ABUI5838 standard; protein; 2481 AA.
DE Protein encoded by Prokaryotic essential gene #1365.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 84.5; DB 6; Length 2481;
Best Local Similarity 24.2%; Pred. No. 6.7e+02;
RESULT 1448
ID ABR62804 standard; protein; 2481 AA.
DE Methicillin resistant Staphylococcus aureus ORF SA1964-fmtB (mrp).
PN WO2003062466-A2.
PD 31-JUL-2003.
PA (UYBR-) UNIV BRISTOL.
Query Match 5.1%; Score 84.5; DB 7; Length 2481;
Best Local Similarity 24.2%; Pred. No. 6.7e+02;
RESULT 1449
ID ADR72871 standard; protein; 22152 AA.
DE Human ovarian cancer-related tumour marker CA125 protein.
PN WO200407513-A2.
PD 10-SEP-2004.
PA (MOUN ) MOUNT SINAI HOSPITAL.
Query Match 5.1%; Score 84.5; DB 8; Length 22152;
Best Local Similarity 27.2%; Pred. No. 1.4e+04;
RESULT 1450
ID AAB11729 standard; protein; 216 AA.
DE Cryptosporidium parvum Iowa isolate GP900, domain 2.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC ) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 216;
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Best Local Similarity 26.7%; Pred. No. 26;
RESULT 1451
ID AAB11734 standard; protein; 216 AA.
DE Cryptosporidium parvum NINC isolate GP900, domain 2.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 216;
Best Local Similarity 26.7%; Pred. No. 26;
RESULT 1452
ID ABJ04047 standard; protein; 216 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 8.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 5; Length 216;
Best Local Similarity 26.7%; Pred. No. 26;
RESULT 1453
ID ABB59598 standard; protein; 330 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 5586.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 84; DB 4; Length 330;
Best Local Similarity 30.8%; Pred. No. 47;
RESULT 1454
ID ADO61979 standard; protein; 335 AA.
DE Transcription factor G2571, SEQ ID 446.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MENDEL) MENDEL BIOTECHNOLOGY INC.
Query Match 5.1%; Score 84; DB 8; Length 335;
Best Local Similarity 26.4%; Pred. No. 48;
RESULT 1455
ID ADM05769 standard; protein; 420 AA.
DE Human protein of the invention SEQ ID NO:4454.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 84; DB 7; Length 420;
Best Local Similarity 19.5%; Pred. No. 66;
RESULT 1456
ID ABB67668 standard; protein; 459 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 29796.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 84; DB 4; Length 459;
Best Local Similarity 24.2%; Pred. No. 74;
RESULT 1457
ID ABB47318 standard; protein; 793 AA.
DE Listeria monocytogenes protein #22.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 5.1%; Score 84; DB 5; Length 793;
Best Local Similarity 22.4%; Pred. No. 1.6e+02;
RESULT 1458
ID ABU32765 standard; protein; 793 AA.
DE Protein encoded by Prokaryotic essential gene #18292.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.1%; Score 84; DB 6; Length 793;
Best Local Similarity 22.4%; Pred. No. 1.6e+02;
RESULT 1459
ID AAB41835 standard; protein; 833 AA.
DE Human ORFX ORF1599 polypeptide sequence SEQ ID NO:3198.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 84; DB 3; Length 833;
Best Local Similarity 20.0%; Pred. No. 1.7e+02;
RESULT 1460
ID ADH71762 standard; protein; 834 AA.
DE Human protein of the invention NOV28k SEQ ID NO:658.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 84; DB 8; Length 834;
Best Local Similarity 23.3%; Pred. No. 1.7e+02;
RESULT 1461
ID ADC30924 standard; protein; 845 AA.
DE Human novel polypeptide sequence, SEQ ID NO:1006.
PN WO2003029271-A2.
PD 10-APR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.1%; Score 84; DB 7; Length 845;
Best Local Similarity 19.5%; Pred. No. 1.7e+02;
RESULT 1462
ID AAU91290 standard; protein; 905 AA.
DE Human NOV51 protein.
PN WO200216600-A2.
PD 28-FEB-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.1%; Score 84; DB 5; Length 905;
Best Local Similarity 23.2%; Pred. No. 1.9e+02;
RESULT 1463
ID AAR11993 standard; protein; 920 AA.
DE Glutamate receptor 5-1.
PN WO9106648-A.
PD 16-MAY-1991.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.1%; Score 84; DB 2; Length 920;
Best Local Similarity 22.2%; Pred. No. 1.9e+02;
RESULT 1464
ID ADO67713 standard; protein; 933 AA.
DE Novel human protein sequence #2379.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.1%; Score 84; DB 8; Length 933;
Best Local Similarity 20.2%; Pred. No. 2e+02;
RESULT 1465
ID ADI27184 standard; protein; 996 AA.
DE Mouse LRP binding family protein #20.
PN WO2003106657-A2.
PD 24-DEC-2003.
PA (STOW-) STOWERS INST MEDICAL RES.
Query Match 5.1%; Score 84; DB 8; Length 996;
Best Local Similarity 22.7%; Pred. No. 2.1e+02;
RESULT 1466
ID ADS43638 standard; protein; 1075 AA.
DE Bacterial polypeptide #22068.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.1%; Score 84; DB 8; Length 1075;
Best Local Similarity 24.2%; Pred. No. 2.4e+02;
RESULT 1467
ID ADN33134 standard; protein; 1084 AA.
DE Human transporter and ion channel (TRICH) protein SeqID19.
PN WO2004035755-A2.
PD 29-APR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.1%; Score 84; DB 8; Length 1084;
Best Local Similarity 19.4%; Pred. No. 2.4e+02;
RESULT 1468
ID ABP73029 standard; protein; 1228 AA.
DE Amino acid sequence of the GuxA polypeptide.
PN WO2003012109-A1.
PD 13-FEB-2003.

PA (MIDE) MIDWEST RES INST.
Query Match 5.1%; Score 84; DB 6; Length 1228;
Best Local Similarity 22.1%; Pred. No. 2.9e+02;
RESULT 1469
ID ADH36636 standard; protein; 1228 AA.
DE Acidothermus cellulolyticus glycoside hydrolase, GuxA.
PN US2003104522-A1.
PD 05-JUN-2003.
PA (DING/) DING S.
PA (ADNE/) ADNEY W S.
PA (VINZ/) VINZANT T B.
PA (HIMM/) HIMMEL M E.
PA (DECK/) DECKER S R.
Query Match 5.1%; Score 84; DB 8; Length 1228;
Best Local Similarity 22.1%; Pred. No. 2.9e+02;
RESULT 1470
ID ABB70925 standard; protein; 1291 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 39567.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.1%; Score 84; DB 4; Length 1291;
Best Local Similarity 19.3%; Pred. No. 3.1e+02;
RESULT 1471
ID AAB36091 standard; protein; 1362 AA.
DE Putative P. abyssi amylopullulanase.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 5.1%; Score 84; DB 4; Length 1362;
Best Local Similarity 26.5%; Pred. No. 3.3e+02;
RESULT 1472
ID AAW48299 standard; protein; 1721 AA.
DE Cryptosporidium parvum GP900 antigen.
PN WO9806430-A1.
PD 19-FEB-1998.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 2; Length 1721;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 1473
ID AAB11727 standard; protein; 1721 AA.
DE Portion of Cryptosporidium parvum NINC isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 1721;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 1474
ID ABJ04045 standard; protein; 1721 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 6.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 5; Length 1721;
Best Local Similarity 26.7%; Pred. No. 4.5e+02;
RESULT 1475
ID AAB11726 standard; protein; 1837 AA.
DE Cryptosporidium parvum Iowa isolate GP900.
PN US6071518-A.
PD 06-JUN-2000.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 3; Length 1837;
Best Local Similarity 26.7%; Pred. No. 5e+02;
RESULT 1476
ID ABJ04044 standard; protein; 1837 AA.
DE C parvum GP900 protein fragment SEQ ID NO: 5.
PN WO200194631-A1.
PD 13-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 5.1%; Score 84; DB 5; Length 1837;
Best Local Similarity 26.7%; Pred. No. 5e+02;
RESULT 1477

ID ABUS3165 standard; protein; 143 AA.
DE Human testes-derived DKFzptres3_2a11 homologue #25.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 143;
Best Local Similarity 30.7%; Pred. No. 17;
RESULT 1478
ID ABUS3163 standard; protein; 247 AA.
DE Human testes-derived DKFzptres3_2a11 homologue #23.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 247;
Best Local Similarity 30.7%; Pred. No. 35;
RESULT 1479
ID ABUS3158 standard; protein; 260 AA.
DE Human testes-derived DKFzptres3_2a11 homologue #18.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 260;
Best Local Similarity 30.7%; Pred. No. 38;
RESULT 1480
ID ADD55680 standard; protein; 352 AA.
DE Thalecress environmental stress-related protein #19.
PN US2003131386-A1.
PD 10-JUL-2003.
PA (SAMA/) SAMAHA R.
PA (HEAR/) HEARD J.
PA (JIAN/) JIANG C.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (KEDD/) KEDDIE J.
PA (RATC/) RATCLIFFE O.
PA (PIIG/) PILGRIM M.
PA (ADAM/) ADAM L.
PA (BROU/) BROUN P.
PA (ZHAN/) ZHANG J.
Query Match 5.0%; Score 83.5; DB 7; Length 352;
Best Local Similarity 19.8%; Pred. No. 57;
RESULT 1481
ID ADO01723 standard; protein; 352 AA.
DE Thalecress transcription factor protein #68.
PN US2004045049-A1.
PD 04-MAR-2004.
PA (ZHAN/) ZHANG J.
PA (FROM/) FROMM M E.
PA (HEAR/) HEARD J E.
PA (RIEC/) RIECHMANN J L.
PA (ADAM/) ADAM L J.
PA (BROU/) BROUN P E.
PA (PINE/) PINEDA O.
PA (REUB/) REUBER T L.
PA (KEDD/) KEDDIE J S.
PA (YUGG/) YU G.
PA (JIAN/) JIANG C.
PA (SAMA/) SAMAHA R S.
PA (PIIG/) PILGRIM M L.
PA (CREE/) CREELMAN R A.
PA (DUBE/) DUBELL A N.
PA (RATC/) RATCLIFFE O.
PA (KUMI/) KUMIMOTO R.
PA (SHER/) SHERMAN B K.
Query Match 5.0%; Score 83.5; DB 8; Length 352;
Best Local Similarity 19.8%; Pred. No. 57;
RESULT 1482
ID ABUS3157 standard; protein; 368 AA.
DE Human testes-derived DKFzptres3_2a11 homologue #17.
PN WO200112659-A2.
PD 22-FEB-2001.

PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 368;
Best Local Similarity 30.7%; Pred. No. 61;
RESULT 1483
ID ABUS3156 standard; protein; 385 AA.
DE Human testes-derived DKFZphtes3_2all homologue #16.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 385;
Best Local Similarity 30.7%; Pred. No. 65;
RESULT 1484
ID ABUS3159 standard; protein; 386 AA.
DE Human testes-derived DKFZphtes3_2all homologue #19.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 386;
Best Local Similarity 30.7%; Pred. No. 65;
RESULT 1485
ID ABUS3161 standard; protein; 387 AA.
DE Human testes-derived DKFZphtes3_2all homologue #21.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 387;
Best Local Similarity 30.7%; Pred. No. 65;
RESULT 1486
ID AAM50241 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase.
PN US6297055-B1.
PD 02-OCT-2001.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.0%; Score 83.5; DB 4; Length 393;
Best Local Similarity 26.5%; Pred. No. 67;
RESULT 1487
ID AAU76423 standard; protein; 393 AA.
DE Wheat tyrosine decarboxylase clone wri.pk0059.g9.
PN US2002009801-A1.
PD 24-JAN-2002.
PA (FALC) FALCO S C.
PA (FAMO) FAMODU O O.
PA (OROZ) OROZCO E R.
Query Match 5.0%; Score 83.5; DB 5; Length 393;
Best Local Similarity 26.5%; Pred. No. 67;
RESULT 1488
ID ABUS3160 standard; protein; 395 AA.
DE Human testes-derived DKFZphtes3_2all homologue #20.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 395;
Best Local Similarity 30.7%; Pred. No. 67;
RESULT 1489
ID ABB69710 standard; protein; 399 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 35922.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.0%; Score 83.5; DB 4; Length 399;
Best Local Similarity 26.2%; Pred. No. 68;
RESULT 1490
ID ADA19428 standard; protein; 498 AA.
DE Mouse CD30 amino acid sequence.
PN WO2003066674-A2.
PD 14-AUG-2003.
PA (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
Query Match 5.0%; Score 83.5; DB 6; Length 498;
Best Local Similarity 20.5%; Pred. No. 92;
RESULT 1491
ID ABB10349 standard; protein; 553 AA.
DE Human cDNA SEQ ID NO: 657.
PN WO200154474-A2.

PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.0%; Score 83.5; DB 4; Length 553;
Best Local Similarity 22.9%; Pred. No. 1.1e+02;
RESULT 1492
ID ABP66936 standard; protein; 553 AA.
DE Human polypeptide SEQ ID NO 657.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 5.0%; Score 83.5; DB 5; Length 553;
Best Local Similarity 22.9%; Pred. No. 1.1e+02;
RESULT 1493
ID AAM12713 standard; protein; 562 AA.
DE hRIP, a protein critical for HIV replication.
PN WO9701648-A1.
PD 16-JAN-1997.
PA (UYNA-) UNIV MASSACHUSETTS MEDICAL CENT.
Query Match 5.0%; Score 83.5; DB 2; Length 562;
Best Local Similarity 23.4%; Pred. No. 1.1e+02;
RESULT 1494
ID ADO00991 standard; protein; 562 AA.
DE Human homologue of Fruit fly AD-related protein CG3365.
PN US2004067535-A1.
PD 08-APR-2004.
PA (LIFE-) LIFE SCI DEV CORP.
Query Match 5.0%; Score 83.5; DB 8; Length 562;
Best Local Similarity 23.4%; Pred. No. 1.1e+02;
RESULT 1495
ID ADP55222 standard; protein; 562 AA.
DE Human PRO protein sequence SEQ ID NO:1198.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 5.0%; Score 83.5; DB 8; Length 562;
Best Local Similarity 23.4%; Pred. No. 1.1e+02;
RESULT 1496
ID ADP04689 standard; protein; 643 AA.
DE Sea squirt protein with tissue specific expression in development Seq284.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 5.0%; Score 83.5; DB 8; Length 643;
Best Local Similarity 21.9%; Pred. No. 1.3e+02;
RESULT 1497
ID AAU33234 standard; protein; 644 AA.
DE Novel human secreted protein #3725.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.0%; Score 83.5; DB 4; Length 644;
Best Local Similarity 23.4%; Pred. No. 1.3e+02;
RESULT 1498
ID ABUS3144 standard; protein; 717 AA.
DE Human testes-derived DKFZphtes3_2all homologue #4.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 5.0%; Score 83.5; DB 4; Length 717;
Best Local Similarity 30.7%; Pred. No. 1.5e+02;
RESULT 1499
ID AAR77024 standard; protein; 879 AA.
DE Canine herpesvirus gb homologue.
PN WO9526751-A1.
PD 12-OCT-1995.
PA (VIRO-) VIROGENETICS CORP.
Query Match 5.0%; Score 83.5; DB 2; Length 879;
Best Local Similarity 30.9%; Pred. No. 2e+02;
RESULT 1500
ID AAO16418 standard; protein; 2759 AA.
DE Human nucleic acid-associated protein (NAAP) - SEQ ID NO 15.

PN WO2003000864-A2.
PD 03-JAN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.0%; Score 83.5; DB 6; Length 2759;
Best Local Similarity 20.2%; Pred. No. 9.7e+02;